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Alu and B1 Repeats Have Been Selectively Retained in the Upstream and Intronic Regions of Genes of Specific Functional Classes

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ABSTRACT

ALU and B1 repeats are mobile elements that originated in an initial duplication of the 7SL RNA gene prior to the primate-rodent split about 80 million years ago and currently account for a substantial fraction of the human and mouse genome respectively. Following the primate-rodent split, ALU and B1 elements spread independently in each of the two genomes in a seemingly random manner, and, according to the prevailing hypothesis, negative selection shaped their final distribution in each genome by forcing the selective loss of certain ALU and B1 copies. In this paper, contrary to the prevailing hypothesis, we present evidence that ALU and B1 elements have been selectively retained in the upstream and intronic regions of genes belonging to specific functional classes, while at the same time we found no evidence for selective loss of these elements in any functional class. A subset of the functional links we discovered corresponds to functions where ALU involvement has actually been experimentally validated, whereas the majority of the functional links we report are novel. Finally, the unexpected finding that ALU and B1 elements show similar biases in their distribution across functional classes despite having spread independently in their respective genomes, further supports our claim that the extant instances of ALU and B1 elements are the result of positive selection.

INTRODUCTION

Identifiable repeat elements cover a very large fraction of the human and mouse genomes, and even though they are quite diverse at the sequence level, they can be assigned to a fairly small number of families (Deininger and Batzer 2002). ALU and B elements belong to the Short Interspersed Nuclear Element (SINE) family, members of which exist in several mammalian genomes, where they have spread in great copy numbers (Batzer and Deininger 2002; Kazazian 2004; Schmid 2003). One member-class of the SINE family, the ALU class, is the most abundant in the human genome among all types of mobile elements. ALU elements (ALUs) originated in the duplication and subsequent fusion of the 7SL RNA gene at the beginning of the radiation of primates (Kriegs, Churakov, Jurka, Brosius and Schmitz 2007; Quentin 1992). B1 elements (B1s) belong to the same repeat family and have also descended from the 7SL RNA. Following the primate-rodent split, copies of ALUs and B1s have amplified and duplicated *independently* in the two genomes while accumulating mutations. The extent of the acquired mutations is such that extant instances of archetypal ALUs and B1s bear little resemblance to one another or to the original 7SL RNA gene.

In earlier work, the ALU distribution in the human genome was studied in terms of several genomic features in order to understand how they spread in the genome: it was shown that ALU elements are predominant in R bands and inversely distributed with respect to L1 elements (Korenberg and Rykowski 1988), correlated with GC-rich parts of the genome (Belle, Webster and Eyre-Walker 2005; Grover, Mukerji, Bhatnagar, Kannan and Brahmachari 2004), gene and intron density (Grover, Mukerji, Bhatnagar, Kannan and Brahmachari 2004; Hackenberg, Bernaola-Galván, Carpena and Oliver 2005; Medstrand, van de Lagemaat and Mager 2002), enriched in isochores (Hackenberg, Bernaola-Galván, Carpena and Oliver 2005), segmental duplications (Jurka, Kohany, Pavlicek, Kapitonov and Jurka 2004) and transcription factor binding sites (Polak and Domany 2006). Another study of ALUs, B1s and related SINEs across mammalian genomes demonstrated their presence in primates, rodents, and tree-shrews and their absence in other mammals (Vassetzky, Ten and Kramerov 2003). There have also been attempts to associate ALU elements with functional classes of genes. In (Grover, Majumder, Rao, Brahmachari and Mukerji 2003), ALUs located on chromosomes 21 and 22, were found to be over-represented in a limited set of functional classes. Housekeeping genes vs. tissue-specific genes were also found to have preferences for ALUs (Ganapathi, Srivastava, Sutar, Kumar, Dasgupta, Pal Singh, Brahmachari and Brahmachari 2005). In (Polak and Domany 2006), the authors considered for their analysis only 5kb upstream of known genes, and a limited set of functional classes for over-representation or under-representation of ALUs.

In what follows, we extend previous work by studying and comparing the distributions of extant instances of both ALUs and B1s (as well as related B2 and B4 elements[1]) in both *upstream and intronic regions* of known protein-coding genes in order to contribute to the understanding of their *evolutionary history*. More specifically, we test whether their current distributions in the human and mouse genomes are a result of positive or negative selection across functional classes of genes.

RESULTS

ALU and B element densities vary as a function of their upstream/downstream distance from gene transcript start positions

Following the primate-rodent split, ALU and B elements spread throughout the human and mouse genomes: ALU elements currently number ~1.1 million copies and cover about 5.4% of the human genome (in the sense orientation), while B elements number ~1.2 million copies and cover about 3.6% of the mouse genome (in the sense orientation).

We studied ALU and B element densities separately for all combinations of: (a) *distance* from gene transcript start positions, (b) *direction* (upstream vs. downstream), and (c) *orientation* (sense vs. antisense). In the case of downstream direction, we computed ALU and B element densities separately for intronic and exonic regions. For a detailed description of the computation method and all relevant definitions, see Methods section. Our results demonstrate that ALU and B elements are significantly over-represented[2] in the *upstream* regions of genes, and that the highest densities are observed within the window ending at 16kb upstream of gene transcript start positions. Similarly, ALU and B elements are significantly over-represented in the *intronic downstream* regions of genes, and, just as in the upstream case, the highest densities are observed in the window ending at 16kb downstream of the gene transcript start positions. However, in introns, the over-representation is significantly more pronounced in the antisense orientation. Finally, there is a significant under-representation of ALU and B elements in *exons* but the effect of distance is not as pronounced as in the upstream and intronic downstream cases.

These results are shown in detail in Figure 1 for ALU elements in human and in Figure 2 for B elements in mouse: we plot ALU and B element densities upstream and downstream of known genes as a function of distance from the gene transcript start positions. Green and red curves correspond to ALU and

[1] From this point on, we will be referring to B1, B2 and B4 elements collectively as "B elements".

[2] For a detailed explanation of how we determine *significance* and how we compute *p-values* for all cases of over-representation and under-representation, see Methods.

B densities in the sense and antisense orientation respectively. In the downstream case, we distinguish between exonic and intronic regions.

Human ALU elements have been selectively retained in upstream and intronic regions of genes of specific functional classes

We first associated ALU elements to functional classes by performing a genome-wide analysis on the latest release of the human genome annotations and applying a *distribution-free statistical test* with *multiple hypothesis testing correction*. Unlike (Polak and Domany 2006), where only 5kb upstream of known genes were considered, we considered the 0kb-16kb window for the upstream analysis, i.e. the window where we find that the ALU density is maximized (see above). In addition, we: (a) examined the possibility that *intronic* instances might also be linked to specific functional classes, and (b) treated sense and antisense orientations seperately. As a result, we were able to associate with ALUs at least four times more functional classes than we would have been able to, had we only considered 5kb upstream regions. Finally, after determining the functional associations, we conducted *additional experiments* to pinpoint the most likely explanation for the observed functional biases.

We applied the following statistical test in order to determine potential biases in the positioning of ALU elements within upstream and intronic regions of genes belonging to specific functional classes. After labeling each gene's upstream or intronic region with the GO terms attributed to the corresponding spliced transcripts, we tested whether ALU densities are *significantly higher* in the upstream or intronic regions of genes associated with certain GO terms. *Density* is defined as the fraction of the upstream or intronic region of a given gene that is covered by ALU instances. For a more formal definition of density and a detailed description of the statistical method used here we refer the reader to the Methods section.

Using this approach we found that upstream and intronic ALU instances are not randomly distributed, but instead are located, significantly more frequently than expected, inside upstream and intronic regions (in either the sense or antisense direction) of genes belonging to specific sets of functions. These functional classes are listed in Table 1, and in the Supplement, we report the p-values for each of the terms shown in Table 1.

In order to validate our computational results, we looked in the existing literature for *experimental evidence* linking ALUs to specific functions and compared these ALU-linked functions to the GO terms listed in Table 1. ALUs have been implicated in alternative splicing, RNA editing and translation regulation (Hasler and Strub 2006; Vidal, Mougneau, Glaichenhaus, Vaigot, Darmon and Cuzin 1993), shown to repress transcription following heat shock (Mariner, Walters, Espinoza, Drullinger, Wagner,

Kugel and Goodrich 2008), and also shown to affect genomic organization and evolution, through insertion mutation and recombination (Batzer and Deininger 2002; Deininger, Moran, Batzer and Kazazian 2003). For most of these functions, we were able to find related GO terms in Table 1: RNA splicing, translation, chromatin remodeling, and DNA recombination. In Figure 3, we verify that for these GO terms, the ALU densities of associated genes in upstream and intronic regions are significantly higher than we would expect in a randomly chosen set of genes. Interestingly, most of functional classes reported in Table 1 have not been linked to ALUs, suggesting potential novel regulatory roles for these elements.

In search for the most likely interpretation of the functional biases of ALU instances in upstream and intronic regions reported in Table 1, we explored three alternative scenarios, and conducted further computational experiments in order to prove or disprove them. One possible explanation for our findings could be that ALU elements were *selectively retained* through natural selection in the genes of these functional classes, because they play a positive role in the function of these genes and offer a selective advantage. If these insertions had had a neutral effect, no functional biases would have been observed in our analysis. If, on the other hand, they had had a negative effect, they would have been selected against during evolution, especially when we consider that insertions in upstream regions of genes, where regulatory signals are located, could easily disrupt normal function. Not surprisingly, an obvious case of negative selection is found in the *exonic* regions where not only ALUs are under-represented (see Figure 1), but also no functional biases are observed, in other words, the negative selection of ALUs in exonic regions is active across all functional classes.

A second possible explanation could be that genes in these functional classes tend to tolerate mobile element insertions better than the rest of the genes. To corroborate or refute this hypothesis, we tested whether other types of mobile repeat elements are enriched in these functional classes and, in general, *found no such bias* except in the antisense intronic case, where LINE elements are over-represented in a small subset of the functional classes associated with antisense intronic ALU instances (only 25 out of 94). Moreover, none of these common classes is related to recombination, chromatin remodeling, splicing or translation. In the rest of the cases no other type of mobile repeat elements is over-represented in ALU-associated functional classes.

A third alternative explanation could be that certain ALU instances were selectively lost after the initial random spreading, and, in fact, this scenario corresponds to the prevailing hypothesis. However, when we tested whether ALU elements are under-represented in the upstream or intronic regions of genes of specific functional classes, we *found no such bias*. This suggests that ALU instances have been *lost randomly* across functional classes.

Based on the above analysis, we conclude that there has been a positive selection of ALUs in the upstream and intronic regions of the genes that belong to the functional classes reported in Table 1. This finding suggests that ALUs likely play an active role in the entire set of functions listed in Table 1, and not only in the small subset which has already been reported in the literature.

Mouse B1 elements have *independently* been retained in the upstream and intronic regions of genes of similar functional classes to human ALUs

B1 and ALU repeat families both descended from an initial duplication of the 7SL RNA gene (Batzer and Deininger 2002) before the primate-rodent split, i.e. more that 80 million years ago. However, after the primate-rodent split, ALU and B elements spread *independently*, accumulated mutations and, over time, substantially diverged from the 7SL RNA sequence from which they originated (Batzer and Deininger 2002). Consequently, extant B1 elements should be very different from ALU elements at the sequence level. We confirmed the lack of sequence similarity between ALU and B1 elements in two ways. First, in Figure 4, we show that the average pair-wise similarity among ALU elements is 71.5±11.1%, whereas the expected similarity is 45.3±4.4% as determined using shuffled versions of the ALU sequences. The average pair-wise similarity for B1 elements is 70.1±10.8%, whereas the expected similarity is 45.1±2.5%. In contrast, the average pair-wise similarity between extant ALU monomers and B1s is only 51.1±4.7% and very close to the expected similarity value of 44.2±2.7%. Second, using human/mouse whole-genome alignments we found that ALUs and B1s are located overwhelmingly in non-conserved regions of the human and mouse genomes: the figures are ~99.9% in the case of ALUs and ~96.4% in the case of B elements (~95.8% for B1s, ~96.9% for B2s and ~96.5% for B4s).

Next, we applied the same statistical analysis used in the previous section, in order to look for enrichment of B elements in specific functional classes of genes. Given that, as shown abose, B elements are so *different* from ALU elements at the sequence level, and that the current distribution of ALU and B elements has been shaped *independently* in the each of the two genomes through initial random spreading and subsequent loss of certain copies, one would expect that the functional associations of B elements in upstream and intronic regions of genes would be different from the ones described in the previous section. However, we find that the set of functions associated with B elements contains 83.2% (expected = 12.2±2.0%) of the functions associated with ALUs. The fact that this result is observed independently in the mouse genome further strengthens our claim that these two types of SINE elements have been *selectively retained* in genes of certain functional classes, rather than selectively lost from certain genes.

Nevertheless, we examined an alternative scenario: since ALU and B elements lie in non-conserved regions of human and mouse, we tested whether certain functional classes of genes tend to have non-conserved upstream and intronic regions (effectively defining the differences between these two organisms), and whether these functional classes overlap with those associated with ALU and B elements. We found that the overlap between the set of GO terms associated with non-conserved regions and the set of GO terms associated with ALU elements is only *five* in the combined sense/antisense intronic regions, and *zero* in the combined sense/antisense upstream regions. The common GO terms in the intronic case are general high-level terms (e.g metabolism, binding, etc.), and do not include recombination, chromatin remodeling, splicing or translation. Therefore, we conclude that lack of conservation of ALU and B elements does not explain the observed functional biases.

Functional biases of Alu and B element instances entend to all ALU and B element sub-families

Human ALUs belong to one of three main sub-families AluS, AluJ and AluY, with approximately 660,000, 283,000 and 148,000 copies respectively in the human genome. We repeated the above GO term analysis separately for each ALU sub-family and found that all three ALU sub-families are significantly over-represented in the upstream and intronic regions of genes of certain functional classes. Using the same cutoff on the adjusted p-values, we obtained 244 significant GO terms for the AluS sub-family, 200 for the AluJ sub-family and 116 for the AluY sub-family. The relationships of these three sets to one another are depicted in the form of a Venn diagram in Figure 5. A qualitative interpretation of the Venn diagram is that the AluS GO term set is an approximate superset of the AluJ set (86.0% of the AluJ set members are also members of the AluS set; expected overlap is 7.7±1.6%), which in turn is an approximate superset of the AluY set (93.1% of the AluY set members are also members of the AluJ set; expected overlap is 6.6±2.3%). The AluY set is 100% covered by the AluS set. The computed p-values for all sub-families, for both upstream and intronic regions, and for both sense and antisense orientations can be found in the Supplement.

Similarly, in the mouse genome there are B1, B2 and B4 elements with approximately 417,000, 363,000 and 390,000 copies respectively. Using the same method and cutoff, we found 293, 260 and 232 significant GO terms for B1, B2 and B4 elements respectively. Unlike ALU sub-families, where the number of significant GO terms depends on the age of the sub-family, here all three types of elements have comparable numbers of significant GO terms associated with them. Also, pair-wise intersection of these lists of GO terms show high similarities, measured using the Jaccard coefficient between each pair of sets: 65.6% between B1 and B2 (expected similarity = 4.6±0.8%), 54.0% between B1 and B4

(expected similarity = 4.4±0.9%), and 56.2% between B2 and B4% (expected similarity = 4.0±0.9%). The computed p-values for B1, B2 and B4 elements, for both upstream and intronic regions, and for both sense and antisense orientations can be found in the Supplement.

DISCUSSION

Our analyses reveal that *both upstream and intronic regions* in human and mouse are significantly enriched in ALU and B elements respectively. Surprisingly, we find that ALU and B elements are significantly enriched across similar functional classes in human and mouse, even though these two types of elements have spread independently in the two genomes, following the primate-rodent split. In contrast, we find no depletion across functional classes, a finding which suggests that the final distribution of ALU and B elements across the two genomes is unlikely to be the result of a selective loss of some of their randomly retrotransposed copies. A simpler explanation suggests that they have been *selectively retained* in the upstream and intronic regions of genes belonging to the functional classes presented in Table 1, because they offered some selective advantage thus increasing each organism's chances of survival. Indeed, a subset of the functional associations we uncovered in this paper has been reported in the literature, thus supporting the merit of our computational approach, while the rest of the functions suggest possible avenues to specific experimental tests.

Most importantly, our analysis suggests that SINEs are *implicated in gene regulation* effected through the upstream and intronic regions of specific genes, and contributes to an increasing body of literature attributing functional relevance to repeat elements which were initially 'dismissed' and labeled "junk DNA" (Ohno 1972). Indeed, soon after the advent of genomic sequencing, reports of mobile elements that were exapted into novel genes and regulatory elements through retrotransposion (Brosius 1999; Hamdi, Nishio, Tavis, Zielinski and Dugaiczyk 2000; Nekrutenko and Li 2001) or exonization (Lin, Shen, Tye, Cai, Jiang, Davidson and Xing 2008) started appearing in the literature. Individual instances of various types of repeat elements were shown to cause disease but to also drive genomic evolution in a positive manner (Batzer and Deininger 2002; Deininger, Moran, Batzer and Kazazian 2003). Recent reports also discuss findings suggesting that the role of mobile elements in genomic evolution, organization and cell process regulation may be significantly more important than previously thought (Berry, Hannenhalli, Leipzig and Bushman 2006; Czech, Malone, Zhou, Stark, Schlingeheyde, Dus, Perrimon, Kellis, Wohlschlegel, Sachidanandam et al. 2008; Lowe, Bejerano and Haussler 2007; Tay, Zhang, Thomson, Lim and Rigoutsos 2008; Watanabe, Totoki, Toyoda, Kaneda, Kuramochi-Miyagawa, Obata, Chiba, Kohara, Kono, Nakano et al. 2008).

Interestingly, ALU and B elements are not conserved between human and mouse. For nearly three decades, most searches for regulatory elements made explicit or implicit use of the assumption of equivalence between sequence conservation and function. However, recent work has shown that the human genome regions can be classified into three broad categories with respect to the extent of their evolutionary conservation and their coding potential: (a) sequences that are under *strong evolutionary constraints* (~5% of the human genome (Margulies, Cooper, Asimenos, Thomas, Dewey, Siepel, Birney, Keefe, Schwartz, Hou et al. 2007; Siepel, Bejerano, Pedersen, Hinrichs, Hou, Rosenbloom, Clawson, Spieth, Hillier, Richards et al. 2005)); (b) *conserved non-exonic sequences* that are more frequent than expected (Dermitzakis, Reymond and Antonarakis 2005) but do not necessarily comprise functional elements (Nobrega, Zhu, Plajzer-Frick, Afzal and Rubin 2004); and (c) *non-conserved, non-exonic sequences*, a category with an unexpected high number of functional elements (ENCODE 2007). Such findings increasingly question whether sequence conservation is a necessary and sufficient condition for function. Indeed, recent publications have revealed the existence of *regulatory elements* that are not conserved between human and mouse (Fisher, Grice, Vinton, Bessling and McCallion 2006; Lal, Kim, Abdelmohsen, Kuwano, Pullmann, Srikantan, Subrahmanyam, Martindale, Yang, Ahmed et al. 2008; McGaughey, Vinton, Huynh, Al-Saif, Beer and McCallion 2008; Rigoutsos, Huynh, Miranda, Tsirigos, McHardy and Platt 2006; Tay, Zhang, Thomson, Lim and Rigoutsos 2008; Tay, Tam, Ang, Gaughwin, Yang, Wang, Liu, George, Ng, Perera et al. 2008; Tsirigos and Rigoutsos 2008).

In closing, it is worth emphasizing that in our analysis *antisense intronic regions* are significantly more enriched in ALU and B elements than sense intronic regions, unlike in the upstream case, where no significant difference is observed between sense and antisense. In view of this finding, and taking into account previous work showing evidence of widespread occurrence of antisense transcription in introns (Shendure and Church 2002; Yelin, Dahary, Sorek, Levanon, Goldstein, Shoshan, Diber, Biton, Tamir, Khosravi et al. 2003) as well as correlation of non-coding antisense intronic RNA levels with tumor differentiation (Reis, Nakaya, Louro, Canavez, Flatschart, Almeida, Egidio, Paquola, Machado, Festa et al. 2004), it is reasonable to conjecture that antisense intronic sequences may play an important role in regulation. Conceivably, this conjectured activity may be coordinated with instances of ALU and B elements located upstream of protein-coding genes. Taken together, these findings hint at the existence of a potentially very complex web of interactions among upstream regions, introns, and repeat elements in the context of cell process regulation.

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METHODS

Data sources

We obtained genome chromosome sequences and genomic region coordinates for transcripts, exons, introns as well as Gene Ontology (GO) annotations (biological processes and molecular functions) from ENSEMBL release 52. Human/mouse pairwise alignments and repeat regions corresponding to the same genome assembly versions (NCBI36 for human and NCBIM37 for mouse) were obtained from UCSC Genome Browser.

Computing densities and associated p-values

We define *density* of a given type of elements (for example ALU or B elements) in a given genomic region as the fraction of the region that is covered by the instances of these elements. We calculated the densities of ALU and B elements in *genomic regions* obtained from all combinations of: (a) *distance* from gene transcript start positions (1, 2, 4, 8, 16, 32, 64, 128, 256 and 512kb), (b) *direction* (upstream and downstream), and (c) *orientation* (sense and antisense). Each genomic region was identified as follows:

(1) for each gene transcript with transcript start position *s*, we identified its upstream (downstream) region at distance *d* as the region covering *d* nucleotides upstream (downstream) of position *s*

(2) for each gene transcript, we identified its downstream exonic region at distance *d* as the intersection of its downstream region at distance *d* and its set of exons

(3) for each gene transcript, we identified its downstream intronic region at distance *d* as the intersection of its downstream region at distance *d* and its set of introns

(4) the final genomic region was determined as the union of all the corresponding gene transcript regions; for example, the upstream region, is the union of the upstream regions of all gene transcripts.

The *expected* ALU and B element densities were calculated on the entire human and mouse genome respectively. All density calculations were performed using *resampling* and the results are shown as mean and standard deviation on Figure 1 for human and Figure 2 for mouse. P-values were computed in each case using Student's T test between the observed and expected, or between sense and antisense in the intronic downstream case. For a wide range of distances (i.e. 4kb-256kb), both upstream and downstream, the p-values are practically zero.

Identifying significant GO terms and computing adjusted p-values

For each gene, we identified: (a) its *upstream region* as the union of the upstream regions of all of its transcripts (b) its *intronic region* as the union of the introns of all of its transcripts, (c) its associated GO term set as the union of the GO term sets associated with its transcripts, and (d) the densities of ALU and B elements in the gene's upstream and intronic regions (separately for sense and antisense orientation). Then, each GO term *x* was tested for significance by *comparing two distributions* of ALU/B densities in upstream and intronic regions: the distribution of densities of the genes that have term *x* on their list versus the distribution of densities of the genes that do not have *x*. Using *random permutations*, we calculated the *adjusted p-values* for each GO term, thus accounting for multiple hypothesis testing. We consider significant those GO terms whose *adjusted p-value* is less than 0.01. The *unadjusted p-values* reported in the Supplement are calculated using a *t*-test approximation, since in the case of very low p-values, the number of required permutations would be computationally infeasible. However, both methods yield the same results in terms of adjusted p-values, demonstrating that the underlying distributional assumption of the t-test is valid. In any case, the results shown in Table 1, are obtained using the random permutation method, and *do not depend on any distributional assumption*.

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FIGURE LEGENDS

Figure 1: ALU densities upstream and downstream of known genes as a function of distance from the gene transcript start position. Green and red curves correspond to ALU instances in the sense and antisense orientation respectively. Downstream regions are separated in exonic and intronic parts. There is a clear over-representation of ALU instances upstream of known genes and in the intronic regions, particularly in the antisense direction. In contrast, ALUs are under-represented in exons.

Figure 2: B element (B1, B2, B4) densities upstream and downstream of known genes as a function of distance from the gene transcript start position. Green and red curves correspond to B element instances in the sense and antisense orientation respectively. Downstream regions are separated in exonic and intronic parts. As in the case of ALUs, there is a clear over-representation of B element instances upstream of known genes and in the intronic regions, particularly in the antisense direction. In contrast, B elements are under-represented in exons.

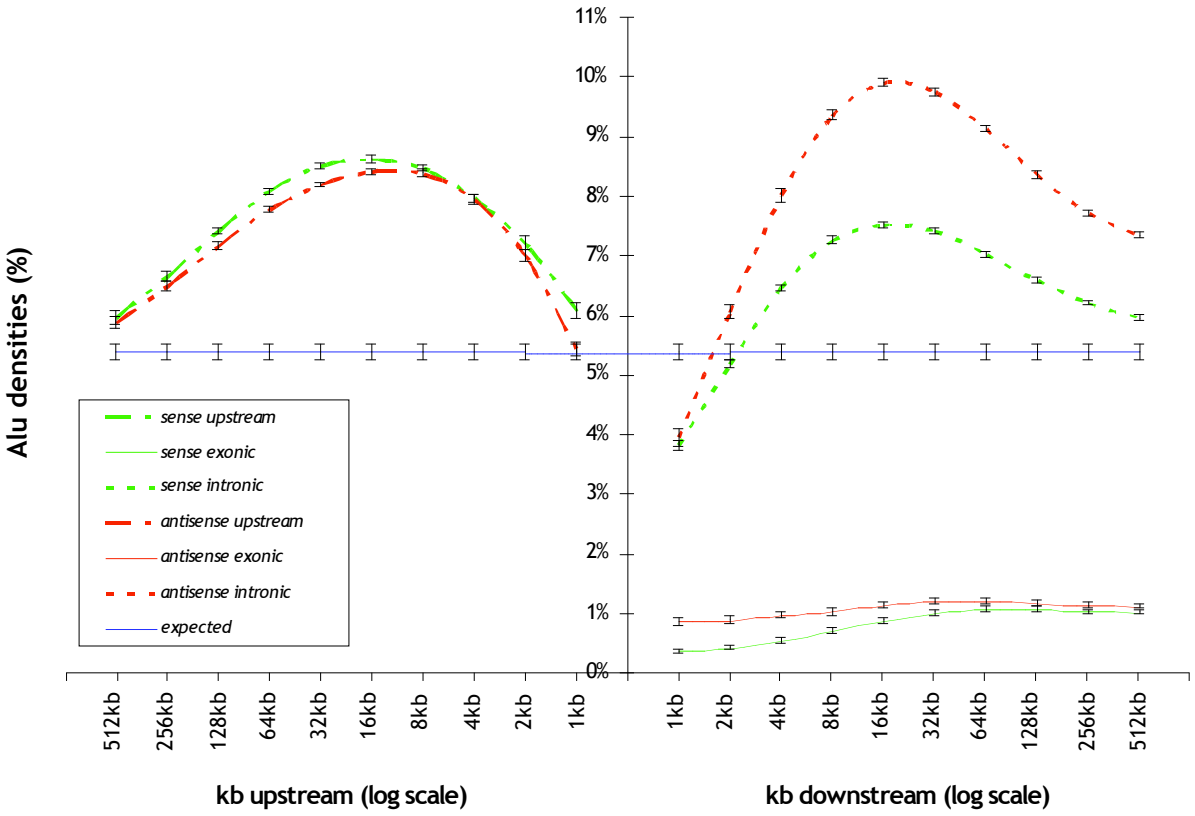
Figure 3: ALU densities upstream and downstream of known genes as a function of distance from the gene transcript start position. Green and red curves correspond to ALU instances in the sense and antisense orientation respectively. Here, we show only the subset of the curves of Figure 1 with the highest densities, i.e. sense upstream and antisense intronic downstream, and compare it the corresponding densities of the genes which belong to the experimentally validated functional classes: DNA recombination, chromatin remodeling, splicing and translation.

Figure 4: Average pair-wise sequence similarities involving ALU and B1 elements. We have carried out pair-wise comparisons involving a) only ALUs, b) only B1s, and c) ALU monomers with B1s.

Figure 5: Venn diagram showing the relationships among the three sets of significant GO terms corresponding to each ALU sub-family. Note that the AluS GO term set is an approximate superset of the AluJ set, which in turn is an approximate superset of the AluY set – see test for details.

TABLE LEGENDS

Table 1: Significantly over-represented GO terms for ALU and B elements. In the interest of clarity of the presentation we *only* show GO terms at GO hierarchy level ≥ 6; the entire list of GO terms can be found in the Supplement. The colors in the columns labeled "ALU" and "B" show for each GO term whether it is associated with upstream, sense intronic, or antisense intronic regions: (a) GO terms associated with upstream ALU/B instances are colored cyan, (b) GO terms associated with *sense* intronic instances of ALU/B instances are colored green, and (c) GO terms associated with *antisense* intronic ALU/B instances are colored red. Significant GO terms are considered those terms whose *adjusted p-values* are less than 0.01 (see Methods). The actual adjusted and unadjusted p-values for each type of element and for each region and orientation can be found in the Supplement. The *GO terms are organized* in such a way so that related GO terms are located as close as possible to one another (note that this is not an easy problem, since the GO hierarchy is not a tree).



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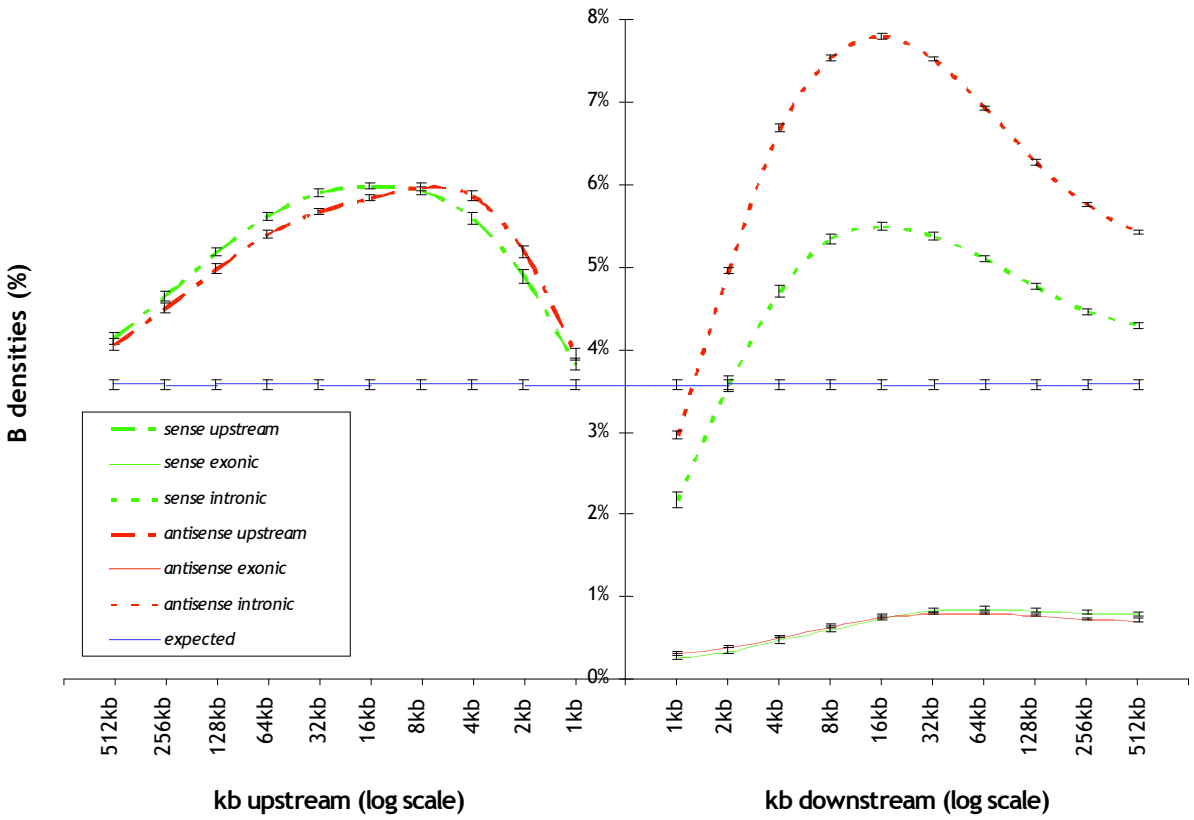

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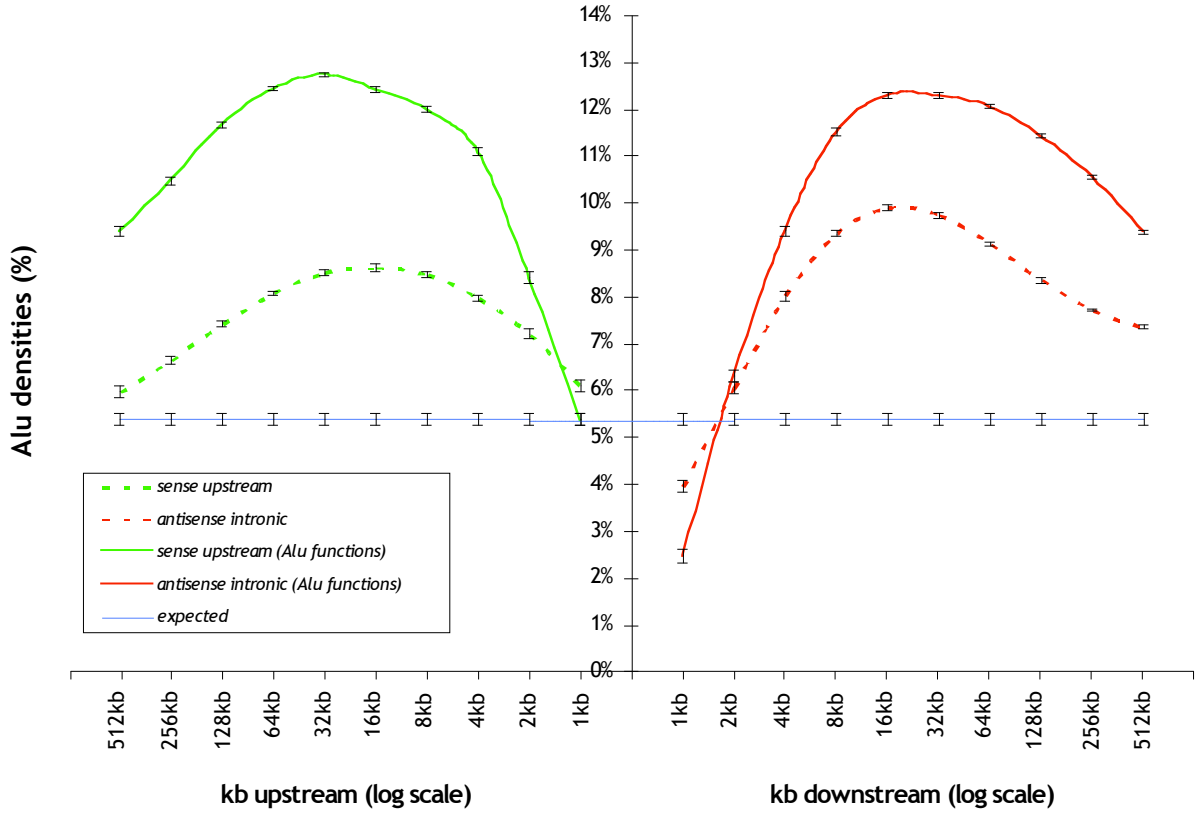

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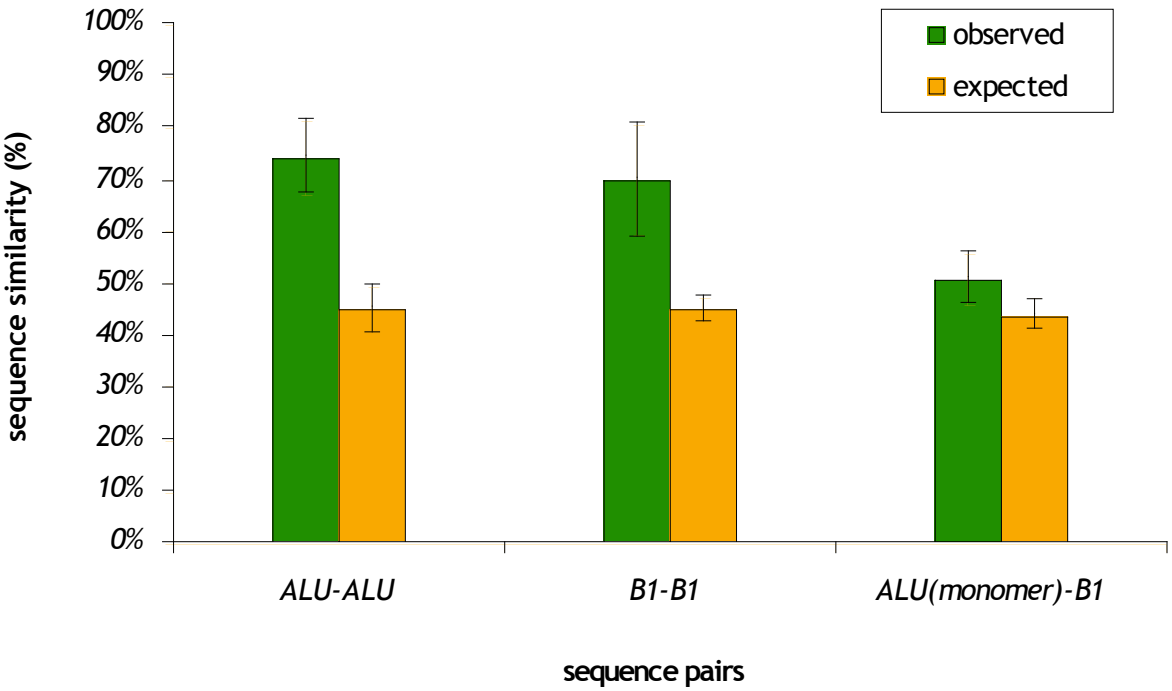

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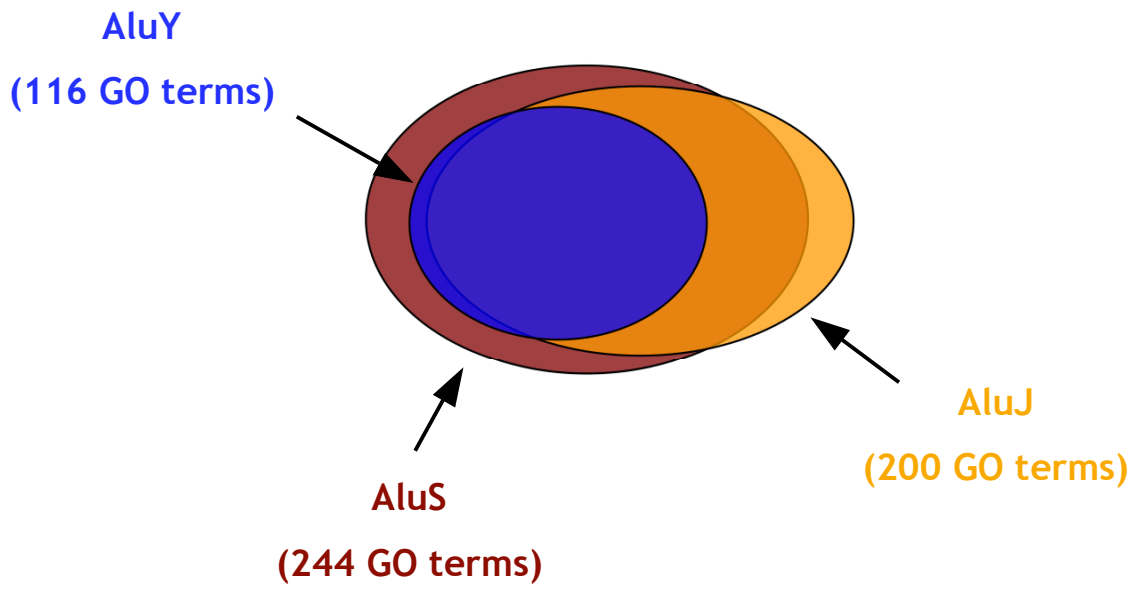

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	human		mouse		
GO term id	genes	ALU	genes	B	GO term description
GO:0016279	29		24		protein-lysine N-methyltransferase activity
GO:0018024	29		24		histone-lysine N-methyltransferase activity
GO:0042054	37		33		histone methyltransferase activity
GO:0016278	29		24		lysine N-methyltransferase activity
GO:0004713	556		572		protein-tyrosine kinase activity
GO:0004674	541		564		protein serine/threonine kinase activity
GO:0017111	761		725		nucleoside-triphosphatase activity
GO:0016887	378		363		ATPase activity
GO:0042623	292		274		ATPase activity, coupled
GO:0003924	261		241		GTPase activity
GO:0004721	174		161		phosphoprotein phosphatase activity
GO:0004842	161		151		ubiquitin-protein ligase activity
GO:0030983	23		12		mismatched DNA binding
GO:0045934	389		357		negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism
GO:0051053	23		18		negative regulation of DNA metabolism
GO:0008156	18		12		negative regulation of DNA replication

GO:0016481	358				335				negative regulation of transcription
GO:0045449	2723				2515				regulation of transcription
GO:0006355	2554				2363				regulation of transcription, DNA-dependent
GO:0051052	73				48				regulation of DNA metabolism
GO:0006445	60				31				regulation of translation
GO:0006446	44				22				regulation of translational initiation
GO:0043065	299				254				positive regulation of apoptosis
GO:0006917	250				190				induction of apoptosis
GO:0012502	251				190				induction of programmed cell death
GO:0043066	276				226				negative regulation of apoptosis
GO:0043414	50				74				biopolymer methylation
GO:0043037	263				165				translation
GO:0006414	108				24				translational elongation
GO:0006413	69				65				translational initiation
GO:0043632	237				162				modification-dependent macromolecule catabolism
GO:0019941	237				162				modification-dependent protein catabolism
GO:0006511	234				159				ubiquitin-dependent protein catabolism
GO:0043161	100				29				proteasomal ubiquitin-dependent protein catabolism
GO:0030433	18				11				ER-associated protein catabolism
GO:0006401	51				35				RNA catabolism
GO:0006402	34				29				mRNA catabolism
GO:0000184	21				16				mRNA catabolism, nonsense-mediated decay
GO:0044257	262				185				cellular protein catabolism
GO:0051603	259				183				proteolysis during cellular protein catabolism
GO:0006515	18				12				misfolded or incompletely synthesized protein catabolism
GO:0016310	878				873				phosphorylation
GO:0006468	727				750				protein amino acid phosphorylation
GO:0006310	112				86				DNA recombination
GO:0006260	223				167				DNA replication
GO:0006261	120				74				DNA-dependent DNA replication
GO:0045005	31				15				maintenance of fidelity during DNA-dependent DNA replication
GO:0006323	418				378				DNA packaging

GO:0006325	414				376				establishment and/or maintenance of chromatin architecture
GO:0016568	216				192				chromatin modification
GO:0016569	58				55				covalent chromatin modification
GO:0006338	56				49				chromatin remodeling
GO:0006396	504				411				RNA processing
GO:0006397	307				244				mRNA processing
GO:0000398	161				51				nuclear mRNA splicing, via spliceosome
GO:0000387	28				4				spliceosomal snRNP biogenesis
GO:0000245	36				20				spliceosome assembly
GO:0008380	278				194				RNA splicing
GO:0000375	161				51				RNA splicing, via transesterification reactions
GO:0000377	161				51				RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0043631	12				13				RNA polyadenylation
GO:0016071	352				286				mRNA metabolism
GO:0006351	2629				2408				transcription, DNA-dependent
GO:0006352	111				64				transcription initiation
GO:0006367	70				23				transcription initiation from RNA polymerase II promoter
GO:0006354	52				11				RNA elongation
GO:0006368	49				7				RNA elongation from RNA polymerase II promoter
GO:0006366	736				579				transcription from RNA polymerase II promoter
GO:0006508	868				827				proteolysis
GO:0006457	203				150				protein folding
GO:0006464	1918				1805				protein modification
GO:0043543	32				27				protein amino acid acylation
GO:0006473	23				16				protein amino acid acetylation
GO:0006512	603				552				ubiquitin cycle
GO:0031365	11				7				N-terminal protein amino acid modification
GO:0008632	108				78				apoptotic program
GO:0051170	107				83				nuclear import
GO:0006606	105				81				protein import into nucleus
GO:0051168	55				41				nuclear export
GO:0006405	36				21				RNA export from nucleus

GO:0006605	222				228				protein targeting
GO:0051028	80				55				mRNA transport
GO:0007067	224				192				mitosis
GO:0051437	72				0				positive regulation of ubiquitin ligase activity during mitotic cell cycle
GO:0007017	231				219				microtubule-based process
GO:0007001	442				402				chromosome organization and biogenesis (sensu Eukaryota)
GO:0030520	10				4				estrogen receptor signaling pathway

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		Alu+		Alu-		AluJ+		AluJ-		AluS+		AluS-		AluY+		AluY-			
GO term id	genes	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	GO term description	GO term catecory
GO:0000003	515	3.39E-01	1.00E+00	4.40E-01	1.00E+00	7.73E-01	1.00E+00	4.13E-01	1.00E+00	4.65E-01	1.00E+00	3.48E-01	1.00E+00	6.19E-03	3.57E-01	6.70E-01	1.00E+00	reproduction	P
GO:0000018	10	9.45E-03	6.67E-01	8.95E-03	5.03E-01	3.39E-02	1.00E+00	1.45E-02	8.18E-01	1.41E-02	1.00E+00	3.48E-02	1.00E+00	3.54E-01	1.00E+00	6.46E-02	1.00E+00	regulation of DNA recombination	P
GO:0000030	14	9.95E-02	1.00E+00	1.86E-01	1.00E+00	4.19E-01	1.00E+00	5.80E-01	1.00E+00	2.99E-02	1.00E+00	1.95E-01	1.00E+00	7.76E-01	1.00E+00	7.39E-02	1.00E+00	mannosyltransferase activity	F
GO:0000041	75	1.05E-01	1.00E+00	3.98E-02	1.00E+00	6.89E-01	1.00E+00	8.45E-02	1.00E+00	7.60E-02	1.00E+00	1.79E-02	8.81E-01	2.69E-01	1.00E+00	7.66E-01	1.00E+00	transition metal ion transport	P
GO:0000045	11	9.61E-02	1.00E+00	6.21E-03	3.60E-01	1.64E-01	1.00E+00	1.18E-01	1.00E+00	4.23E-02	1.00E+00	4.98E-03	2.70E-01	7.09E-01	1.00E+00	2.24E-01	1.00E+00	autophagic vacuole formation	P
GO:0000049	21	1.82E-01	1.00E+00	2.41E-02	1.00E+00	9.81E-02	1.00E+00	4.87E-01	1.00E+00	3.62E-01	1.00E+00	1.23E-02	7.39E-01	5.04E-01	1.00E+00	3.16E-01	1.00E+00	tRNA binding	F
GO:0000051	20	7.75E-02	1.00E+00	7.40E-02	1.00E+00	1.25E-01	1.00E+00	1.30E-01	1.00E+00	1.04E-01	1.00E+00	5.24E-02	1.00E+00	1.78E-01	1.00E+00	5.10E-01	1.00E+00	urea cycle intermediate metabolism	P
GO:0000059	17	2.23E-04	2.64E-02	9.78E-05	1.50E-02	4.18E-03	3.27E-01	5.90E-02	1.00E+00	9.64E-04	4.40E-02	1.83E-04	2.60E-02	7.92E-02	1.00E+00	7.71E-02	1.00E+00	protein import into nucleus, docking	P
GO:0000060	23	9.18E-02	1.00E+00	9.53E-02	1.00E+00	1.64E-01	1.00E+00	3.07E-01	1.00E+00	1.16E-01	1.00E+00	6.11E-02	1.00E+00	2.48E-01	1.00E+00	5.37E-01	1.00E+00	protein import into nucleus, translocation	P
GO:0000062	12	2.18E-02	1.00E+00	6.37E-02	1.00E+00	5.54E-02	1.00E+00	2.41E-01	1.00E+00	3.99E-02	1.00E+00	1.21E-01	1.00E+00	7.38E-02	1.00E+00	1.23E-01	1.00E+00	acyl-CoA binding	F
GO:0000070	32	5.20E-02	1.00E+00	1.52E-02	1.00E+00	4.67E-01	1.00E+00	4.75E-03	3.46E-01	7.81E-02	1.00E+00	1.73E-01	1.00E+00	3.07E-02	1.00E+00	3.44E-03	1.85E-01	mitotic sister chromatid segregation	P
GO:0000074	367	1.66E-05	8.00E-03	1.09E-06	8.39E-03	3.22E-03	2.48E-01	5.49E-04	4.70E-02	2.44E-05	5.00E-03	1.26E-05	4.88E-03	5.20E-02	1.00E+00	1.20E-04	2.00E-02	regulation of progression through cell cycle	P
GO:0000075	68	4.03E-03	3.28E-01	3.12E-03	1.97E-01	4.56E-02	1.00E+00	1.56E-02	8.18E-01	7.75E-03	5.39E-01	5.38E-03	2.70E-01	3.53E-01	1.00E+00	1.11E-01	1.00E+00	cell cycle checkpoint	P
GO:0000077	33	7.34E-03	6.34E-01	1.09E-02	6.77E-01	1.57E-02	6.93E-01	2.05E-02	1.00E+00	3.70E-02	1.00E+00	1.31E-02	7.39E-01	1.84E-01	1.00E+00	1.84E-01	1.00E+00	DNA damage checkpoint	P
GO:0000079	50	2.71E-02	1.00E+00	1.66E-02	1.00E+00	1.62E-01	1.00E+00	1.04E-01	1.00E+00	1.32E-02	1.00E+00	3.24E-02	1.00E+00	4.85E-01	1.00E+00	8.02E-02	1.00E+00	regulation of cyclin-dependent protein kinas	P
GO:0000080	16	7.91E-02	1.00E+00	1.56E-02	1.00E+00	5.89E-01	1.00E+00	6.71E-02	1.00E+00	7.75E-02	1.00E+00	2.52E-02	1.00E+00	5.83E-02	1.00E+00	3.07E-02	1.00E+00	G1 phase of mitotic cell cycle	P
GO:0000082	45	8.11E-02	1.00E+00	4.21E-02	1.00E+00	2.65E-01	1.00E+00	5.20E-03	3.46E-01	3.09E-02	1.00E+00	1.39E-01	1.00E+00	5.32E-01	1.00E+00	3.00E-01	1.00E+00	G1/S transition of mitotic cell cycle	P
GO:0000084	16	7.20E-02	1.00E+00	7.58E-02	1.00E+00	1.22E-01	1.00E+00	4.24E-01	1.00E+00	8.76E-02	1.00E+00	1.28E-01	1.00E+00	1.22E-01	1.00E+00	2.98E-02	1.00E+00	S phase of mitotic cell cycle	P
GO:0000086	20	8.65E-03	6.34E-01	7.02E-03	3.60E-01	5.73E-04	3.60E-02	4.45E-02	1.00E+00	6.67E-02	1.00E+00	1.51E-02	7.39E-01	7.01E-02	1.00E+00	9.09E-02	1.00E+00	G2/M transition of mitotic cell cycle	P
GO:0000087	226	1.33E-09	8.06E-04	1.58E-12	0.00E+00	1.59E-03	2.48E-01	4.64E-11	0.00E+00	4.47E-09	9.64E-04	2.14E-08	8.37E-04	1.03E-03	7.07E-02	3.00E-06	1.88E-03	M phase of mitotic cell cycle	P
GO:0000096	21	2.64E-01	1.00E+00	6.98E-02	1.00E+00	2.10E-01	1.00E+00	1.41E-01	1.00E+00	2.20E-01	1.00E+00	6.07E-02	1.00E+00	9.67E-01	1.00E+00	9.66E-01	1.00E+00	sulfur amino acid metabolism	P
GO:0000097	14	2.40E-01	1.00E+00	1.37E-01	1.00E+00	9.10E-02	1.00E+00	4.18E-01	1.00E+00	2.53E-01	1.00E+00	8.63E-02	1.00E+00	9.57E-01	1.00E+00	8.85E-01	1.00E+00	sulfur amino acid biosynthesis	P
GO:0000118	27	3.89E-01	1.00E+00	7.47E-02	1.00E+00	1.57E-01	1.00E+00	6.35E-01	1.00E+00	3.54E-01	1.00E+00	2.93E-02	1.00E+00	9.83E-01	1.00E+00	2.10E-01	1.00E+00	histone deacetylase complex	C
GO:0000119	25	5.52E-04	3.37E-02	1.72E-03	9.10E-02	1.62E-02	6.93E-01	1.70E-02	8.18E-01	3.23E-03	2.85E-01	1.02E-03	5.49E-02	8.52E-03	6.30E-01	2.50E-01	1.00E+00	mediator complex	C
GO:0000122	191	1.18E-02	6.67E-01	4.18E-02	1.00E+00	2.30E-01	1.00E+00	1.16E-01	1.00E+00	3.85E-03	2.85E-01	6.20E-02	1.00E+00	3.00E-01	1.00E+00	1.57E-01	1.00E+00	negative regulation of transcription from RN	P
GO:0000123	12	1.42E-03	2.02E-01	9.99E-08	4.97E-03	4.53E-03	3.27E-01	2.60E-04	2.70E-02	2.04E-02	1.00E+00	6.96E-06	4.88E-03	3.84E-02	1.00E+00	7.25E-03	4.81E-01	histone acetyltransferase complex	C
GO:0000139	350	5.87E-02	1.00E+00	1.39E-03	9.10E-02	9.08E-02	1.00E+00	4.84E-02	1.00E+00	9.07E-02	1.00E+00	8.12E-04	5.49E-02	8.77E-02	1.00E+00	3.13E-01	1.00E+00	Golgi membrane	C
GO:0000146	15	2.75E-01	1.00E+00	1.72E-01	1.00E+00	2.88E-01	1.00E+00	2.26E-01	1.00E+00	2.17E-01	1.00E+00	1.61E-01	1.00E+00	7.69E-01	1.00E+00	2.81E-01	1.00E+00	microfilament motor activity	F
GO:0000149	29	7.70E-02	1.00E+00	3.62E-01	1.00E+00	4.40E-02	1.00E+00	2.65E-01	1.00E+00	1.77E-01	1.00E+00	5.76E-01	1.00E+00	2.70E-01	1.00E+00	3.17E-01	1.00E+00	SNARE binding	F
GO:0000151	95	2.19E-02	1.00E+00	3.23E-03	1.97E-01	4.19E-03	3.27E-01	2.00E-02	1.00E+00	2.35E-01	1.00E+00	2.93E-03	2.39E-01	5.97E-02	1.00E+00	2.70E-01	1.00E+00	ubiquitin ligase complex	C
GO:0000152	16	1.51E-01	1.00E+00	9.01E-02	1.00E+00	2.67E-01	1.00E+00	1.61E-01	1.00E+00	5.17E-01	1.00E+00	1.62E-01	1.00E+00	5.50E-03	3.57E-01	7.56E-02	1.00E+00	nuclear ubiquitin ligase complex	C
GO:0000155	13	2.63E-01	1.00E+00	5.31E-01	1.00E+00	2.31E-01	1.00E+00	5.59E-01	1.00E+00	1.78E-01	1.00E+00	7.09E-01	1.00E+00	9.39E-01	1.00E+00	5.66E-02	1.00E+00	two-component sensor activity	F
GO:0000159	23	2.00E-01	1.00E+00	6.14E-03	3.60E-01	3.34E-01	1.00E+00	3.51E-02	1.00E+00	1.99E-01	1.00E+00	1.06E-02	7.39E-01	4.59E-01	1.00E+00	1.90E-01	1.00E+00	protein phosphatase type 2A complex	C
GO:0000160	11	6.79E-01	1.00E+00	8.00E-01	1.00E+00	4.01E-01	1.00E+00	5.63E-01	1.00E+00	6.44E-01	1.00E+00	9.26E-01	1.00E+00	9.43E-01	1.00E+00	5.26E-01	1.00E+00	two-component signal transduction system	P
GO:0000165	188	1.36E-03	2.02E-01	3.01E-03	1.97E-01	3.40E-02	1.00E+00	3.88E-03	2.41E-01	6.89E-04	4.00E-02	1.52E-02	7.39E-01	2.22E-01	1.00E+00	1.24E-02	6.47E-01	MAPKKK cascade	P
GO:0000166	2329	1.73E-32	0.00E+00	0.00E+00	0.00E+00	4.61E-17	0.00E+00	1.42E-20	0.00E+00	2.78E-28	0.00E+00	3.43E-43	0.00E+00	1.66E-11	0.00E+00	1.02E-12	0.00E+00	nucleotide binding	F
GO:0000175	10	3.76E-02	1.00E+00	4.22E-01	1.00E+00	1.52E-01	1.00E+00	4.91E-01	1.00E+00	4.17E-02	1.00E+00	7.48E-01	1.00E+00	1.08E-01	1.00E+00	1.45E-01	1.00E+00	3'-5'-exoribonuclease activity	F
GO:0000178	12	2.99E-02	1.00E+00	6.65E-01	1.00E+00	8.80E-02	1.00E+00	6.13E-01	1.00E+00	5.51E-02	1.00E+00	8.73E-01	1.00E+00	8.55E-02	1.00E+00	3.01E-01	1.00E+00	exosome (RNase complex)	C
GO:0000184	21	6.00E-06	7.00E-03	6.76E-05	1.00E-02	2.78E-04	3.60E-02	3.56E-03	2.02E-01	1.05E-04	1.70E-02	4.25E-04	4.10E-02	2.45E-02	1.00E+00	5.89E-03	3.60E-01	mRNA catabolism, nonsense-mediated dec	P
GO:0000186	16	4.15E-01	1.00E+00	3.77E-01	1.00E+00	4.95E-01	1.00E+00	8.26E-01	1.00E+00	2.86E-01	1.00E+00	4.20E-01	1.00E+00	5.96E-01	1.00E+00	9.62E-02	1.00E+00	activation of MAPKK activity	P
GO:0000187	69	2.60E-02	1.00E+00	1.12E-02	6.77E-01	2.99E-02	1.00E+00	1.67E-02	8.18E-01	4.93E-02	1.00E+00	1.68E-02	8.60E-01	2.05E-01	1.00E+00	1.21E-01	1.00E+00	activation of MAPK activity	P
GO:0000188	20	1.79E-01	1.00E+00	4.77E-01	1.00E+00	2.08E-01	1.00E+00	7.05E-01	1.00E+00	1.86E-01	1.00E+00	3.88E-01	1.00E+00	5.88E-01	1.00E+00	3.01E-01	1.00E+00	inactivation of MAPK activity	P
GO:0000209	15	3.30E-01	1.00E+00	5.02E-01	1.00E+00	1.70E-01	1.00E+00	4.59E-01	1.00E+00	3.64E-01	1.00E+00	4.49E-01	1.00E+00	8.27E-01	1.00E+00	7.53E-01	1.00E+00	protein polyubiquitination	P
GO:0000226	100	4.55E-04	3.37E-02	1.66E-02	1.00E+00	2.16E-05	6.00E-03	1.40E-01	1.00E+00	9.10E-03	5.39E-01	3.04E-02	1.00E+00	1.45E-02	6.47E-01	5.83E-02	1.00E+00	microtubule cytoskeleton organization and b	P
GO:0000228	115	4.94E-04	3.37E-02	1.09E-04	1.50E-02	1.29E-02	5.32E-01	1.09E-02	8.18E-01	5.24E-04	2.20E-02	1.44E-04	1.70E-02	1.10E-01	1.00E+00	6.52E-02	1.00E+00	nuclear chromosome	C
GO:0000242	12	3.33E-02	1.00E+00	1.97E-01	1.00E+00	2.39E-02	1.00E+00	4.10E-01	1.00E+00	9.44E-02	1.00E+00	2.93E-01	1.00E+00	2.53E-02	1.00E+00	8.97E-03	4.81E-01	pericentriolar material	C
GO:0000245	35	3.61E-04	3.37E-02	2.91E-05	9.58E-03	1.72E-03	2.48E-01	6.22E-04	4.70E-02	3.51E-03	2.85E-01	2.42E-04	2.60E-02	2.95E-02	1.00E+00	1.27E-01	1.00E+00	spliceosome assembly	P
GO:0000267	853	1.64E-02	6.67E-01	1.47E-03	9.10E-02	2.01E-01	1.00E+00	7.71E-02	1.00E+00	1.19E-02	5.39E-01	5.64E-04	5.49E-02	9.00E-02	1.00E+00	2.34E-01	1.00E+00	cell fraction	C
GO:0000271	47	2.81E-01	1.00E+00	1.75E-01	1.00E+00	7.42E-01	1.00E+00	7.06E-01	1.00E+00	1.74E-01	1.00E+00	1.22E-01	1.00E+00	4.66E-01	1.00E+00	2.17E-01	1.00E+00	polysaccharide biosynthesis	P
GO:0000272	16	9.96E-01	1.00E+00	7.76E-01	1.00E+00	7.09E-01	1.00E+00	6.87E-01	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	8.11E-01	1.00E+00	8.95E-01	1.00E+00	polysaccharide catabolism	P
GO:0000278	385	5.87E-13	0.00E+00	4.76E-16	0.00E+00	1.11E-04	1.20E-02	4.13E-11	0.00E+00	8.84E-13	0.00E+00	5.17E-12	0.00E+00	6.39E-04	6.50E-02	2.81E-07	1.88E-03	mitotic cell cycle	P
GO:0000279	298	6.27E-11	0.00E+00	1.01E-14	0.00E+00	5.58E-04	3.60E-02	1.11E-11	0.00E+00	1.55E-10	0.00E+00	2.45E-10	0.00E+00	1.61E-03	1.68E-01	8.30E-07	1.88E-03	M phase	P
GO:0000287	420	6.30E-05	1.10E-02	1.10E-09	0.00E+00	6.41E-03	4.60E-01	3.65E-06	8.00E-03	4.46E-05	6.35E-03	3.46E-08	8.37E-04	2.45E-01	1.00E+00	1.84E-04	2.00E-02	magnesium ion binding	F
GO:0000299	12	6.68E-02	1.00E+00	3.89E-01	1.00E+00	3.27E-01	1.00E+00	7.10E-01	1.00E+00	6.69E-02	1.00E+00	2.20E-01	1.00E+00	3.53E-02	1.00E+00	7.77E-01	1.00E+00	integral to membrane of membrane fraction	C
GO:0000302	35	3.44E-02	1.00E+00	4.78E-02	1.00E+00	3.44E-01	1.00E+00	5.70E-02	1.00E+00	1.15E-02	5.39E-01	1.08E-01	1.00E+00	3.88E-01	1.00E+00	6.85E-02	1.00E+00	response to reactive oxygen species	P
GO:0000313	48	1.30E-02	6.67E-01	1.19E-01	1.00E+00	3.22E-03	2.48E-01	1.36E-01	1.00E+00	2.57E-01	1.00E+00	2.33E-01	1.00E+00	2.61E-03	1.95E-01	2.71E-01	1.00E+00	organellar ribosome	C
GO:0000314	18	3.80E-02	1.00E+00	2.41E-01	1.00E+00	1.18E-02	5.32E-01	4.21E-01	1.00E+00	1.64E-01	1.00E+00	2.56E-01	1.00E+00	1.23E-01	1.00E+00	5.15E-01	1.00E+00	organellar small ribosomal subunit	C
GO:0000315	17	4.74E-01	1.00E+00	1.57E-01	1.00E+00	5.42E-01	1.00E+00	3.42E-02	1.00E+00	5.84E-01	1.00E+00	2.13E-01	1.00E+00	1.32E-01	1.00E+00	3.97E-01	1.00E+00	organellar large ribosomal subunit	C
GO:0000323	209	1.10E-03	9.60E-02	1.11E-03	9.10E-02	1.95E-01	1.00E+00	3.73E-02	1.00E+00	2.75E-04	1.70E-02	4.42E-03	2.70E-01	1.49E-01	1.00E+00	3.98E-03	1.85E-01	lytic vacuole	C
GO:0000375	156	1.25E-15	0.00E+00	3.78E-19	0.00E+00	6.88E-07	2.42E-03	9.68E-08	9.71E-04	1.13E-13	0.00E+00	1.59E-16	0.00E+00	9.54E-06	5.44E-03	2.34E-08	7.71E-04	RNA splicing, via transesterification reactior	P
GO:0000377	156	1.25E-15	0.00E+00	3.78E-19	0.00E+00	6.88E-07	2.42E-03	9.68E-08	9.71E-04	1.13E-13	0.00E+00	1.59E-16	0.00E+00	9.54E-06	5.44E-03	2.34E-08	7.71E-04	RNA splicing, via transesterification reactior	P
GO:0000387	27	4.22E-06	7.00E-03	3.72E-05	9.58E-03	2.12E-04	2.40E-02	2.89E-02	1.00E+00	7.27E-05	1.70E-02	3.78E-05	1.20E-02	1.27E-01	1.00E+00	1.76E-02	1.00E+00	spliceosomal snRNP biogenesis	P
GO:0000398	156	1.25E-15	0.00E+00	3.78E-19	0.00E+00	6.88E-07	2.42E-03	9.68E-08	9.71E-04	1.13E-13	0.00E+00	1.59E-16	0.00E+00	9.54E-06	5.44E-03	2.34E-08	7.71E-04	nuclear mRNA splicing, via spliceosome	P
GO:0000502	49	4.60E-03	3.28E-01	3.00E-04	4.19E-02	3.74E-01	1.00E+00	3.12E-02	1.00E+00	6.97E-04	4.00E-02	1.09E-03	5.49E-02	1.97E-01	1.00E+00	1.12E-03	9.16E-02	proteasome complex (sensu Eukaryota)	C
GO:0000718	21	2.08E-02	1.00E+00	2.63E-02	1.00E+00	2.05E-02	1.00E+00	4.51E-02	1.00E+00	7.11E-02	1.00E+00	4.62E-02	1.00E+00	1.16E-01	1.00E+00	4.49E-01	1.00E+00	nucleotide-excision repair, DNA damage rer	P
GO:0000723	28	2.75E-02	1.00E+00	1.08E-01	1.00E+00	1.70E-02	6.93E-01	7.87E-01	1.00E+00	9.41E-02	1.00E+00	5.27E-02	1.00E+00	2.11E-01	1.00E+00	3.50E-01	1.00E+00	telomere maintenance	P
GO:0000724	15	9.19E-02	1.00E+00	3.88E-02	1.00E+00	2.00E-02	1.00E+00	3.57E-01	1.00E+00	5.51E-01	1.00E+00	2.18E-02	1.00E+00	2.60E-01	1.00E+00	1.24E-01	1.00E+00	double-strand break repair via homologous	P
GO:0000725	15	9.19E-02	1.00E+00	3.88E-02	1.00E+00	2.00E-02	1.00E+00	3.57E-01	1.00E+00	5.51E-01	1.00E+00	2.18E-02	1.00E+00	2.60E-01	1.00E+00	1.24E-01	1.00E+00	recombinational repair	P
GO:0000726	12	2.59E-01	1.00E+00	3.71E-01	1.00E+00	1.34E-01	1.00E+00	9.80E-01	1.00E+00	4.54E-01	1.00E+00	2.07E-02	1.00E+00	1.99E-01	1.00E+00	9.96E-01	1.00E+00	non-recombinational repair	P
GO:0000775	88	9.07E-04	8.30E-02	7.37E-05	1.00E-02	8.29E-03	4.60E-01	5.89E-03	3.46E-01	1.90E-03	1.76E-01	1.06E-04	1.70E-02	3.01E-01	1.00E+00	3.12E-02	1.00E+00	chromosome, pericentric region	C
GO:0000776	47	1.28E-02	6.67E-01	2.98E-03	1.97E-01	2.11E-02	1.00E+00	2.41E-02	1.00E+00	2.97E-02	1.00E+00	3.95E-03	2.70E-01	2.72E-01	1.00E+00	7.39E-02	1.00E+00	kinetochore	C
GO:0000777	30	2.35E-02	1.00E+00	8.66E-02	1.00E+00	2.53E-02	1.00E+00	8.84E-02	1.00E+00	4.44E-02	1.00E+00	1.16E-01	1.00E+00	4.63E-01	1.00E+00	1.89E-01	1.00E+00	condensed chromosome kinetochore	C
GO:0000779	35	1.33E-02	6.67E-01	1.12E-01	1.00E+00	2.87E-02	1.00E+00	2.28E-01	1.00E+00	2.67E-02	1.00E+00	1.09E-01	1.00E+00	2.66E-01	1.00E+00	2.40E-01	1.00E+00	condensed chromosome, pericentric region	C

GO:0000781	25	2.11E-02	1.00E+00	6.78E-02	1.00E+00	3.49E-02	1.00E+00	4.85E-01	1.00E+00	6.42E-02	1.00E+00	3.59E-02	1.00E+00	5.47E-02	1.00E+00	4.96E-01	1.00E+00	chromosome, telomeric region	C
GO:0000784	10	1.02E-01	1.00E+00	2.25E-01	1.00E+00	1.54E-01	1.00E+00	7.12E-01	1.00E+00	1.44E-01	1.00E+00	1.04E-01	1.00E+00	1.27E-01	1.00E+00	6.67E-01	1.00E+00	nuclear chromosome, telomeric region	C
GO:0000785	311	1.16E-05	7.00E-03	4.32E-05	9.58E-03	1.82E-01	1.00E+00	2.52E-01	1.00E+00	2.02E-06	2.60E-03	1.31E-04	1.70E-02	4.73E-03	3.57E-01	7.94E-06	1.88E-03	chromatin	C
GO:0000786	158	6.87E-03	5.17E-01	1.65E-02	1.00E+00	9.60E-01	1.00E+00	9.39E-01	1.00E+00	5.65E-04	4.00E-02	1.04E-02	7.39E-01	2.52E-02	1.00E+00	2.39E-03	1.40E-01	nucleosome	C
GO:0000790	34	1.12E-02	6.67E-01	1.32E-01	1.00E+00	8.81E-02	1.00E+00	2.39E-01	1.00E+00	1.66E-02	1.00E+00	1.75E-01	1.00E+00	1.52E-01	1.00E+00	1.07E-01	1.00E+00	nuclear chromatin	C
GO:0000792	35	3.87E-02	1.00E+00	2.62E-02	1.00E+00	1.11E-01	1.00E+00	4.03E-01	1.00E+00	4.54E-02	1.00E+00	3.16E-02	1.00E+00	1.92E-01	1.00E+00	1.59E-02	8.49E-01	heterochromatin	C
GO:0000793	84	3.18E-04	3.37E-02	5.29E-04	6.90E-02	1.14E-02	5.32E-01	4.43E-03	3.46E-01	4.62E-04	2.20E-02	1.80E-03	1.61E-01	7.71E-02	1.00E+00	4.74E-02	1.00E+00	condensed chromosome	C
GO:0000794	39	2.99E-02	1.00E+00	8.78E-05	1.50E-02	1.20E-01	1.00E+00	6.34E-02	1.00E+00	2.26E-02	1.00E+00	7.52E-05	1.70E-02	2.66E-01	1.00E+00	2.85E-01	1.00E+00	condensed nuclear chromosome	C
GO:0000795	17	2.97E-01	1.00E+00	2.86E-04	4.19E-02	2.30E-01	1.00E+00	1.53E-01	1.00E+00	2.21E-01	1.00E+00	1.18E-03	6.40E-02	9.53E-01	1.00E+00	1.90E-01	1.00E+00	synaptonemal complex	C
GO:0000803	12	1.68E-01	1.00E+00	4.46E-01	1.00E+00	6.12E-01	1.00E+00	8.93E-01	1.00E+00	2.42E-01	1.00E+00	4.21E-01	1.00E+00	1.30E-01	1.00E+00	3.20E-01	1.00E+00	sex chromosome	C
GO:0000819	33	3.38E-02	1.00E+00	8.21E-03	3.60E-01	4.00E-01	1.00E+00	2.73E-03	1.47E-01	4.97E-02	1.00E+00	1.08E-01	1.00E+00	3.92E-02	1.00E+00	2.84E-03	1.85E-01	sister chromatid segregation	P
GO:0000902	602	2.75E-01	1.00E+00	4.82E-02	1.00E+00	3.41E-02	1.00E+00	1.23E-02	8.18E-01	2.89E-01	1.00E+00	1.58E-01	1.00E+00	7.85E-01	1.00E+00	6.07E-02	1.00E+00	cell morphogenesis	P
GO:0000904	202	9.72E-01	1.00E+00	8.64E-01	1.00E+00	7.48E-01	1.00E+00	9.43E-01	1.00E+00	9.66E-01	1.00E+00	8.66E-01	1.00E+00	9.39E-01	1.00E+00	2.62E-01	1.00E+00	cellular morphogenesis during differentiatio	P
GO:0000910	32	7.18E-02	1.00E+00	7.66E-04	6.90E-02	8.72E-02	1.00E+00	1.57E-02	8.18E-01	3.06E-02	1.00E+00	1.56E-03	1.61E-01	9.37E-01	1.00E+00	2.60E-02	1.00E+00	cytokinesis	P
GO:0000922	25	1.90E-02	1.00E+00	7.01E-02	1.00E+00	2.88E-03	2.48E-01	1.98E-01	1.00E+00	6.99E-02	1.00E+00	5.38E-02	1.00E+00	1.57E-01	1.00E+00	3.94E-01	1.00E+00	spindle pole	C
GO:0000930	10	4.76E-02	1.00E+00	8.04E-01	1.00E+00	2.88E-02	1.00E+00	8.95E-01	1.00E+00	1.46E-01	1.00E+00	8.65E-01	1.00E+00	7.81E-02	1.00E+00	2.19E-01	1.00E+00	gamma-tubulin complex	C
GO:0001501	317	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	skeletal development	P
GO:0001502	16	8.03E-01	1.00E+00	9.00E-01	1.00E+00	9.85E-01	1.00E+00	9.42E-01	1.00E+00	6.50E-01	1.00E+00	7.43E-01	1.00E+00	6.20E-01	1.00E+00	9.84E-01	1.00E+00	cartilage condensation	P
GO:0001503	145	4.83E-01	1.00E+00	6.39E-01	1.00E+00	5.69E-01	1.00E+00	3.87E-01	1.00E+00	3.14E-01	1.00E+00	6.90E-01	1.00E+00	9.48E-01	1.00E+00	6.46E-01	1.00E+00	ossification	P
GO:0001505	102	9.85E-01	1.00E+00	8.68E-01	1.00E+00	8.34E-01	1.00E+00	5.11E-01	1.00E+00	9.80E-01	1.00E+00	8.92E-01	1.00E+00	9.78E-01	1.00E+00	9.24E-01	1.00E+00	regulation of neurotransmitter levels	P
GO:0001508	50	2.51E-01	1.00E+00	2.70E-01	1.00E+00	4.98E-02	1.00E+00	1.72E-01	1.00E+00	5.66E-01	1.00E+00	3.31E-01	1.00E+00	2.35E-01	1.00E+00	4.27E-01	1.00E+00	regulation of action potential	P
GO:0001518	14	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.90E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	voltage-gated sodium channel complex	C
GO:0001522	14	2.34E-01	1.00E+00	3.73E-01	1.00E+00	4.75E-01	1.00E+00	5.18E-01	1.00E+00	1.45E-01	1.00E+00	6.36E-01	1.00E+00	4.34E-01	1.00E+00	5.05E-02	1.00E+00	pseudouridine synthesis	P
GO:0001523	13	9.62E-01	1.00E+00	8.54E-01	1.00E+00	4.47E-01	1.00E+00	4.89E-01	1.00E+00	1.00E+00	1.00E+00	9.27E-01	1.00E+00	1.33E-01	1.00E+00	5.81E-01	1.00E+00	retinoid metabolism	P
GO:0001525	158	8.67E-01	1.00E+00	4.90E-01	1.00E+00	8.55E-01	1.00E+00	5.27E-01	1.00E+00	8.75E-01	1.00E+00	6.36E-01	1.00E+00	4.42E-01	1.00E+00	8.98E-02	1.00E+00	angiogenesis	P
GO:0001533	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.42E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	cornified envelope	C
GO:0001539	47	4.43E-01	1.00E+00	4.03E-01	1.00E+00	2.52E-01	1.00E+00	3.21E-01	1.00E+00	4.85E-01	1.00E+00	7.14E-01	1.00E+00	5.81E-01	1.00E+00	7.84E-02	1.00E+00	ciliary or flagellar motility	P
GO:0001540	10	3.06E-01	1.00E+00	7.93E-01	1.00E+00	1.04E-01	1.00E+00	5.00E-01	1.00E+00	4.38E-01	1.00E+00	9.66E-01	1.00E+00	3.66E-01	1.00E+00	6.61E-02	1.00E+00	beta-amyloid binding	F
GO:0001541	24	1.39E-01	1.00E+00	2.82E-01	1.00E+00	1.30E-01	1.00E+00	1.73E-01	1.00E+00	1.32E-01	1.00E+00	3.42E-01	1.00E+00	6.17E-01	1.00E+00	3.79E-01	1.00E+00	ovarian follicle development	P
GO:0001558	167	2.80E-01	1.00E+00	4.02E-02	1.00E+00	2.35E-02	1.00E+00	9.84E-03	7.13E-01	4.58E-01	1.00E+00	1.40E-01	1.00E+00	6.65E-01	1.00E+00	7.74E-02	1.00E+00	regulation of cell growth	P
GO:0001565	15	4.66E-01	1.00E+00	1.05E-01	1.00E+00	5.59E-01	1.00E+00	3.26E-01	1.00E+00	4.71E-01	1.00E+00	7.08E-02	1.00E+00	5.43E-01	1.00E+00	3.36E-01	1.00E+00	phorbol ester receptor activity	F
GO:0001568	226	9.28E-01	1.00E+00	5.55E-01	1.00E+00	8.98E-01	1.00E+00	5.14E-01	1.00E+00	9.58E-01	1.00E+00	7.96E-01	1.00E+00	3.22E-01	1.00E+00	3.95E-02	1.00E+00	blood vessel development	P
GO:0001569	17	9.36E-01	1.00E+00	9.99E-01	1.00E+00	7.50E-01	1.00E+00	9.96E-01	1.00E+00	9.75E-01	1.00E+00	9.86E-01	1.00E+00	8.51E-01	1.00E+00	1.00E+00	1.00E+00	patterning of blood vessels	P
GO:0001570	25	4.71E-01	1.00E+00	3.74E-01	1.00E+00	6.95E-01	1.00E+00	4.18E-01	1.00E+00	3.97E-01	1.00E+00	4.62E-01	1.00E+00	2.47E-01	1.00E+00	3.65E-01	1.00E+00	vasculogenesis	P
GO:0001584	1078	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	rhodopsin-like receptor activity	F
GO:0001595	67	9.96E-01	1.00E+00	9.17E-01	1.00E+00	9.50E-01	1.00E+00	8.95E-01	1.00E+00	9.79E-01	1.00E+00	8.49E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	angiotensin receptor activity	F
GO:0001603	19	3.84E-01	1.00E+00	1.99E-01	1.00E+00	1.37E-01	1.00E+00	4.30E-01	1.00E+00	4.05E-01	1.00E+00	1.07E-01	1.00E+00	9.46E-01	1.00E+00	7.24E-01	1.00E+00	vasopressin-like receptor activity	F
GO:0001608	129	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.24E-01	1.00E+00	9.97E-01	1.00E+00	nucleotide receptor activity, G-protein coupl	F
GO:0001614	136	9.97E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	9.88E-01	1.00E+00	9.49E-01	1.00E+00	9.96E-01	1.00E+00	purinergic nucleotide receptor activity	F
GO:0001619	21	2.26E-01	1.00E+00	2.73E-01	1.00E+00	4.79E-01	1.00E+00	4.00E-01	1.00E+00	1.85E-01	1.00E+00	2.50E-01	1.00E+00	4.02E-01	1.00E+00	4.03E-01	1.00E+00	lysosphingolipid and lysophosphatidic acid r	F
GO:0001633	35	9.72E-01	1.00E+00	9.64E-01	1.00E+00	9.94E-01	1.00E+00	9.83E-01	1.00E+00	9.85E-01	1.00E+00	9.71E-01	1.00E+00	4.79E-01	1.00E+00	3.64E-01	1.00E+00	secretin-like receptor activity	F
GO:0001637	58	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.49E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein chemoattractant receptor activity	F
GO:0001649	46	6.92E-01	1.00E+00	7.51E-01	1.00E+00	9.91E-01	1.00E+00	7.33E-01	1.00E+00	4.20E-01	1.00E+00	8.61E-01	1.00E+00	8.33E-01	1.00E+00	1.50E-01	1.00E+00	osteoblast differentiation	P
GO:0001653	415	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity	F
GO:0001654	80	5.67E-01	1.00E+00	9.25E-01	1.00E+00	2.81E-01	1.00E+00	7.43E-01	1.00E+00	5.41E-01	1.00E+00	9.68E-01	1.00E+00	8.74E-01	1.00E+00	3.09E-01	1.00E+00	eye development	P
GO:0001655	82	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.56E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.51E-01	1.00E+00	urogenital system development	P
GO:0001656	41	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.08E-01	1.00E+00	metanephros development	P
GO:0001657	33	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.78E-01	1.00E+00	ureteric bud development	P
GO:0001658	20	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.98E-01	1.00E+00	6.63E-01	1.00E+00	ureteric bud branching	P
GO:0001659	227	1.86E-01	1.00E+00	2.94E-01	1.00E+00	2.18E-02	1.00E+00	1.73E-01	1.00E+00	4.57E-01	1.00E+00	3.54E-01	1.00E+00	2.23E-01	1.00E+00	6.59E-01	1.00E+00	thermoregulation	P
GO:0001662	10	6.94E-01	1.00E+00	6.36E-01	1.00E+00	2.70E-01	1.00E+00	6.62E-01	1.00E+00	9.55E-01	1.00E+00	5.42E-01	1.00E+00	5.80E-01	1.00E+00	5.03E-01	1.00E+00	behavioral fear response	P
GO:0001664	85	8.48E-01	1.00E+00	9.60E-01	1.00E+00	7.05E-01	1.00E+00	6.97E-01	1.00E+00	9.42E-01	1.00E+00	8.89E-01	1.00E+00	3.29E-01	1.00E+00	1.00E+00	1.00E+00	G-protein-coupled receptor binding	F
GO:0001666	75	1.62E-02	6.67E-01	2.26E-02	1.00E+00	8.83E-03	4.60E-01	3.38E-02	1.00E+00	2.63E-02	1.00E+00	5.37E-02	1.00E+00	2.47E-01	1.00E+00	1.30E-01	1.00E+00	response to hypoxia	P
GO:0001669	32	8.73E-01	1.00E+00	4.71E-01	1.00E+00	9.99E-01	1.00E+00	4.84E-01	1.00E+00	7.74E-01	1.00E+00	4.01E-01	1.00E+00	2.48E-01	1.00E+00	6.74E-01	1.00E+00	acrosome	C
GO:0001701	114	1.10E-03	9.60E-02	1.02E-02	5.18E-01	5.87E-02	1.00E+00	1.89E-02	1.00E+00	2.10E-03	2.85E-01	1.23E-02	7.39E-01	5.87E-03	3.57E-01	2.76E-01	1.00E+00	embryonic development (sensu Mammalia)	P
GO:0001702	14	2.02E-01	1.00E+00	2.89E-01	1.00E+00	4.68E-01	1.00E+00	4.84E-01	1.00E+00	1.92E-01	1.00E+00	2.14E-01	1.00E+00	5.72E-01	1.00E+00	3.75E-01	1.00E+00	gastrulation (sensu Deuterostomia)	P
GO:0001704	37	3.85E-01	1.00E+00	3.22E-01	1.00E+00	4.25E-01	1.00E+00	8.41E-01	1.00E+00	3.57E-01	1.00E+00	4.74E-01	1.00E+00	4.65E-01	1.00E+00	4.30E-02	1.00E+00	formation of primary germ layer	P
GO:0001707	33	2.59E-01	1.00E+00	2.03E-01	1.00E+00	3.83E-01	1.00E+00	6.22E-01	1.00E+00	2.35E-01	1.00E+00	3.16E-01	1.00E+00	3.83E-01	1.00E+00	4.60E-02	1.00E+00	mesoderm formation	P
GO:0001708	28	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-01	1.00E+00	8.98E-01	1.00E+00	cell fate specification	P
GO:0001709	35	9.72E-01	1.00E+00	9.92E-01	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	9.73E-01	1.00E+00	7.67E-01	1.00E+00	8.01E-01	1.00E+00	cell fate determination	P
GO:0001725	18	2.34E-02	1.00E+00	1.67E-02	1.00E+00	2.92E-02	1.00E+00	1.13E-01	1.00E+00	1.12E-02	5.39E-01	1.69E-02	8.60E-01	9.17E-01	1.00E+00	5.95E-01	1.00E+00	stress fiber	C
GO:0001726	46	1.57E-02	6.67E-01	4.30E-03	1.97E-01	1.10E-01	1.00E+00	6.23E-02	1.00E+00	7.56E-03	5.39E-01	1.16E-02	7.39E-01	3.00E-01	1.00E+00	1.66E-02	8.49E-01	ruffle	C
GO:0001727	26	2.76E-02	1.00E+00	2.33E-02	1.00E+00	3.13E-02	1.00E+00	8.18E-02	1.00E+00	1.06E-01	1.00E+00	3.68E-02	1.00E+00	1.51E-01	1.00E+00	1.55E-01	1.00E+00	lipid kinase activity	F
GO:0001739	12	1.68E-01	1.00E+00	4.46E-01	1.00E+00	6.12E-01	1.00E+00	8.93E-01	1.00E+00	2.42E-01	1.00E+00	4.21E-01	1.00E+00	1.30E-01	1.00E+00	3.20E-01	1.00E+00	sex chromatin	C
GO:0001750	13	9.91E-01	1.00E+00	6.59E-01	1.00E+00	4.26E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	4.84E-01	1.00E+00	9.91E-01	1.00E+00	5.29E-01	1.00E+00	photoreceptor outer segment	C
GO:0001755	19	9.68E-01	1.00E+00	9.14E-01	1.00E+00	8.57E-01	1.00E+00	9.92E-01	1.00E+00	9.87E-01	1.00E+00	8.10E-01	1.00E+00	6.54E-01	1.00E+00	8.78E-01	1.00E+00	neural crest cell migration	P
GO:0001756	28	7.38E-01	1.00E+00	8.34E-01	1.00E+00	4.24E-01	1.00E+00	7.92E-01	1.00E+00	7.15E-01	1.00E+00	8.14E-01	1.00E+00	9.55E-01	1.00E+00	6.46E-01	1.00E+00	somitogenesis	P
GO:0001759	13	7.62E-01	1.00E+00	9.91E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	5.49E-01	1.00E+00	9.50E-01	1.00E+00	9.16E-01	1.00E+00	9.67E-01	1.00E+00	induction of an organ	P
GO:0001763	61	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	morphogenesis of a branching structure	P
GO:0001764	60	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.85E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	9.95E-01	1.00E+00	neuron migration	P
GO:0001772	24	4.34E-02	1.00E+00	4.82E-01	1.00E+00	1.25E-02	5.32E-01	5.68E-01	1.00E+00	1.21E-01	1.00E+00	6.26E-01	1.00E+00	1.17E-01	1.00E+00	3.73E-01	1.00E+00	immunological synapse	C
GO:0001775	284	3.31E-02	1.00E+00	1.11E-02	6.77E-01	2.68E-02	1.00E+00	1.65E-02	8.18E-01	4.67E-02	1.00E+00	3.03E-02	1.00E+00	3.73E-01	1.00E+00	5.12E-02	1.00E+00	cell activation	P
GO:0001776	31	2.48E-02	1.00E+00	7.73E-02	1.00E+00	8.30E-02	1.00E+00	5.74E-02	1.00E+00	2.38E-02	1.00E+00	6.58E-02	1.00E+00	1.03E-01	1.00E+00	2.91E-01	1.00E+00	leukocyte homeostasis	P
GO:0001782	10	7.46E-02	1.00E+00	3.04E-01	1.00E+00	1.18E-01	1.00E+00	2.89E-01	1.00E+00	4.75E-02	1.00E+00	4.03E-01	1.00E+00	9.44E-01	1.00E+00	1.73E-01	1.00E+00	B cell homeostasis	P
GO:0001816	130	2.90E-01	1.00E+00	1.64E-01	1.00E+00	2.24E-01	1.00E+00	8.29E-02	1.00E+00	3.80E-01	1.00E+00	2.50E-01	1.00E+00	2.77E-01	1.00E+00	3.70E-01	1.00E+00	cytokine production	P

GO:0001817	18	6.05E-01	1.00E+00	7.90E-01	1.00E+00	5.63E-01	1.00E+00	2.06E-01	1.00E+00	6.42E-01	1.00E+00	8.80E-01	1.00E+00	3.16E-01	1.00E+00	9.64E-01	1.00E+00	regulation of cytokine production	P
GO:0001819	12	2.27E-01	1.00E+00	5.92E-01	1.00E+00	2.66E-01	1.00E+00	2.61E-01	1.00E+00	2.99E-01	1.00E+00	6.90E-01	1.00E+00	1.98E-01	1.00E+00	7.47E-01	1.00E+00	positive regulation of cytokine production	P
GO:0001822	72	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.27E-01	1.00E+00	kidney development	P
GO:0001824	33	3.32E-04	3.37E-02	1.42E-03	9.10E-02	1.98E-02	1.00E+00	6.81E-03	4.53E-01	4.11E-04	2.20E-02	5.92E-03	3.51E-01	2.99E-02	1.00E+00	2.22E-02	1.00E+00	blastocyst development	P
GO:0001825	12	4.30E-03	3.28E-01	5.14E-03	3.60E-01	6.16E-02	1.00E+00	2.47E-02	1.00E+00	2.17E-03	2.85E-01	4.13E-02	1.00E+00	8.42E-02	1.00E+00	1.80E-02	1.00E+00	blastocyst formation	P
GO:0001829	10	1.37E-02	6.67E-01	2.28E-02	1.00E+00	1.68E-01	1.00E+00	2.32E-02	1.00E+00	1.09E-02	5.39E-01	1.53E-01	1.00E+00	4.43E-02	1.00E+00	8.11E-03	4.81E-01	trophectodermal cell differentiation	P
GO:0001832	11	7.61E-02	1.00E+00	1.72E-01	1.00E+00	1.86E-01	1.00E+00	2.74E-01	1.00E+00	8.12E-02	1.00E+00	2.05E-01	1.00E+00	1.35E-01	1.00E+00	1.01E-01	1.00E+00	blastocyst growth	P
GO:0001836	16	1.87E-03	2.02E-01	8.55E-04	6.90E-02	2.11E-02	1.00E+00	1.45E-03	1.15E-01	1.57E-03	1.76E-01	7.44E-03	5.30E-01	3.23E-02	1.00E+00	9.02E-03	4.81E-01	release of cytochrome c from mitochondria	P
GO:0001837	13	7.40E-01	1.00E+00	4.32E-01	1.00E+00	7.85E-01	1.00E+00	4.79E-01	1.00E+00	7.67E-01	1.00E+00	4.69E-01	1.00E+00	7.26E-01	1.00E+00	2.55E-01	1.00E+00	epithelial to mesenchymal transition	P
GO:0001838	40	3.87E-01	1.00E+00	2.80E-01	1.00E+00	2.72E-01	1.00E+00	5.11E-01	1.00E+00	4.06E-01	1.00E+00	2.43E-01	1.00E+00	6.72E-01	1.00E+00	1.48E-01	1.00E+00	embryonic epithelial tube formation	P
GO:0001839	39	5.21E-01	1.00E+00	3.28E-01	1.00E+00	2.80E-01	1.00E+00	5.10E-01	1.00E+00	5.25E-01	1.00E+00	2.57E-01	1.00E+00	7.97E-01	1.00E+00	2.86E-01	1.00E+00	neural plate morphogenesis	P
GO:0001841	37	4.52E-01	1.00E+00	2.62E-01	1.00E+00	2.45E-01	1.00E+00	4.03E-01	1.00E+00	4.95E-01	1.00E+00	2.31E-01	1.00E+00	7.16E-01	1.00E+00	2.10E-01	1.00E+00	neural tube formation	P
GO:0001843	27	3.76E-01	1.00E+00	2.35E-01	1.00E+00	4.00E-02	1.00E+00	3.99E-01	1.00E+00	6.55E-01	1.00E+00	2.18E-01	1.00E+00	6.72E-01	1.00E+00	2.03E-01	1.00E+00	neural tube closure	P
GO:0001871	127	9.29E-01	1.00E+00	9.82E-01	1.00E+00	6.80E-01	1.00E+00	8.81E-01	1.00E+00	8.89E-01	1.00E+00	9.58E-01	1.00E+00	9.61E-01	1.00E+00	9.88E-01	1.00E+00	pattern binding	F
GO:0001889	26	2.16E-01	1.00E+00	5.65E-02	1.00E+00	4.81E-01	1.00E+00	8.22E-02	1.00E+00	2.47E-01	1.00E+00	9.02E-02	1.00E+00	1.35E-01	1.00E+00	1.44E-01	1.00E+00	liver development	P
GO:0001890	34	6.42E-02	1.00E+00	3.71E-02	1.00E+00	1.88E-01	1.00E+00	7.02E-02	1.00E+00	1.16E-01	1.00E+00	6.04E-02	1.00E+00	5.37E-02	1.00E+00	2.85E-01	1.00E+00	placenta development	P
GO:0001892	14	3.06E-02	1.00E+00	1.10E-02	6.77E-01	7.39E-02	1.00E+00	5.31E-03	3.46E-01	3.85E-02	1.00E+00	9.65E-02	1.00E+00	7.97E-02	1.00E+00	1.19E-01	1.00E+00	embryonic placenta development	P
GO:0001894	41	3.63E-02	1.00E+00	4.73E-02	1.00E+00	1.01E-01	1.00E+00	7.37E-02	1.00E+00	2.15E-02	1.00E+00	2.83E-02	1.00E+00	2.97E-01	1.00E+00	2.22E-01	1.00E+00	tissue homeostasis	P
GO:0001906	23	9.33E-01	1.00E+00	4.50E-01	1.00E+00	8.40E-01	1.00E+00	3.61E-01	1.00E+00	8.91E-01	1.00E+00	3.78E-01	1.00E+00	5.73E-01	1.00E+00	8.53E-01	1.00E+00	cell killing	P
GO:0001909	20	7.99E-01	1.00E+00	3.74E-01	1.00E+00	7.27E-01	1.00E+00	2.82E-01	1.00E+00	7.51E-01	1.00E+00	3.44E-01	1.00E+00	4.88E-01	1.00E+00	8.03E-01	1.00E+00	leukocyte mediated cytotoxicity	P
GO:0001910	12	9.66E-01	1.00E+00	9.18E-01	1.00E+00	9.50E-01	1.00E+00	3.45E-01	1.00E+00	9.17E-01	1.00E+00	9.19E-01	1.00E+00	6.51E-01	1.00E+00	9.89E-01	1.00E+00	regulation of leukocyte mediated cytotoxicity	P
GO:0001932	89	8.54E-01	1.00E+00	9.08E-01	1.00E+00	3.89E-01	1.00E+00	3.87E-01	1.00E+00	8.23E-01	1.00E+00	9.44E-01	1.00E+00	9.82E-01	1.00E+00	9.45E-01	1.00E+00	regulation of protein amino acid phosphoryl	P
GO:0001933	13	2.06E-02	1.00E+00	2.81E-02	1.00E+00	2.26E-03	2.48E-01	5.28E-02	1.00E+00	2.95E-02	1.00E+00	6.95E-02	1.00E+00	3.51E-01	1.00E+00	2.37E-01	1.00E+00	negative regulation of protein amino acid ph	P
GO:0001934	43	8.80E-01	1.00E+00	8.70E-01	1.00E+00	3.47E-01	1.00E+00	3.46E-01	1.00E+00	8.86E-01	1.00E+00	9.56E-01	1.00E+00	9.66E-01	1.00E+00	7.15E-01	1.00E+00	positive regulation of protein amino acid ph	P
GO:0001935	29	4.24E-01	1.00E+00	2.66E-01	1.00E+00	7.87E-01	1.00E+00	1.80E-01	1.00E+00	3.21E-01	1.00E+00	4.49E-01	1.00E+00	3.98E-01	1.00E+00	2.26E-01	1.00E+00	endothelial cell proliferation	P
GO:0001936	24	5.52E-01	1.00E+00	4.22E-01	1.00E+00	8.14E-01	1.00E+00	2.93E-01	1.00E+00	4.78E-01	1.00E+00	6.40E-01	1.00E+00	5.19E-01	1.00E+00	2.38E-01	1.00E+00	regulation of endothelial cell proliferation	P
GO:0001937	15	4.75E-01	1.00E+00	5.70E-01	1.00E+00	4.32E-01	1.00E+00	2.42E-01	1.00E+00	6.08E-01	1.00E+00	7.51E-01	1.00E+00	3.45E-01	1.00E+00	6.72E-01	1.00E+00	negative regulation of endothelial cell prolife	P
GO:0001938	10	7.76E-01	1.00E+00	2.83E-01	1.00E+00	9.90E-01	1.00E+00	3.14E-01	1.00E+00	4.61E-01	1.00E+00	5.00E-01	1.00E+00	8.21E-01	1.00E+00	3.70E-02	1.00E+00	positive regulation of endothelial cell prolife	P
GO:0001942	34	9.86E-01	1.00E+00	9.72E-01	1.00E+00	9.89E-01	1.00E+00	9.70E-01	1.00E+00	9.62E-01	1.00E+00	9.69E-01	1.00E+00	9.79E-01	1.00E+00	3.61E-01	1.00E+00	hair follicle development	P
GO:0001944	230	9.56E-01	1.00E+00	6.02E-01	1.00E+00	9.33E-01	1.00E+00	5.46E-01	1.00E+00	9.76E-01	1.00E+00	8.34E-01	1.00E+00	3.33E-01	1.00E+00	4.14E-02	1.00E+00	vasculature development	P
GO:0001947	15	3.02E-01	1.00E+00	2.59E-01	1.00E+00	4.83E-01	1.00E+00	2.24E-01	1.00E+00	3.71E-01	1.00E+00	3.44E-01	1.00E+00	1.23E-01	1.00E+00	2.81E-01	1.00E+00	heart looping	P
GO:0001948	14	3.20E-01	1.00E+00	6.47E-02	1.00E+00	1.05E-01	1.00E+00	5.52E-01	1.00E+00	5.21E-01	1.00E+00	4.74E-02	1.00E+00	3.15E-01	1.00E+00	3.24E-02	1.00E+00	glycoprotein binding	F
GO:0001952	18	7.98E-01	1.00E+00	6.19E-01	1.00E+00	6.40E-01	1.00E+00	3.89E-01	1.00E+00	7.02E-01	1.00E+00	7.67E-01	1.00E+00	9.58E-01	1.00E+00	4.03E-01	1.00E+00	regulation of cell-matrix adhesion	P
GO:0001974	14	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	7.82E-01	1.00E+00	8.39E-01	1.00E+00	blood vessel remodeling	P
GO:0001976	20	8.94E-01	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	9.69E-01	1.00E+00	8.82E-01	1.00E+00	1.00E+00	1.00E+00	1.39E-01	1.00E+00	6.58E-01	1.00E+00	fast regulation of arterial pressure	P
GO:0001990	17	9.47E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	9.20E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	2.40E-01	1.00E+00	6.21E-01	1.00E+00	regulation of blood pressure by hormones	P
GO:0002009	121	9.91E-01	1.00E+00	8.69E-01	1.00E+00	9.30E-01	1.00E+00	8.71E-01	1.00E+00	9.74E-01	1.00E+00	8.70E-01	1.00E+00	9.56E-01	1.00E+00	5.52E-01	1.00E+00	morphogenesis of an epithelium	P
GO:0002026	10	7.34E-01	1.00E+00	5.82E-01	1.00E+00	5.87E-01	1.00E+00	9.91E-01	1.00E+00	6.40E-01	1.00E+00	2.94E-01	1.00E+00	7.50E-01	1.00E+00	9.50E-01	1.00E+00	cardiac inotropy	P
GO:0002053	10	6.36E-01	1.00E+00	9.23E-01	1.00E+00	9.37E-01	1.00E+00	8.89E-01	1.00E+00	3.81E-01	1.00E+00	9.46E-01	1.00E+00	8.68E-01	1.00E+00	3.79E-01	1.00E+00	positive regulation of mesenchymal cell pro	P
GO:0002062	19	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	9.99E-01	1.00E+00	9.46E-01	1.00E+00	chondrocyte differentiation	P
GO:0002064	12	6.55E-01	1.00E+00	9.80E-01	1.00E+00	4.34E-01	1.00E+00	9.12E-01	1.00E+00	6.93E-01	1.00E+00	9.94E-01	1.00E+00	6.11E-01	1.00E+00	9.62E-01	1.00E+00	epithelial cell development	P
GO:0002088	12	5.66E-01	1.00E+00	6.66E-01	1.00E+00	2.46E-01	1.00E+00	5.07E-01	1.00E+00	8.28E-01	1.00E+00	6.38E-01	1.00E+00	3.54E-01	1.00E+00	8.17E-01	1.00E+00	lens development (sensu Vertebrata)	P
GO:0002200	29	3.06E-01	1.00E+00	9.50E-02	1.00E+00	5.29E-01	1.00E+00	2.63E-01	1.00E+00	1.72E-01	1.00E+00	7.11E-02	1.00E+00	9.36E-01	1.00E+00	5.50E-01	1.00E+00	somatic diversification of immune receptors	P
GO:0002204	24	3.70E-01	1.00E+00	8.52E-02	1.00E+00	5.33E-01	1.00E+00	2.44E-01	1.00E+00	2.26E-01	1.00E+00	6.59E-02	1.00E+00	9.92E-01	1.00E+00	5.55E-01	1.00E+00	somatic recombination of immunoglobulin g	P
GO:0002208	24	3.70E-01	1.00E+00	8.52E-02	1.00E+00	5.33E-01	1.00E+00	2.44E-01	1.00E+00	2.26E-01	1.00E+00	6.59E-02	1.00E+00	9.92E-01	1.00E+00	5.55E-01	1.00E+00	somatic diversification of immunoglobulins	P
GO:0002209	10	6.94E-01	1.00E+00	6.36E-01	1.00E+00	2.70E-01	1.00E+00	6.62E-01	1.00E+00	9.55E-01	1.00E+00	5.42E-01	1.00E+00	5.80E-01	1.00E+00	5.03E-01	1.00E+00	behavioral defense response	P
GO:0002217	572	1.00E+00	1.00E+00	9.55E-01	1.00E+00	9.99E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	9.12E-01	1.00E+00	9.85E-01	1.00E+00	9.24E-01	1.00E+00	physiological defense response	P
GO:0002228	16	7.90E-01	1.00E+00	4.29E-01	1.00E+00	6.82E-01	1.00E+00	6.47E-01	1.00E+00	8.04E-01	1.00E+00	3.42E-01	1.00E+00	3.19E-01	1.00E+00	6.64E-01	1.00E+00	natural killer cell mediated immunity	P
GO:0002245	547	9.90E-01	1.00E+00	5.06E-01	1.00E+00	8.23E-01	1.00E+00	3.75E-01	1.00E+00	9.93E-01	1.00E+00	4.95E-01	1.00E+00	9.03E-01	1.00E+00	6.02E-01	1.00E+00	physiological response to wounding	P
GO:0002250	151	5.50E-01	1.00E+00	2.70E-01	1.00E+00	4.90E-01	1.00E+00	4.29E-01	1.00E+00	5.49E-01	1.00E+00	1.93E-01	1.00E+00	5.56E-01	1.00E+00	7.43E-01	1.00E+00	adaptive immune response	P
GO:0002252	183	3.66E-01	1.00E+00	3.22E-01	1.00E+00	4.48E-01	1.00E+00	5.13E-01	1.00E+00	2.91E-01	1.00E+00	2.46E-01	1.00E+00	6.34E-01	1.00E+00	6.35E-01	1.00E+00	immune effector process	P
GO:0002253	76	2.96E-01	1.00E+00	4.44E-01	1.00E+00	5.70E-01	1.00E+00	5.73E-01	1.00E+00	1.85E-01	1.00E+00	4.58E-01	1.00E+00	6.90E-01	1.00E+00	2.53E-01	1.00E+00	activation of immune response	P
GO:0002260	23	3.63E-02	1.00E+00	8.32E-02	1.00E+00	7.37E-02	1.00E+00	8.19E-02	1.00E+00	2.71E-02	1.00E+00	6.72E-02	1.00E+00	4.18E-01	1.00E+00	2.20E-01	1.00E+00	lymphocyte homeostasis	P
GO:0002263	17	2.07E-01	1.00E+00	1.01E-01	1.00E+00	7.41E-02	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	7.10E-02	1.00E+00	5.04E-01	1.00E+00	2.81E-01	1.00E+00	cell activation during immune response	P
GO:0002274	36	4.63E-01	1.00E+00	1.87E-01	1.00E+00	2.77E-01	1.00E+00	8.05E-02	1.00E+00	4.23E-01	1.00E+00	2.93E-01	1.00E+00	9.20E-01	1.00E+00	2.36E-01	1.00E+00	myeloid leukocyte activation	P
GO:0002285	15	4.69E-01	1.00E+00	3.04E-01	1.00E+00	1.82E-01	1.00E+00	5.00E-01	1.00E+00	6.17E-01	1.00E+00	2.22E-01	1.00E+00	6.89E-01	1.00E+00	8.12E-01	1.00E+00	lymphocyte activation during immune respo	P
GO:0002286	13	5.38E-01	1.00E+00	2.98E-01	1.00E+00	2.53E-01	1.00E+00	5.03E-01	1.00E+00	6.23E-01	1.00E+00	2.03E-01	1.00E+00	8.54E-01	1.00E+00	8.19E-01	1.00E+00	T cell activation during immune response	P
GO:0002292	13	5.38E-01	1.00E+00	2.98E-01	1.00E+00	2.53E-01	1.00E+00	5.03E-01	1.00E+00	6.23E-01	1.00E+00	2.03E-01	1.00E+00	8.54E-01	1.00E+00	8.19E-01	1.00E+00	T cell differentiation during immune respons	P
GO:0002293	13	5.38E-01	1.00E+00	2.98E-01	1.00E+00	2.53E-01	1.00E+00	5.03E-01	1.00E+00	6.23E-01	1.00E+00	2.03E-01	1.00E+00	8.54E-01	1.00E+00	8.19E-01	1.00E+00	alpha-beta T cell differentiation during immu	P
GO:0002294	13	5.38E-01	1.00E+00	2.98E-01	1.00E+00	2.53E-01	1.00E+00	5.03E-01	1.00E+00	6.23E-01	1.00E+00	2.03E-01	1.00E+00	8.54E-01	1.00E+00	8.19E-01	1.00E+00	CD4-positive, alpha-beta T cell differentiatic	P
GO:0002366	17	2.07E-01	1.00E+00	1.01E-01	1.00E+00	7.41E-02	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	7.10E-02	1.00E+00	5.04E-01	1.00E+00	2.81E-01	1.00E+00	leukocyte activation during immune respons	P
GO:0002367	13	3.80E-01	1.00E+00	6.77E-01	1.00E+00	7.88E-01	1.00E+00	8.68E-01	1.00E+00	3.02E-01	1.00E+00	5.37E-01	1.00E+00	2.87E-01	1.00E+00	5.87E-01	1.00E+00	cytokine production during immune respons	P
GO:0002376	994	9.15E-01	1.00E+00	7.28E-01	1.00E+00	9.63E-01	1.00E+00	6.24E-01	1.00E+00	8.51E-01	1.00E+00	7.26E-01	1.00E+00	6.19E-01	1.00E+00	6.99E-01	1.00E+00	immune system process	P
GO:0002377	39	1.99E-01	1.00E+00	1.04E-01	1.00E+00	5.66E-01	1.00E+00	2.50E-01	1.00E+00	8.43E-02	1.00E+00	8.23E-02	1.00E+00	9.47E-01	1.00E+00	5.43E-01	1.00E+00	immunoglobulin production	P
GO:0002381	25	4.14E-01	1.00E+00	1.12E-01	1.00E+00	5.87E-01	1.00E+00	2.45E-01	1.00E+00	2.45E-01	1.00E+00	9.33E-02	1.00E+00	9.96E-01	1.00E+00	6.13E-01	1.00E+00	immunoglobulin production during immune	P
GO:0002429	37	9.30E-03	6.67E-01	2.31E-01	1.00E+00	8.56E-02	1.00E+00	2.85E-01	1.00E+00	8.92E-03	5.39E-01	2.39E-01	1.00E+00	3.73E-01	1.00E+00	3.04E-01	1.00E+00	immune response-activating cell surface re	P
GO:0002437	59	4.72E-01	1.00E+00	3.08E-01	1.00E+00	2.23E-01	1.00E+00	6.24E-01	1.00E+00	5.76E-01	1.00E+00	2.08E-01	1.00E+00	5.59E-01	1.00E+00	4.31E-01	1.00E+00	inflammatory response to antigenic stimulus	P
GO:0002438	54	5.07E-01	1.00E+00	3.69E-01	1.00E+00	1.86E-01	1.00E+00	5.72E-01	1.00E+00	6.72E-01	1.00E+00	2.54E-01	1.00E+00	5.45E-01	1.00E+00	6.86E-01	1.00E+00	acute inflammatory response to antigenic st	P
GO:0002440	47	2.72E-01	1.00E+00	2.02E-01	1.00E+00	6.47E-01	1.00E+00	5.42E-01	1.00E+00	1.22E-01	1.00E+00	1.08E-01	1.00E+00	9.62E-01	1.00E+00	7.18E-01	1.00E+00	production of molecular mediator of immune	P
GO:0002443	159	3.59E-01	1.00E+00	2.28E-01	1.00E+00	4.21E-01	1.00E+00	2.88E-01	1.00E+00	3.23E-01	1.00E+00	1.89E-01	1.00E+00	4.44E-01	1.00E+00	7.10E-01	1.00E+00	leukocyte mediated immunity	P
GO:0002444	12	1.15E-02	6.67E-01	1.63E-01	1.00E+00	5.53E-03	4.19E-01	2.02E-01	1.00E+00	1.22E-02	5.39E-01	2.37E-01	1.00E+00	8.00E-01	1.00E+00	1.64E-01	1.00E+00	myeloid leukocyte mediated immunity	P
GO:0002449	149	5.51E-01	1.00E+00	3.09E-01	1.00E+00	6.65E-01	1.00E+00	3.97E-01	1.00E+00	5.01E-01	1.00E+00	2.08E-01	1.00E+00	4.15E-01	1.00E+00	8.76E-01	1.00E+00	lymphocyte mediated immunity	P
GO:0002455	30	9.79E-01	1.00E+00	9.01E-01	1.00E+00	9.94E-01	1.00E+00	6.79E-01	1.00E+00	9.15E-01	1.00E+00	8.25E-01	1.00E+00	9.29E-01	1.00E+00	9.26E-01	1.00E+00	humoral immune response mediated by circ	P
GO:0002456	18	1.03E-01	1.00E+00	1.65E-01	1.00E+00	3.42E-01	1.00E+00	3.14E-01	1.00E+00	8.89E-02	1.00E+00	1.55E-01	1.00E+00	8.10E-02	1.00E+00	3.64E-01	1.00E+00	T cell mediated immunity	P
GO:0002460	151	5.50E-01	1.00E+00	2.70E-01	1.00E+00	4.90E-01	1.00E+00	4.29E-01	1.00E+00	5.49E-01	1.00E+00	1.93E-01	1.00E+00	5.56E-01	1.00E+00	7.43E-01	1.00E+00	adaptive immune response (sensu Gnathos	P

GO:0002474	16	9.28E-01	1.00E+00	7.37E-01	1.00E+00	9.08E-01	1.00E+00	3.00E-01	1.00E+00	9.17E-01	1.00E+00	6.91E-01	1.00E+00	5.47E-01	1.00E+00	9.92E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0002504	19	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.95E-01	1.00E+00	5.85E-01	1.00E+00	7.64E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0002520	264	1.99E-02	1.00E+00	4.54E-02	1.00E+00	7.91E-02	1.00E+00	2.07E-02	1.00E+00	9.61E-03	5.39E-01	1.63E-01	1.00E+00	5.70E-01	1.00E+00	9.12E-02	1.00E+00	immune system development	P
GO:0002521	138	3.18E-01	1.00E+00	2.35E-01	1.00E+00	2.56E-01	1.00E+00	3.68E-01	1.00E+00	2.81E-01	1.00E+00	3.30E-01	1.00E+00	8.48E-01	1.00E+00	6.97E-02	1.00E+00	leukocyte differentiation	P
GO:0002524	54	5.07E-01	1.00E+00	3.69E-01	1.00E+00	1.86E-01	1.00E+00	5.72E-01	1.00E+00	6.72E-01	1.00E+00	2.54E-01	1.00E+00	5.45E-01	1.00E+00	6.86E-01	1.00E+00	hypersensitivity	P
GO:0002526	126	9.91E-01	1.00E+00	9.14E-01	1.00E+00	9.00E-01	1.00E+00	8.75E-01	1.00E+00	9.97E-01	1.00E+00	8.52E-01	1.00E+00	6.26E-01	1.00E+00	9.52E-01	1.00E+00	acute inflammatory response	P
GO:0002541	36	9.93E-01	1.00E+00	8.64E-01	1.00E+00	9.91E-01	1.00E+00	8.52E-01	1.00E+00	9.73E-01	1.00E+00	7.80E-01	1.00E+00	9.20E-01	1.00E+00	6.29E-01	1.00E+00	activation of plasma proteins during acute i	P
GO:0002562	26	3.15E-01	1.00E+00	6.83E-02	1.00E+00	6.39E-01	1.00E+00	2.09E-01	1.00E+00	1.77E-01	1.00E+00	6.13E-02	1.00E+00	8.54E-01	1.00E+00	3.84E-01	1.00E+00	somatic diversification of immune receptors	P
GO:0002573	45	7.94E-01	1.00E+00	4.65E-01	1.00E+00	4.63E-01	1.00E+00	5.19E-01	1.00E+00	8.37E-01	1.00E+00	5.14E-01	1.00E+00	9.85E-01	1.00E+00	2.55E-01	1.00E+00	myeloid leukocyte differentiation	P
GO:0002682	121	5.15E-01	1.00E+00	3.31E-01	1.00E+00	7.21E-01	1.00E+00	4.77E-01	1.00E+00	3.91E-01	1.00E+00	4.50E-01	1.00E+00	6.21E-01	1.00E+00	8.95E-02	1.00E+00	regulation of immune system process	P
GO:0002683	15	1.78E-01	1.00E+00	1.08E-01	1.00E+00	1.21E-01	1.00E+00	2.17E-01	1.00E+00	2.79E-01	1.00E+00	1.24E-01	1.00E+00	8.91E-02	1.00E+00	1.14E-01	1.00E+00	negative regulation of immune system proc	P
GO:0002684	103	5.65E-01	1.00E+00	6.18E-01	1.00E+00	8.27E-01	1.00E+00	6.40E-01	1.00E+00	3.85E-01	1.00E+00	6.69E-01	1.00E+00	7.60E-01	1.00E+00	2.62E-01	1.00E+00	positive regulation of immune system proce	P
GO:0002697	20	5.96E-01	1.00E+00	6.92E-01	1.00E+00	4.59E-01	1.00E+00	7.19E-01	1.00E+00	6.46E-01	1.00E+00	5.96E-01	1.00E+00	5.18E-01	1.00E+00	9.26E-01	1.00E+00	regulation of immune effector process	P
GO:0002699	17	8.81E-01	1.00E+00	8.73E-01	1.00E+00	8.66E-01	1.00E+00	7.67E-01	1.00E+00	7.99E-01	1.00E+00	7.59E-01	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of immune effector proce	P
GO:0002703	19	4.95E-01	1.00E+00	6.51E-01	1.00E+00	3.92E-01	1.00E+00	6.94E-01	1.00E+00	5.47E-01	1.00E+00	5.50E-01	1.00E+00	4.48E-01	1.00E+00	9.00E-01	1.00E+00	regulation of leukocyte mediated immunity	P
GO:0002705	16	8.13E-01	1.00E+00	8.41E-01	1.00E+00	8.13E-01	1.00E+00	7.42E-01	1.00E+00	7.13E-01	1.00E+00	7.17E-01	1.00E+00	8.50E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of leukocyte mediated im	P
GO:0002706	19	4.95E-01	1.00E+00	6.51E-01	1.00E+00	3.92E-01	1.00E+00	6.94E-01	1.00E+00	5.47E-01	1.00E+00	5.50E-01	1.00E+00	4.48E-01	1.00E+00	9.00E-01	1.00E+00	regulation of lymphocyte mediated immunity	P
GO:0002708	16	8.13E-01	1.00E+00	8.41E-01	1.00E+00	8.13E-01	1.00E+00	7.42E-01	1.00E+00	7.13E-01	1.00E+00	7.17E-01	1.00E+00	8.50E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of lymphocyte mediated	P
GO:0002757	40	7.82E-03	6.34E-01	1.92E-01	1.00E+00	6.75E-02	1.00E+00	2.30E-01	1.00E+00	7.49E-03	5.39E-01	2.27E-01	1.00E+00	3.64E-01	1.00E+00	1.66E-01	1.00E+00	immune response-activating signal transdu	P
GO:0002761	22	9.67E-01	1.00E+00	7.60E-01	1.00E+00	9.60E-01	1.00E+00	7.66E-01	1.00E+00	9.32E-01	1.00E+00	7.33E-01	1.00E+00	9.65E-01	1.00E+00	6.22E-01	1.00E+00	regulation of myeloid leukocyte differentiatic	P
GO:0002762	13	9.78E-01	1.00E+00	6.19E-01	1.00E+00	9.95E-01	1.00E+00	7.22E-01	1.00E+00	9.58E-01	1.00E+00	5.07E-01	1.00E+00	8.71E-01	1.00E+00	8.43E-01	1.00E+00	negative regulation of myeloid leukocyte dif	P
GO:0002764	42	1.38E-02	6.67E-01	2.23E-01	1.00E+00	1.12E-01	1.00E+00	2.79E-01	1.00E+00	9.85E-03	5.39E-01	2.52E-01	1.00E+00	4.46E-01	1.00E+00	2.18E-01	1.00E+00	immune response-regulating signal transdu	P
GO:0002768	39	1.68E-02	6.67E-01	2.70E-01	1.00E+00	1.42E-01	1.00E+00	3.44E-01	1.00E+00	1.18E-02	5.39E-01	2.67E-01	1.00E+00	4.56E-01	1.00E+00	3.86E-01	1.00E+00	immune response-regulating cell surface re	P
GO:0002790	42	7.59E-01	1.00E+00	6.99E-01	1.00E+00	4.74E-01	1.00E+00	8.70E-01	1.00E+00	6.81E-01	1.00E+00	5.77E-01	1.00E+00	9.86E-01	1.00E+00	6.65E-01	1.00E+00	peptide secretion	P
GO:0002819	19	1.56E-01	1.00E+00	3.42E-01	1.00E+00	1.98E-01	1.00E+00	4.02E-01	1.00E+00	1.33E-01	1.00E+00	2.76E-01	1.00E+00	4.44E-01	1.00E+00	7.28E-01	1.00E+00	regulation of adaptive immune response	P
GO:0002821	14	3.22E-01	1.00E+00	5.03E-01	1.00E+00	5.86E-01	1.00E+00	4.01E-01	1.00E+00	1.88E-01	1.00E+00	4.46E-01	1.00E+00	8.48E-01	1.00E+00	8.67E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002822	19	1.56E-01	1.00E+00	3.42E-01	1.00E+00	1.98E-01	1.00E+00	4.02E-01	1.00E+00	1.33E-01	1.00E+00	2.76E-01	1.00E+00	4.44E-01	1.00E+00	7.28E-01	1.00E+00	regulation of adaptive immune response (se	P
GO:0002824	14	3.22E-01	1.00E+00	5.03E-01	1.00E+00	5.86E-01	1.00E+00	4.01E-01	1.00E+00	1.88E-01	1.00E+00	4.46E-01	1.00E+00	8.48E-01	1.00E+00	8.67E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0003674	16170	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.37E-34	0.00E+00	2.38E-44	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.90E-24	0.00E+00	8.51E-30	0.00E+00	molecular_function	F
GO:0003676	3675	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.80E-17	0.00E+00	4.03E-22	0.00E+00	2.80E-45	0.00E+00	0.00E+00	0.00E+00	4.03E-18	0.00E+00	2.92E-21	0.00E+00	nucleic acid binding	F
GO:0003677	2636	1.23E-20	0.00E+00	2.00E-26	0.00E+00	7.95E-07	2.42E-03	1.05E-10	0.00E+00	4.56E-20	0.00E+00	1.80E-23	0.00E+00	5.41E-10	0.00E+00	5.61E-11	7.71E-04	DNA binding	F
GO:0003678	37	3.53E-02	1.00E+00	9.75E-03	5.18E-01	2.11E-02	1.00E+00	1.73E-01	1.00E+00	1.96E-01	1.00E+00	4.98E-03	2.70E-01	3.17E-02	1.00E+00	4.23E-01	1.00E+00	DNA helicase activity	F
GO:0003682	123	3.52E-03	2.73E-01	2.39E-04	4.19E-02	1.79E-01	1.00E+00	1.32E-02	8.18E-01	3.71E-03	2.85E-01	4.13E-04	4.10E-02	4.42E-02	1.00E+00	4.76E-03	3.60E-01	chromatin binding	F
GO:0003684	53	3.02E-02	1.00E+00	4.45E-02	1.00E+00	4.34E-02	1.00E+00	1.62E-02	8.18E-01	9.81E-02	1.00E+00	1.09E-01	1.00E+00	3.36E-02	1.00E+00	2.98E-01	1.00E+00	damaged DNA binding	F
GO:0003688	11	9.75E-02	1.00E+00	1.96E-02	1.00E+00	3.22E-01	1.00E+00	5.86E-02	1.00E+00	5.15E-02	1.00E+00	1.24E-01	1.00E+00	6.48E-01	1.00E+00	1.87E-01	1.00E+00	DNA replication origin binding	F
GO:0003690	68	4.70E-03	3.28E-01	2.13E-02	1.00E+00	7.79E-02	1.00E+00	5.65E-02	1.00E+00	4.15E-03	2.85E-01	1.92E-02	1.00E+00	1.02E-01	1.00E+00	6.87E-01	1.00E+00	double-stranded DNA binding	F
GO:0003697	49	1.13E-03	9.60E-02	1.68E-04	1.50E-02	2.01E-02	1.00E+00	2.10E-02	1.00E+00	2.69E-03	2.85E-01	6.54E-04	5.49E-02	5.04E-02	1.00E+00	3.38E-03	1.85E-01	single-stranded DNA binding	F
GO:0003700	1045	1.12E-01	1.00E+00	2.70E-01	1.00E+00	1.84E-01	1.00E+00	1.93E-01	1.00E+00	1.01E-01	1.00E+00	3.96E-01	1.00E+00	4.18E-01	1.00E+00	3.34E-01	1.00E+00	transcription factor activity	F
GO:0003702	229	1.50E-04	2.50E-02	4.53E-04	6.90E-02	3.70E-03	3.27E-01	3.73E-04	4.20E-02	2.94E-04	1.70E-02	2.87E-03	2.39E-01	1.82E-02	9.11E-01	1.66E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003704	36	4.35E-01	1.00E+00	3.06E-01	1.00E+00	8.18E-01	1.00E+00	1.40E-01	1.00E+00	2.64E-01	1.00E+00	3.87E-01	1.00E+00	7.41E-01	1.00E+00	5.28E-01	1.00E+00	specific RNA polymerase II transcription fac	F
GO:0003705	34	5.78E-01	1.00E+00	2.88E-01	1.00E+00	7.89E-01	1.00E+00	3.13E-01	1.00E+00	5.28E-01	1.00E+00	2.74E-01	1.00E+00	3.33E-01	1.00E+00	8.29E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003707	56	5.02E-01	1.00E+00	6.20E-01	1.00E+00	1.52E-01	1.00E+00	1.62E-01	1.00E+00	5.24E-01	1.00E+00	7.87E-01	1.00E+00	9.02E-01	1.00E+00	8.02E-01	1.00E+00	steroid hormone receptor activity	F
GO:0003708	27	7.91E-01	1.00E+00	8.83E-01	1.00E+00	5.92E-01	1.00E+00	9.72E-01	1.00E+00	6.68E-01	1.00E+00	8.34E-01	1.00E+00	1.00E+00	1.00E+00	6.93E-01	1.00E+00	retinoic acid receptor activity	F
GO:0003709	10	2.02E-04	2.50E-02	2.32E-02	1.00E+00	4.40E-02	1.00E+00	2.14E-01	1.00E+00	8.61E-04	4.40E-02	3.15E-02	1.00E+00	1.65E-01	1.00E+00	1.31E-01	1.00E+00	RNA polymerase III transcription factor acti	F
GO:0003711	21	1.11E-02	6.67E-01	2.84E-02	1.00E+00	4.69E-02	1.00E+00	2.48E-01	1.00E+00	2.35E-02	1.00E+00	4.08E-02	1.00E+00	2.70E-02	1.00E+00	3.00E-02	1.00E+00	transcriptional elongation regulator activity	F
GO:0003712	310	4.45E-09	8.06E-04	5.29E-08	4.97E-03	7.62E-07	2.42E-03	3.13E-06	8.00E-03	2.29E-08	9.64E-04	3.06E-06	2.97E-03	4.36E-02	1.00E+00	3.04E-03	1.85E-01	transcription cofactor activity	F
GO:0003713	184	2.68E-07	1.95E-03	1.50E-07	4.97E-03	8.05E-07	2.42E-03	8.99E-05	1.20E-02	7.50E-06	2.88E-03	3.08E-06	2.97E-03	2.02E-02	9.11E-01	7.56E-03	4.81E-01	transcription coactivator activity	F
GO:0003714	119	1.66E-03	2.02E-01	9.14E-03	5.03E-01	3.50E-02	1.00E+00	3.61E-03	2.02E-01	4.67E-04	2.20E-02	4.76E-02	1.00E+00	3.74E-01	1.00E+00	3.76E-02	1.00E+00	transcription corepressor activity	F
GO:0003723	719	2.01E-35	0.00E+00	2.23E-34	0.00E+00	3.26E-19	0.00E+00	1.14E-14	0.00E+00	9.28E-31	0.00E+00	1.86E-29	0.00E+00	6.31E-10	0.00E+00	9.54E-13	0.00E+00	RNA binding	F
GO:0003724	27	5.45E-05	1.10E-02	9.31E-04	6.90E-02	5.03E-04	3.60E-02	1.18E-02	8.18E-01	1.10E-02	5.39E-01	3.35E-04	3.07E-02	3.29E-02	1.00E+00	5.92E-01	1.00E+00	RNA helicase activity	F
GO:0003725	35	6.79E-02	1.00E+00	4.60E-03	3.60E-01	1.74E-01	1.00E+00	4.85E-02	1.00E+00	9.76E-02	1.00E+00	1.69E-02	8.60E-01	1.30E-01	1.00E+00	2.79E-02	1.00E+00	double-stranded RNA binding	F
GO:0003727	23	3.81E-03	3.28E-01	3.06E-02	1.00E+00	5.69E-02	1.00E+00	2.40E-01	1.00E+00	8.09E-03	5.39E-01	3.80E-02	1.00E+00	1.87E-02	9.11E-01	3.32E-02	1.00E+00	single-stranded RNA binding	F
GO:0003729	48	2.87E-03	2.39E-01	1.11E-03	9.10E-02	2.45E-03	2.48E-01	2.31E-02	1.00E+00	1.19E-02	5.39E-01	8.11E-03	7.39E-01	7.04E-02	1.00E+00	2.50E-04	2.70E-02	mRNA binding	F
GO:0003735	291	1.44E-11	0.00E+00	5.86E-05	9.58E-03	3.22E-05	6.00E-03	9.93E-02	1.00E+00	1.07E-09	9.64E-04	5.13E-05	1.70E-02	1.37E-06	1.95E-03	5.13E-03	3.60E-01	structural constituent of ribosome	F
GO:0003743	63	1.99E-07	1.95E-03	6.71E-08	4.97E-03	2.01E-04	2.40E-02	2.00E-03	1.24E-01	5.90E-07	2.45E-03	1.25E-06	2.97E-03	1.00E-02	6.30E-01	1.42E-03	9.16E-02	translation initiation factor activity	F
GO:0003746	18	1.13E-01	1.00E+00	4.46E-02	1.00E+00	5.20E-01	1.00E+00	1.74E-01	1.00E+00	7.32E-02	1.00E+00	3.23E-02	1.00E+00	2.01E-01	1.00E+00	1.94E-01	1.00E+00	translation elongation factor activity	F
GO:0003755	44	1.21E-02	6.67E-01	7.29E-02	1.00E+00	2.59E-02	1.00E+00	2.67E-01	1.00E+00	5.20E-02	1.00E+00	6.74E-02	1.00E+00	9.55E-03	6.30E-01	3.43E-01	1.00E+00	peptidyl-prolyl cis-trans isomerase activity	F
GO:0003774	161	8.93E-03	6.34E-01	1.50E-04	1.50E-02	1.01E-03	9.80E-02	1.28E-03	1.15E-01	3.47E-02	1.00E+00	2.50E-04	2.60E-02	3.64E-01	1.00E+00	2.04E-01	1.00E+00	motor activity	F
GO:0003777	82	5.65E-03	3.50E-01	2.75E-02	1.00E+00	1.34E-03	9.80E-02	5.51E-03	3.46E-01	1.47E-02	1.00E+00	5.80E-02	1.00E+00	4.57E-01	1.00E+00	6.98E-01	1.00E+00	microtubule motor activity	F
GO:0003779	325	1.15E-02	6.67E-01	8.30E-05	1.00E-02	3.99E-04	3.60E-02	9.31E-03	7.13E-01	2.14E-02	1.00E+00	9.13E-05	1.70E-02	9.10E-01	1.00E+00	1.18E-02	6.47E-01	actin binding	F
GO:0003796	12	6.80E-01	1.00E+00	8.40E-01	1.00E+00	4.26E-01	1.00E+00	4.82E-01	1.00E+00	8.38E-01	1.00E+00	9.03E-01	1.00E+00	3.81E-01	1.00E+00	8.62E-01	1.00E+00	lysozyme activity	F
GO:0003823	62	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.20E-01	1.00E+00	9.38E-01	1.00E+00	antigen binding	F
GO:0003824	5697	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.28E-25	0.00E+00	7.25E-29	0.00E+00	3.64E-42	0.00E+00	0.00E+00	0.00E+00	1.19E-11	0.00E+00	9.15E-21	0.00E+00	catalytic activity	F
GO:0003840	13	1.98E-01	1.00E+00	3.01E-01	1.00E+00	2.39E-01	1.00E+00	5.66E-01	1.00E+00	2.34E-01	1.00E+00	2.46E-01	1.00E+00	4.60E-01	1.00E+00	3.63E-01	1.00E+00	gamma-glutamyltransferase activity	F
GO:0003854	17	8.71E-01	1.00E+00	1.00E+00	1.00E+00	8.01E-01	1.00E+00	9.98E-01	1.00E+00	9.52E-01	1.00E+00	9.99E-01	1.00E+00	3.73E-01	1.00E+00	9.42E-01	1.00E+00	3-beta-hydroxy-delta5-steroid dehydrogena	F
GO:0003887	30	2.56E-02	1.00E+00	5.95E-02	1.00E+00	2.91E-01	1.00E+00	5.95E-02	1.00E+00	2.76E-03	2.85E-01	9.32E-02	1.00E+00	9.87E-01	1.00E+00	2.70E-01	1.00E+00	DNA-directed DNA polymerase activity	F
GO:0003899	49	4.29E-04	3.37E-02	1.24E-03	9.10E-02	9.26E-03	4.60E-01	4.39E-03	3.46E-01	1.30E-02	1.00E+00	1.56E-02	7.63E-01	4.65E-04	6.50E-02	9.08E-02	1.00E+00	DNA-directed RNA polymerase activity	F
GO:0003916	22	6.00E-02	1.00E+00	5.53E-01	1.00E+00	2.43E-01	1.00E+00	1.49E-01	1.00E+00	1.17E-01	1.00E+00	6.76E-01	1.00E+00	1.45E-01	1.00E+00	8.57E-01	1.00E+00	DNA topoisomerase activity	F
GO:0003918	17	1.63E-01	1.00E+00	6.39E-01	1.00E+00	1.77E-01	1.00E+00	2.26E-01	1.00E+00	3.36E-01	1.00E+00	8.03E-01	1.00E+00	2.31E-01	1.00E+00	6.53E-01	1.00E+00	DNA topoisomerase (ATP-hydrolyzing) activ	F
GO:0003924	259	1.49E-06	1.95E-03	7.86E-05	1.00E-02	1.37E-02	6.93E-01	4.35E-02	1.00E+00	1.40E-06	2.60E-03	2.36E-05	7.63E-03	8.42E-05	2.50E-02	3.31E-02	1.00E+00	GTPase activity	F
GO:0003950	24	1.93E-01	1.00E+00	5.42E-02	1.00E+00	3.51E-01	1.00E+00	7.42E-03	4.55E-01	2.18E-01	1.00E+00	2.10E-01	1.00E+00	3.69E-01	1.00E+00	3.19E-01	1.00E+00	NAD+ ADP-ribosyltransferase activity	F
GO:0003954	45	3.52E-03	2.73E-01	3.45E-02	1.00E+00	6.59E-02	1.00E+00	1.29E-01	1.00E+00	6.96E-03	5.39E-01	8.39E-02	1.00E+00	4.53E-02	1.00E+00	7.89E-02	1.00E+00	NADH dehydrogenase activity	F
GO:0003993	16	1.07E-01	1.00E+00	3.20E-01	1.00E+00	4.23E-02	1.00E+00	6.68E-02	1.00E+00	1.47E-01	1.00E+00	6.89E-01	1.00E+00	3.00E-01	1.00E+00	5.66E-01	1.00E+00	acid phosphatase activity	F
GO:0003995	16	1.99E-01	1.00E+00	2.06E-01	1.00E+00	5.45E-02	1.00E+00	1.05E-01	1.00E+00	2.31E-01	1.00E+00	2.73E-01	1.00E+00	9.07E-01	1.00E+00	4.66E-01	1.00E+00	acyl-CoA dehydrogenase activity	F
GO:0004003	24	2.40E-01	1.00E+00	5.58E-02	1.00E+00	3.01E-01	1.00E+00	2.17E-01	1.00E+00	3.76E-01	1.00E+00	4.81E-02	1.00E+00	1.46E-01	1.00E+00	4.38E-01	1.00E+00	ATP-dependent DNA helicase activity	F

GO:0004004	19	6.64E-04	3.44E-02	4.64E-03	3.60E-01	1.01E-02	4.60E-01	1.39E-02	8.18E-01	3.30E-02	1.00E+00	3.73E-03	2.70E-01	1.51E-02	6.47E-01	3.20E-01	1.00E+00	ATP-dependent RNA helicase activity	F
GO:0004012	15	7.00E-01	1.00E+00	4.71E-01	1.00E+00	5.16E-01	1.00E+00	4.16E-01	1.00E+00	4.38E-01	1.00E+00	6.16E-01	1.00E+00	1.00E+00	1.00E+00	1.46E-01	1.00E+00	phospholipid-translocating ATPase activity	F
GO:0004016	11	7.48E-01	1.00E+00	9.86E-02	1.00E+00	8.14E-01	1.00E+00	6.77E-02	1.00E+00	4.88E-01	1.00E+00	7.87E-02	1.00E+00	9.28E-01	1.00E+00	5.92E-01	1.00E+00	adenylate cyclase activity	F
GO:0004022	33	7.91E-01	1.00E+00	6.18E-01	1.00E+00	8.35E-01	1.00E+00	5.17E-01	1.00E+00	8.04E-01	1.00E+00	7.04E-01	1.00E+00	1.15E-01	1.00E+00	1.51E-01	1.00E+00	alcohol dehydrogenase activity	F
GO:0004033	15	7.94E-01	1.00E+00	6.58E-01	1.00E+00	3.19E-01	1.00E+00	8.78E-01	1.00E+00	9.31E-01	1.00E+00	5.84E-01	1.00E+00	8.35E-01	1.00E+00	6.06E-01	1.00E+00	aldo-keto reductase activity	F
GO:0004065	12	5.20E-01	1.00E+00	4.14E-01	1.00E+00	2.92E-01	1.00E+00	2.55E-01	1.00E+00	8.27E-01	1.00E+00	3.29E-01	1.00E+00	4.78E-01	1.00E+00	1.00E+00	1.00E+00	arylsulfatase activity	F
GO:0004089	21	4.51E-02	1.00E+00	1.35E-01	1.00E+00	7.14E-02	1.00E+00	4.06E-02	1.00E+00	4.06E-02	1.00E+00	1.79E-01	1.00E+00	5.63E-01	1.00E+00	4.94E-01	1.00E+00	carbonate dehydratase activity	F
GO:0004091	23	1.04E-04	1.60E-02	4.29E-02	1.00E+00	7.76E-05	1.20E-02	9.23E-04	5.90E-02	8.30E-04	4.40E-02	2.81E-01	1.00E+00	5.96E-01	1.00E+00	1.05E-01	1.00E+00	carboxylesterase activity	F
GO:0004104	13	1.99E-01	1.00E+00	2.39E-01	1.00E+00	4.35E-02	1.00E+00	4.39E-02	1.00E+00	2.82E-01	1.00E+00	4.57E-01	1.00E+00	7.18E-01	1.00E+00	3.24E-01	1.00E+00	cholinesterase activity	F
GO:0004112	25	9.70E-01	1.00E+00	9.38E-01	1.00E+00	9.12E-01	1.00E+00	6.94E-01	1.00E+00	9.58E-01	1.00E+00	9.59E-01	1.00E+00	8.95E-01	1.00E+00	9.48E-01	1.00E+00	cyclic-nucleotide phosphodiesterase activity	F
GO:0004114	24	9.85E-01	1.00E+00	9.98E-01	1.00E+00	9.39E-01	1.00E+00	9.75E-01	1.00E+00	9.84E-01	1.00E+00	9.96E-01	1.00E+00	8.69E-01	1.00E+00	9.98E-01	1.00E+00	3',5'-cyclic-nucleotide phosphodiesterase ac	F
GO:0004129	28	2.16E-01	1.00E+00	6.64E-02	1.00E+00	1.17E-01	1.00E+00	1.83E-01	1.00E+00	2.84E-01	1.00E+00	7.30E-02	1.00E+00	8.97E-01	1.00E+00	1.47E-01	1.00E+00	cytochrome-c oxidase activity	F
GO:0004143	15	6.19E-01	1.00E+00	6.29E-01	1.00E+00	3.18E-01	1.00E+00	9.11E-01	1.00E+00	5.97E-01	1.00E+00	4.20E-01	1.00E+00	9.82E-01	1.00E+00	5.46E-01	1.00E+00	diacylglycerol kinase activity	F
GO:0004175	459	5.29E-02	1.00E+00	8.45E-03	5.03E-01	7.65E-02	1.00E+00	7.90E-02	1.00E+00	7.22E-02	1.00E+00	1.23E-02	7.39E-01	1.69E-01	1.00E+00	2.03E-02	1.00E+00	endopeptidase activity	F
GO:0004176	19	2.31E-02	1.00E+00	4.18E-01	1.00E+00	2.62E-02	1.00E+00	8.71E-01	1.00E+00	5.03E-02	1.00E+00	3.69E-01	1.00E+00	3.60E-02	1.00E+00	2.14E-01	1.00E+00	ATP-dependent peptidase activity	F
GO:0004177	46	2.58E-01	1.00E+00	5.81E-02	1.00E+00	3.31E-01	1.00E+00	5.33E-02	1.00E+00	3.44E-01	1.00E+00	1.08E-01	1.00E+00	1.63E-01	1.00E+00	1.16E-01	1.00E+00	aminopeptidase activity	F
GO:0004179	11	6.28E-01	1.00E+00	2.00E-01	1.00E+00	9.45E-01	1.00E+00	2.76E-01	1.00E+00	5.55E-01	1.00E+00	3.54E-01	1.00E+00	2.65E-01	1.00E+00	8.43E-02	1.00E+00	membrane alanyl aminopeptidase activity	F
GO:0004180	43	9.37E-01	1.00E+00	8.91E-01	1.00E+00	7.06E-01	1.00E+00	8.93E-01	1.00E+00	9.46E-01	1.00E+00	8.92E-01	1.00E+00	7.39E-01	1.00E+00	6.16E-01	1.00E+00	carboxypeptidase activity	F
GO:0004181	30	9.79E-01	1.00E+00	9.79E-01	1.00E+00	5.76E-01	1.00E+00	9.20E-01	1.00E+00	9.97E-01	1.00E+00	9.77E-01	1.00E+00	7.79E-01	1.00E+00	7.71E-01	1.00E+00	metallocarboxypeptidase activity	F
GO:0004182	25	9.70E-01	1.00E+00	9.60E-01	1.00E+00	6.12E-01	1.00E+00	9.04E-01	1.00E+00	9.96E-01	1.00E+00	9.23E-01	1.00E+00	6.94E-01	1.00E+00	8.83E-01	1.00E+00	carboxypeptidase A activity	F
GO:0004185	10	5.63E-01	1.00E+00	4.36E-01	1.00E+00	3.35E-01	1.00E+00	8.12E-01	1.00E+00	4.26E-01	1.00E+00	3.11E-01	1.00E+00	1.00E+00	1.00E+00	5.53E-01	1.00E+00	serine carboxypeptidase activity	F
GO:0004190	34	3.32E-02	1.00E+00	5.42E-02	1.00E+00	4.20E-01	1.00E+00	4.99E-01	1.00E+00	2.02E-02	1.00E+00	2.42E-02	1.00E+00	4.15E-02	1.00E+00	2.42E-01	1.00E+00	aspartic-type endopeptidase activity	F
GO:0004194	11	1.08E-01	1.00E+00	4.53E-01	1.00E+00	5.46E-01	1.00E+00	3.99E-01	1.00E+00	1.07E-01	1.00E+00	1.82E-01	1.00E+00	2.82E-01	1.00E+00	1.00E+00	1.00E+00	pepsin A activity	F
GO:0004197	89	1.36E-01	1.00E+00	2.74E-02	1.00E+00	1.18E-01	1.00E+00	1.68E-02	8.18E-01	1.08E-01	1.00E+00	5.91E-02	1.00E+00	5.06E-01	1.00E+00	2.67E-01	1.00E+00	cysteine-type endopeptidase activity	F
GO:0004198	16	3.98E-01	1.00E+00	4.29E-01	1.00E+00	3.83E-01	1.00E+00	2.65E-01	1.00E+00	2.96E-01	1.00E+00	4.93E-01	1.00E+00	7.36E-01	1.00E+00	6.35E-01	1.00E+00	calpain activity	F
GO:0004221	77	5.20E-01	1.00E+00	3.51E-02	1.00E+00	5.07E-01	1.00E+00	4.27E-02	1.00E+00	4.90E-01	1.00E+00	4.76E-02	1.00E+00	5.51E-01	1.00E+00	3.58E-01	1.00E+00	ubiquitin thiolesterase activity	F
GO:0004222	107	8.65E-01	1.00E+00	6.26E-01	1.00E+00	1.06E-01	1.00E+00	9.05E-01	1.00E+00	9.73E-01	1.00E+00	4.02E-01	1.00E+00	9.60E-01	1.00E+00	7.40E-01	1.00E+00	metalloendopeptidase activity	F
GO:0004252	207	9.64E-02	1.00E+00	1.31E-01	1.00E+00	3.43E-01	1.00E+00	1.74E-01	1.00E+00	8.51E-02	1.00E+00	2.66E-01	1.00E+00	1.02E-01	1.00E+00	1.55E-02	8.49E-01	serine-type endopeptidase activity	F
GO:0004289	25	2.19E-01	1.00E+00	2.82E-01	1.00E+00	2.16E-01	1.00E+00	2.71E-01	1.00E+00	2.20E-01	1.00E+00	4.29E-01	1.00E+00	4.42E-01	1.00E+00	1.42E-01	1.00E+00	subtilase activity	F
GO:0004298	21	1.03E-01	1.00E+00	1.70E-02	1.00E+00	6.00E-01	1.00E+00	8.05E-02	1.00E+00	1.09E-01	1.00E+00	2.06E-02	1.00E+00	4.18E-02	1.00E+00	5.55E-02	1.00E+00	threonine endopeptidase activity	F
GO:0004303	11	7.31E-01	1.00E+00	1.90E-01	1.00E+00	6.79E-01	1.00E+00	1.41E-01	1.00E+00	6.65E-01	1.00E+00	2.61E-01	1.00E+00	5.33E-01	1.00E+00	8.01E-02	1.00E+00	estradiol 17-beta-dehydrogenase activity	F
GO:0004364	22	8.17E-01	1.00E+00	9.79E-01	1.00E+00	3.76E-01	1.00E+00	9.36E-01	1.00E+00	9.18E-01	1.00E+00	9.95E-01	1.00E+00	8.59E-01	1.00E+00	1.35E-01	1.00E+00	glutathione transferase activity	F
GO:0004385	10	9.36E-01	1.00E+00	1.97E-01	1.00E+00	7.49E-01	1.00E+00	4.06E-02	1.00E+00	9.57E-01	1.00E+00	7.70E-01	1.00E+00	5.70E-01	1.00E+00	2.86E-01	1.00E+00	guanylate kinase activity	F
GO:0004386	146	1.69E-07	1.95E-03	6.19E-09	4.97E-03	2.81E-07	2.42E-03	4.03E-05	8.00E-03	4.87E-04	2.20E-02	2.23E-08	8.37E-04	3.03E-05	5.44E-03	1.50E-03	9.16E-02	helicase activity	F
GO:0004402	27	2.98E-03	2.39E-01	6.82E-03	3.60E-01	3.24E-02	1.00E+00	3.11E-01	1.00E+00	1.12E-02	5.39E-01	9.28E-03	7.39E-01	1.81E-02	9.11E-01	1.84E-02	1.00E+00	histone acetyltransferase activity	F
GO:0004407	19	2.47E-01	1.00E+00	3.57E-01	1.00E+00	4.57E-01	1.00E+00	7.40E-01	1.00E+00	1.38E-01	1.00E+00	2.19E-01	1.00E+00	5.77E-01	1.00E+00	3.46E-01	1.00E+00	histone deacetylase activity	F
GO:0004428	41	6.98E-04	3.44E-02	8.17E-04	6.90E-02	7.22E-03	4.60E-01	1.09E-04	1.20E-02	6.15E-03	5.39E-01	2.08E-02	1.00E+00	1.13E-02	6.30E-01	5.43E-03	3.60E-01	inositol or phosphatidylinositol kinase activit	F
GO:0004434	26	9.64E-01	1.00E+00	9.95E-01	1.00E+00	9.50E-01	1.00E+00	9.89E-01	1.00E+00	9.80E-01	1.00E+00	9.65E-01	1.00E+00	2.30E-01	1.00E+00	1.00E+00	1.00E+00	inositol or phosphatidylinositol phosphodies	F
GO:0004435	26	9.64E-01	1.00E+00	9.95E-01	1.00E+00	9.50E-01	1.00E+00	9.89E-01	1.00E+00	9.80E-01	1.00E+00	9.65E-01	1.00E+00	2.30E-01	1.00E+00	1.00E+00	1.00E+00	phosphoinositide phospholipase C activity	F
GO:0004437	37	5.70E-01	1.00E+00	1.01E-01	1.00E+00	6.91E-01	1.00E+00	5.10E-01	1.00E+00	7.97E-01	1.00E+00	7.78E-02	1.00E+00	1.24E-02	6.30E-01	1.35E-01	1.00E+00	inositol or phosphatidylinositol phosphatase	F
GO:0004467	10	6.18E-01	1.00E+00	5.72E-01	1.00E+00	8.48E-01	1.00E+00	7.08E-01	1.00E+00	5.67E-01	1.00E+00	4.50E-01	1.00E+00	3.04E-01	1.00E+00	6.03E-01	1.00E+00	long-chain-fatty-acid-CoA ligase activity	F
GO:0004468	27	2.98E-03	2.39E-01	6.82E-03	3.60E-01	3.24E-02	1.00E+00	3.11E-01	1.00E+00	1.12E-02	5.39E-01	9.28E-03	7.39E-01	1.81E-02	9.11E-01	1.84E-02	1.00E+00	lysine N-acetyltransferase activity	F
GO:0004497	136	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.92E-01	1.00E+00	9.95E-01	1.00E+00	monooxygenase activity	F
GO:0004499	21	6.35E-01	1.00E+00	6.70E-01	1.00E+00	6.91E-01	1.00E+00	8.89E-01	1.00E+00	6.02E-01	1.00E+00	4.66E-01	1.00E+00	6.32E-01	1.00E+00	9.94E-01	1.00E+00	dimethylaniline monooxygenase (N-oxide-fo	F
GO:0004518	153	3.91E-04	3.37E-02	1.49E-02	1.00E+00	5.24E-03	4.19E-01	1.40E-01	1.00E+00	1.06E-03	7.80E-02	4.73E-03	2.70E-01	1.86E-01	1.00E+00	4.27E-01	1.00E+00	nuclease activity	F
GO:0004519	93	1.64E-02	6.67E-01	5.51E-02	1.00E+00	6.78E-02	1.00E+00	3.00E-01	1.00E+00	1.37E-02	1.00E+00	2.41E-02	1.00E+00	7.19E-01	1.00E+00	3.15E-01	1.00E+00	endonuclease activity	F
GO:0004520	19	1.43E-01	1.00E+00	4.71E-01	1.00E+00	1.25E-01	1.00E+00	6.91E-01	1.00E+00	1.65E-01	1.00E+00	4.18E-01	1.00E+00	4.78E-01	1.00E+00	3.68E-01	1.00E+00	endodeoxyribonuclease activity	F
GO:0004521	43	2.96E-01	1.00E+00	4.58E-02	1.00E+00	5.28E-01	1.00E+00	4.28E-01	1.00E+00	1.53E-01	1.00E+00	1.04E-02	7.39E-01	9.31E-01	1.00E+00	4.00E-01	1.00E+00	endoribonuclease activity	F
GO:0004522	17	9.88E-01	1.00E+00	8.05E-01	1.00E+00	9.75E-01	1.00E+00	9.84E-01	1.00E+00	8.49E-01	1.00E+00	2.38E-01	1.00E+00	8.39E-01	1.00E+00	9.19E-01	1.00E+00	pancreatic ribonuclease activity	F
GO:0004526	11	1.99E-02	1.00E+00	1.28E-01	1.00E+00	3.59E-02	1.00E+00	7.31E-02	1.00E+00	1.83E-02	1.00E+00	2.14E-01	1.00E+00	6.65E-01	1.00E+00	2.37E-01	1.00E+00	ribonuclease P activity	F
GO:0004527	53	8.59E-02	1.00E+00	2.29E-01	1.00E+00	1.16E-01	1.00E+00	3.26E-01	1.00E+00	1.49E-01	1.00E+00	1.81E-01	1.00E+00	2.18E-01	1.00E+00	5.21E-01	1.00E+00	exonuclease activity	F
GO:0004529	10	9.65E-01	1.00E+00	9.06E-01	1.00E+00	3.21E-01	1.00E+00	6.09E-01	1.00E+00	1.00E+00	1.00E+00	8.95E-01	1.00E+00	8.74E-01	1.00E+00	8.86E-01	1.00E+00	exodeoxyribonuclease activity	F
GO:0004532	13	7.43E-03	6.34E-01	2.04E-01	1.00E+00	6.29E-02	1.00E+00	2.27E-01	1.00E+00	8.49E-03	5.39E-01	4.99E-01	1.00E+00	1.08E-01	1.00E+00	1.17E-01	1.00E+00	exoribonuclease activity	F
GO:0004536	33	5.18E-02	1.00E+00	2.32E-01	1.00E+00	2.74E-02	1.00E+00	3.32E-01	1.00E+00	1.15E-01	1.00E+00	3.05E-01	1.00E+00	1.68E-01	1.00E+00	2.05E-01	1.00E+00	deoxyribonuclease activity	F
GO:0004540	64	2.95E-02	1.00E+00	2.25E-02	1.00E+00	1.52E-01	1.00E+00	3.42E-01	1.00E+00	1.84E-02	1.00E+00	7.49E-03	5.30E-01	7.24E-01	1.00E+00	2.50E-01	1.00E+00	ribonuclease activity	F
GO:0004549	13	2.26E-02	1.00E+00	5.01E-02	1.00E+00	5.72E-02	1.00E+00	8.86E-02	1.00E+00	1.42E-02	1.00E+00	6.62E-02	1.00E+00	7.98E-01	1.00E+00	1.91E-01	1.00E+00	tRNA-specific ribonuclease activity	F
GO:0004550	11	2.48E-02	1.00E+00	1.66E-01	1.00E+00	2.36E-02	1.00E+00	1.63E-01	1.00E+00	3.63E-02	1.00E+00	2.35E-01	1.00E+00	1.88E-01	1.00E+00	2.38E-01	1.00E+00	nucleoside diphosphate kinase activity	F
GO:0004553	130	2.34E-01	1.00E+00	1.23E-01	1.00E+00	5.14E-01	1.00E+00	3.53E-01	1.00E+00	1.61E-01	1.00E+00	1.12E-01	1.00E+00	3.44E-01	1.00E+00	1.82E-01	1.00E+00	hydrolase activity, hydrolyzing O-glycosyl co	F
GO:0004601	47	7.16E-01	1.00E+00	7.96E-01	1.00E+00	6.76E-01	1.00E+00	6.84E-01	1.00E+00	5.11E-01	1.00E+00	8.59E-01	1.00E+00	9.88E-01	1.00E+00	6.52E-01	1.00E+00	peroxidase activity	F
GO:0004602	10	3.68E-01	1.00E+00	4.42E-01	1.00E+00	2.00E-01	1.00E+00	4.43E-01	1.00E+00	3.91E-01	1.00E+00	5.05E-01	1.00E+00	5.78E-01	1.00E+00	2.50E-01	1.00E+00	glutathione peroxidase activity	F
GO:0004620	90	8.39E-01	1.00E+00	9.06E-01	1.00E+00	3.40E-01	1.00E+00	9.90E-01	1.00E+00	9.39E-01	1.00E+00	7.46E-01	1.00E+00	4.20E-01	1.00E+00	6.22E-01	1.00E+00	phospholipase activity	F
GO:0004622	11	9.54E-01	1.00E+00	9.49E-01	1.00E+00	4.28E-01	1.00E+00	9.68E-01	1.00E+00	8.79E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	2.16E-01	1.00E+00	lysophospholipase activity	F
GO:0004623	39	8.39E-01	1.00E+00	6.62E-01	1.00E+00	3.38E-01	1.00E+00	8.31E-01	1.00E+00	8.94E-01	1.00E+00	5.26E-01	1.00E+00	8.74E-01	1.00E+00	4.72E-01	1.00E+00	phospholipase A2 activity	F
GO:0004629	35	9.73E-01	1.00E+00	9.83E-01	1.00E+00	9.42E-01	1.00E+00	9.79E-01	1.00E+00	9.90E-01	1.00E+00	9.39E-01	1.00E+00	1.61E-01	1.00E+00	9.86E-01	1.00E+00	phospholipase C activity	F
GO:0004653	18	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.27E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	polypeptide N-acetylgalactosaminyltransfer	F
GO:0004659	14	2.14E-01	1.00E+00	1.16E-01	1.00E+00	2.94E-01	1.00E+00	1.12E-01	1.00E+00	3.20E-01	1.00E+00	2.09E-01	1.00E+00	2.22E-01	1.00E+00	2.19E-01	1.00E+00	prenyltransferase activity	F
GO:0004672	655	3.21E-04	3.37E-02	9.37E-11	0.00E+00	2.83E-02	1.00E+00	4.73E-07	1.96E-03	1.16E-04	1.70E-02	9.18E-09	8.37E-04	1.63E-01	1.00E+00	5.75E-05	9.00E-03	protein kinase activity	F
GO:0004673	13	2.63E-01	1.00E+00	5.31E-01	1.00E+00	2.31E-01	1.00E+00	5.59E-01	1.00E+00	1.78E-01	1.00E+00	7.09E-01	1.00E+00	9.39E-01	1.00E+00	5.66E-02	1.00E+00	protein histidine kinase activity	F
GO:0004674	534	1.09E-06	1.95E-03	7.82E-15	0.00E+00	2.11E-03	2.48E-01	1.27E-10	0.00E+00	1.13E-06	2.60E-03	2.79E-12	0.00E+00	2.62E-02	1.00E+00	5.92E-05	9.00E-03	protein serine/threonine kinase activity	F
GO:0004675	15	8.19E-01	1.00E+00	4.38E-01	1.00E+00	9.94E-01	1.00E+00	2.79E-01	1.00E+00	6.68E-01	1.00E+00	6.39E-01	1.00E+00	5.46E-01	1.00E+00	1.81E-01	1.00E+00	transmembrane receptor protein serine/thre	F
GO:0004683	28	4.89E-01	1.00E+00	1.12E-01	1.00E+00	7.15E-01	1.00E+00	6.06E-01	1.00E+00	3.87E-01	1.00E+00	5.35E-02	1.00E+00	7.19E-01	1.00E+00	3.64E-01	1.00E+00	calmodulin regulated protein kinase activity	F
GO:0004689	20	6.37E-01	1.00E+00	4.44E-01	1.00E+00	9.29E-01	1.00E+00	8.01E-01	1.00E+00	5.04E-01	1.00E+00	3.83E-01	1.00E+00	7.88E-01	1.00E+00	2.37E-01	1.00E+00	phosphorylase kinase activity	F
GO:0004690	10	4.28E-01	1.00E+00	5.41E-01	1.00E+00	1.76E-01	1.00E+00	3.51E-01	1.00E+00	5.94E-01	1.00E+00	7.67E-01	1.00E+00	5.97E-01	1.00E+00	2.03E-01	1.00E+00	cyclic nucleotide-dependent protein kinase	F
GO:0004693	28	5.80E-03	3.50E-01	1.52E-03	9.10E-02	1.28E-01	1.00E+00	1.17E-01	1.00E+00	9.05E-03	5.39E-01	6.54E-04	5.49E-02	7.74E-02	1.00E+00	1.78E-01	1.00E+00	cyclin-dependent protein kinase activity	F
GO:0004697	15	4.66E-01	1.00E+00	1.05E-01	1.00E+00	5.59E-01	1.00E+00	3.26E-01	1.00E+00	4.71E-01	1.00E+00	7.08E-02	1.00E+00	5.43E-01	1.00E+00	3.36E-01	1.00E+00	protein kinase C activity	F

GO:0004702	58	6.66E-02	1.00E+00	5.17E-02	1.00E+00	3.68E-01	1.00E+00	8.74E-03	7.13E-01	3.76E-02	1.00E+00	1.35E-01	1.00E+00	1.65E-01	1.00E+00	2.40E-01	1.00E+00	receptor signaling protein serine/threonine k	F
GO:0004707	19	7.68E-02	1.00E+00	1.48E-02	1.00E+00	2.19E-01	1.00E+00	3.35E-02	1.00E+00	8.26E-02	1.00E+00	1.27E-02	7.39E-01	4.07E-02	1.00E+00	1.66E-01	1.00E+00	MAP kinase activity	F
GO:0004708	13	7.42E-01	1.00E+00	2.39E-01	1.00E+00	6.04E-01	1.00E+00	1.88E-01	1.00E+00	6.47E-01	1.00E+00	3.03E-01	1.00E+00	9.89E-01	1.00E+00	3.08E-01	1.00E+00	MAP kinase kinase activity	F
GO:0004709	18	1.86E-01	1.00E+00	5.89E-01	1.00E+00	1.06E-01	1.00E+00	6.33E-02	1.00E+00	2.00E-01	1.00E+00	9.15E-01	1.00E+00	8.95E-01	1.00E+00	8.95E-01	1.00E+00	MAP kinase kinase kinase activity	F
GO:0004712	14	7.94E-01	1.00E+00	2.83E-01	1.00E+00	6.00E-01	1.00E+00	1.91E-01	1.00E+00	7.06E-01	1.00E+00	3.84E-01	1.00E+00	9.95E-01	1.00E+00	2.62E-01	1.00E+00	protein threonine/tyrosine kinase activity	F
GO:0004713	552	3.32E-03	2.73E-01	3.48E-10	0.00E+00	1.17E-01	1.00E+00	1.60E-06	2.00E-03	9.18E-04	4.40E-02	1.05E-08	8.37E-04	2.29E-01	1.00E+00	1.33E-04	2.00E-02	protein-tyrosine kinase activity	F
GO:0004714	120	9.99E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	9.09E-01	1.00E+00	8.91E-01	1.00E+00	6.33E-01	1.00E+00	transmembrane receptor protein tyrosine ki	F
GO:0004715	39	2.20E-01	1.00E+00	5.35E-02	1.00E+00	2.68E-01	1.00E+00	6.66E-03	4.53E-01	1.76E-01	1.00E+00	1.18E-01	1.00E+00	5.07E-01	1.00E+00	5.39E-01	1.00E+00	non-membrane spanning protein tyrosine ki	F
GO:0004716	12	1.88E-01	1.00E+00	2.04E-02	1.00E+00	4.96E-01	1.00E+00	9.53E-03	7.13E-01	1.21E-01	1.00E+00	3.01E-02	1.00E+00	1.58E-01	1.00E+00	2.21E-01	1.00E+00	receptor signaling protein tyrosine kinase a	F
GO:0004721	174	1.43E-02	6.67E-01	2.56E-05	9.58E-03	6.47E-02	1.00E+00	1.81E-03	1.24E-01	2.33E-02	1.00E+00	3.06E-05	1.20E-02	1.83E-01	1.00E+00	2.30E-02	1.00E+00	phosphoprotein phosphatase activity	F
GO:0004722	43	4.99E-02	1.00E+00	5.79E-04	6.90E-02	7.74E-02	1.00E+00	5.50E-03	3.46E-01	8.59E-02	1.00E+00	1.23E-03	6.40E-02	2.88E-01	1.00E+00	1.05E-01	1.00E+00	protein serine/threonine phosphatase activit	F
GO:0004725	118	2.79E-01	1.00E+00	2.91E-02	1.00E+00	5.29E-01	1.00E+00	8.21E-02	1.00E+00	2.17E-01	1.00E+00	3.65E-02	1.00E+00	3.95E-01	1.00E+00	7.18E-02	1.00E+00	protein tyrosine phosphatase activity	F
GO:0004745	10	8.74E-01	1.00E+00	9.03E-01	1.00E+00	6.82E-01	1.00E+00	6.17E-01	1.00E+00	9.58E-01	1.00E+00	9.67E-01	1.00E+00	4.94E-01	1.00E+00	6.12E-01	1.00E+00	retinol dehydrogenase activity	F
GO:0004765	10	2.92E-01	1.00E+00	5.78E-01	1.00E+00	4.70E-01	1.00E+00	2.52E-01	1.00E+00	2.44E-01	1.00E+00	6.26E-01	1.00E+00	2.40E-01	1.00E+00	9.73E-01	1.00E+00	shikimate kinase activity	F
GO:0004806	17	3.72E-01	1.00E+00	5.19E-01	1.00E+00	2.85E-01	1.00E+00	9.86E-01	1.00E+00	5.50E-01	1.00E+00	5.39E-01	1.00E+00	2.18E-01	1.00E+00	1.33E-01	1.00E+00	triacylglycerol lipase activity	F
GO:0004812	73	1.46E-03	2.02E-01	4.95E-03	3.60E-01	9.69E-03	4.60E-01	7.68E-02	1.00E+00	2.90E-03	2.85E-01	7.36E-03	5.30E-01	1.06E-01	1.00E+00	9.87E-02	1.00E+00	aminoacyl-tRNA ligase activity	F
GO:0004835	14	1.68E-01	1.00E+00	6.00E-02	1.00E+00	3.41E-01	1.00E+00	6.39E-02	1.00E+00	9.23E-02	1.00E+00	1.18E-01	1.00E+00	6.97E-01	1.00E+00	1.77E-01	1.00E+00	tubulin-tyrosine ligase activity	F
GO:0004842	159	3.53E-06	7.00E-03	3.31E-07	8.39E-03	2.99E-04	3.60E-02	4.87E-04	4.70E-02	1.20E-05	4.00E-03	8.03E-07	2.97E-03	1.28E-01	1.00E+00	7.97E-03	4.81E-01	ubiquitin-protein ligase activity	F
GO:0004843	80	4.90E-01	1.00E+00	1.93E-02	1.00E+00	5.99E-01	1.00E+00	2.52E-02	1.00E+00	4.46E-01	1.00E+00	4.10E-02	1.00E+00	4.48E-01	1.00E+00	1.74E-01	1.00E+00	ubiquitin-specific protease activity	F
GO:0004857	299	8.75E-01	1.00E+00	7.07E-01	1.00E+00	9.97E-01	1.00E+00	7.42E-01	1.00E+00	7.22E-01	1.00E+00	6.55E-01	1.00E+00	2.56E-01	1.00E+00	5.19E-01	1.00E+00	enzyme inhibitor activity	F
GO:0004859	18	5.51E-01	1.00E+00	6.84E-01	1.00E+00	4.21E-01	1.00E+00	8.89E-01	1.00E+00	7.05E-01	1.00E+00	5.16E-01	1.00E+00	3.38E-01	1.00E+00	4.97E-01	1.00E+00	phospholipase inhibitor activity	F
GO:0004860	31	1.68E-01	1.00E+00	8.09E-02	1.00E+00	4.01E-01	1.00E+00	6.11E-02	1.00E+00	9.10E-02	1.00E+00	2.19E-01	1.00E+00	5.71E-01	1.00E+00	1.94E-01	1.00E+00	protein kinase inhibitor activity	F
GO:0004861	10	1.84E-01	1.00E+00	1.52E-01	1.00E+00	5.66E-01	1.00E+00	3.31E-01	1.00E+00	9.61E-02	1.00E+00	2.44E-01	1.00E+00	3.27E-01	1.00E+00	1.48E-01	1.00E+00	cyclin-dependent protein kinase inhibitor ac	F
GO:0004864	25	6.03E-01	1.00E+00	1.87E-01	1.00E+00	8.82E-01	1.00E+00	1.45E-01	1.00E+00	4.41E-01	1.00E+00	3.17E-01	1.00E+00	6.44E-01	1.00E+00	1.19E-01	1.00E+00	protein phosphatase inhibitor activity	F
GO:0004866	169	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	6.57E-01	1.00E+00	9.97E-01	1.00E+00	endopeptidase inhibitor activity	F
GO:0004867	117	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.80E-01	1.00E+00	9.87E-01	1.00E+00	9.73E-01	1.00E+00	6.84E-01	1.00E+00	9.97E-01	1.00E+00	serine-type endopeptidase inhibitor activity	F
GO:0004869	30	9.72E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.11E-01	1.00E+00	9.65E-01	1.00E+00	4.55E-01	1.00E+00	5.33E-01	1.00E+00	cysteine protease inhibitor activity	F
GO:0004871	2793	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	signal transducer activity	F
GO:0004872	2305	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	receptor activity	F
GO:0004879	181	3.94E-01	1.00E+00	4.80E-02	1.00E+00	1.18E-02	5.32E-01	1.66E-02	8.18E-01	6.12E-01	1.00E+00	7.27E-02	1.00E+00	8.37E-01	1.00E+00	3.86E-01	1.00E+00	ligand-dependent nuclear receptor activity	F
GO:0004886	12	9.91E-01	1.00E+00	6.85E-01	1.00E+00	9.63E-01	1.00E+00	8.09E-01	1.00E+00	9.66E-01	1.00E+00	6.39E-01	1.00E+00	1.00E+00	1.00E+00	5.80E-01	1.00E+00	retinoid-X receptor activity	F
GO:0004887	21	2.62E-01	1.00E+00	2.50E-01	1.00E+00	3.75E-01	1.00E+00	3.69E-01	1.00E+00	2.04E-01	1.00E+00	1.85E-01	1.00E+00	6.56E-01	1.00E+00	5.72E-01	1.00E+00	thyroid hormone receptor activity	F
GO:0004888	1691	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor activity	F
GO:0004889	18	2.41E-01	1.00E+00	2.50E-01	1.00E+00	2.79E-01	1.00E+00	1.45E-01	1.00E+00	1.72E-01	1.00E+00	4.20E-01	1.00E+00	9.90E-01	1.00E+00	9.29E-02	1.00E+00	nicotinic acetylcholine-activated cation-sele	F
GO:0004890	32	9.30E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	9.96E-01	1.00E+00	6.07E-01	1.00E+00	1.00E+00	1.00E+00	GABA-A receptor activity	F
GO:0004896	83	8.59E-01	1.00E+00	8.36E-01	1.00E+00	7.85E-01	1.00E+00	8.24E-01	1.00E+00	7.55E-01	1.00E+00	7.25E-01	1.00E+00	9.35E-01	1.00E+00	8.79E-01	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0004907	61	9.65E-01	1.00E+00	9.59E-01	1.00E+00	9.47E-01	1.00E+00	8.34E-01	1.00E+00	8.87E-01	1.00E+00	9.20E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	interleukin receptor activity	F
GO:0004908	28	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	interleukin-1 receptor activity	F
GO:0004918	10	1.00E+00	1.00E+00	7.65E-01	1.00E+00	7.67E-01	1.00E+00	2.28E-01	1.00E+00	9.99E-01	1.00E+00	7.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	interleukin-8 receptor activity	F
GO:0004926	16	1.16E-01	1.00E+00	1.85E-01	1.00E+00	8.43E-02	1.00E+00	5.75E-02	1.00E+00	1.39E-01	1.00E+00	2.63E-01	1.00E+00	5.90E-01	1.00E+00	9.99E-01	1.00E+00	non-G-protein coupled 7TM receptor activit	F
GO:0004930	1212	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor activity	F
GO:0004935	43	9.49E-01	1.00E+00	8.88E-01	1.00E+00	7.54E-01	1.00E+00	5.39E-01	1.00E+00	8.57E-01	1.00E+00	9.42E-01	1.00E+00	9.92E-01	1.00E+00	7.00E-01	1.00E+00	adrenoceptor activity	F
GO:0004936	17	6.99E-01	1.00E+00	5.89E-01	1.00E+00	3.82E-01	1.00E+00	1.53E-01	1.00E+00	7.25E-01	1.00E+00	7.88E-01	1.00E+00	6.64E-01	1.00E+00	9.21E-01	1.00E+00	alpha-adrenergic receptor activity	F
GO:0004938	10	7.83E-02	1.00E+00	3.83E-01	1.00E+00	2.50E-01	1.00E+00	1.51E-01	1.00E+00	9.40E-02	1.00E+00	5.97E-01	1.00E+00	2.47E-01	1.00E+00	7.64E-01	1.00E+00	alpha2-adrenergic receptor activity	F
GO:0004939	11	7.52E-01	1.00E+00	6.25E-01	1.00E+00	6.47E-01	1.00E+00	8.33E-01	1.00E+00	4.64E-01	1.00E+00	4.64E-01	1.00E+00	1.00E+00	1.00E+00	7.84E-01	1.00E+00	beta-adrenergic receptor activity	F
GO:0004942	15	5.02E-02	1.00E+00	6.11E-02	1.00E+00	3.34E-01	1.00E+00	6.02E-02	1.00E+00	1.08E-02	5.39E-01	5.00E-02	1.00E+00	3.91E-01	1.00E+00	5.45E-01	1.00E+00	anaphylatoxin receptor activity	F
GO:0004945	66	9.95E-01	1.00E+00	9.26E-01	1.00E+00	9.50E-01	1.00E+00	9.13E-01	1.00E+00	9.74E-01	1.00E+00	8.48E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	angiotensin type II receptor activity	F
GO:0004946	18	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	bombesin receptor activity	F
GO:0004947	36	9.93E-01	1.00E+00	4.23E-01	1.00E+00	9.96E-01	1.00E+00	7.25E-01	1.00E+00	9.51E-01	1.00E+00	2.38E-01	1.00E+00	9.91E-01	1.00E+00	9.09E-01	1.00E+00	bradykinin receptor activity	F
GO:0004949	50	9.96E-01	1.00E+00	8.73E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	9.45E-01	1.00E+00	8.22E-01	1.00E+00	9.66E-01	1.00E+00	7.32E-01	1.00E+00	cannabinoid receptor activity	F
GO:0004950	58	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.49E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chemokine receptor activity	F
GO:0004952	73	1.18E-01	1.00E+00	5.11E-01	1.00E+00	1.68E-02	6.93E-01	7.47E-01	1.00E+00	3.60E-01	1.00E+00	7.09E-01	1.00E+00	2.85E-01	1.00E+00	1.04E-02	4.81E-01	dopamine receptor activity	F
GO:0004953	17	7.07E-01	1.00E+00	9.33E-01	1.00E+00	1.82E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	7.32E-01	1.00E+00	9.99E-01	1.00E+00	7.23E-01	1.00E+00	icosanoid receptor activity	F
GO:0004954	17	7.07E-01	1.00E+00	9.33E-01	1.00E+00	1.82E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	7.32E-01	1.00E+00	9.99E-01	1.00E+00	7.23E-01	1.00E+00	prostanoid receptor activity	F
GO:0004955	17	7.07E-01	1.00E+00	9.33E-01	1.00E+00	1.82E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	7.32E-01	1.00E+00	9.99E-01	1.00E+00	7.23E-01	1.00E+00	prostaglandin receptor activity	F
GO:0004957	13	8.27E-01	1.00E+00	8.37E-01	1.00E+00	2.09E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	6.08E-01	1.00E+00	9.86E-01	1.00E+00	6.61E-01	1.00E+00	prostaglandin E receptor activity	F
GO:0004965	24	9.38E-01	1.00E+00	9.28E-01	1.00E+00	9.92E-01	1.00E+00	9.48E-01	1.00E+00	9.10E-01	1.00E+00	8.43E-01	1.00E+00	4.74E-01	1.00E+00	7.98E-01	1.00E+00	GABA-B receptor activity	F
GO:0004966	43	4.11E-01	1.00E+00	6.16E-01	1.00E+00	4.70E-01	1.00E+00	3.39E-01	1.00E+00	5.51E-01	1.00E+00	5.94E-01	1.00E+00	1.19E-01	1.00E+00	8.74E-01	1.00E+00	galanin receptor activity	F
GO:0004969	58	4.60E-03	3.28E-01	5.41E-03	3.60E-01	3.03E-02	1.00E+00	1.84E-02	1.00E+00	1.18E-02	5.39E-01	1.52E-02	7.39E-01	1.28E-01	1.00E+00	2.21E-02	1.00E+00	histamine receptor activity	F
GO:0004970	18	9.91E-01	1.00E+00	9.99E-01	1.00E+00	9.58E-01	1.00E+00	9.98E-01	1.00E+00	9.78E-01	1.00E+00	9.60E-01	1.00E+00	8.40E-01	1.00E+00	1.00E+00	1.00E+00	ionotropic glutamate receptor activity	F
GO:0004974	26	9.64E-01	1.00E+00	8.28E-01	1.00E+00	9.91E-01	1.00E+00	8.12E-01	1.00E+00	9.18E-01	1.00E+00	7.27E-01	1.00E+00	9.46E-01	1.00E+00	9.84E-01	1.00E+00	leukotriene receptor activity	F
GO:0004977	188	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	melanocortin receptor activity	F
GO:0004981	21	7.41E-01	1.00E+00	1.00E+00	1.00E+00	8.22E-01	1.00E+00	9.91E-01	1.00E+00	7.22E-01	1.00E+00	1.00E+00	1.00E+00	3.31E-01	1.00E+00	9.56E-01	1.00E+00	muscarinic acetylcholine receptor activity	F
GO:0004982	28	7.57E-01	1.00E+00	2.66E-01	1.00E+00	9.88E-01	1.00E+00	2.91E-01	1.00E+00	4.91E-01	1.00E+00	2.29E-01	1.00E+00	8.38E-01	1.00E+00	5.68E-01	1.00E+00	N-formyl peptide receptor activity	F
GO:0004983	90	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	9.95E-01	1.00E+00	neuropeptide Y receptor activity	F
GO:0004984	455	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	olfactory receptor activity	F
GO:0004985	17	4.52E-01	1.00E+00	9.92E-01	1.00E+00	5.10E-01	1.00E+00	9.93E-01	1.00E+00	5.12E-01	1.00E+00	9.81E-01	1.00E+00	2.61E-01	1.00E+00	7.43E-01	1.00E+00	opioid receptor activity	F
GO:0004992	19	9.95E-01	1.00E+00	7.45E-01	1.00E+00	9.97E-01	1.00E+00	9.93E-01	1.00E+00	9.70E-01	1.00E+00	5.44E-01	1.00E+00	9.57E-01	1.00E+00	7.48E-01	1.00E+00	platelet activating factor receptor activity	F
GO:0004993	13	6.10E-01	1.00E+00	8.81E-01	1.00E+00	5.46E-01	1.00E+00	7.35E-01	1.00E+00	4.16E-01	1.00E+00	9.15E-01	1.00E+00	9.88E-01	1.00E+00	7.22E-01	1.00E+00	serotonin receptor activity	F
GO:0004994	23	8.90E-01	1.00E+00	7.34E-01	1.00E+00	6.67E-01	1.00E+00	8.22E-01	1.00E+00	8.44E-01	1.00E+00	5.92E-01	1.00E+00	9.74E-01	1.00E+00	7.17E-01	1.00E+00	somatostatin receptor activity	F
GO:0005000	13	6.69E-01	1.00E+00	5.65E-01	1.00E+00	3.24E-01	1.00E+00	4.63E-01	1.00E+00	6.01E-01	1.00E+00	5.08E-01	1.00E+00	9.97E-01	1.00E+00	9.86E-01	1.00E+00	vasopressin receptor activity	F
GO:0005001	18	8.40E-01	1.00E+00	6.68E-01	1.00E+00	5.96E-01	1.00E+00	6.22E-01	1.00E+00	9.22E-01	1.00E+00	6.65E-01	1.00E+00	6.06E-01	1.00E+00	6.01E-01	1.00E+00	transmembrane receptor protein tyrosine ph	F
GO:0005003	17	9.27E-01	1.00E+00	8.06E-01	1.00E+00	7.69E-01	1.00E+00	9.24E-01	1.00E+00	8.66E-01	1.00E+00	8.64E-01	1.00E+00	9.61E-01	1.00E+00	3.34E-01	1.00E+00	ephrin receptor activity	F
GO:0005021	71	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.26E-01	1.00E+00	6.83E-01	1.00E+00	vascular endothelial growth factor receptor	F
GO:0005024	15	8.19E-01	1.00E+00	4.38E-01	1.00E+00	9.94E-01	1.00E+00	2.79E-01	1.00E+00	6.68E-01	1.00E+00	6.39E-01	1.00E+00	5.46E-01	1.00E+00	1.81E-01	1.00E+00	transforming growth factor beta receptor ac	F

GO:0005035	10	6.65E-01	1.00E+00	6.36E-01	1.00E+00	9.88E-02	1.00E+00	7.37E-01	1.00E+00	9.75E-01	1.00E+00	6.23E-01	1.00E+00	3.74E-01	1.00E+00	2.69E-01	1.00E+00	death receptor activity	F
GO:0005041	12	2.57E-01	1.00E+00	9.99E-02	1.00E+00	9.40E-01	1.00E+00	6.04E-01	1.00E+00	1.59E-01	1.00E+00	3.55E-02	1.00E+00	1.50E-01	1.00E+00	1.77E-01	1.00E+00	low-density lipoprotein receptor activity	F
GO:0005044	42	9.63E-01	1.00E+00	9.88E-01	1.00E+00	8.57E-01	1.00E+00	8.61E-01	1.00E+00	8.87E-01	1.00E+00	9.54E-01	1.00E+00	9.93E-01	1.00E+00	9.93E-01	1.00E+00	scavenger receptor activity	F
GO:0005048	20	1.49E-01	1.00E+00	4.57E-02	1.00E+00	1.29E-01	1.00E+00	9.41E-02	1.00E+00	1.35E-01	1.00E+00	6.56E-02	1.00E+00	4.51E-01	1.00E+00	2.04E-01	1.00E+00	signal sequence binding	F
GO:0005057	168	4.63E-02	1.00E+00	6.15E-03	3.60E-01	2.12E-01	1.00E+00	4.71E-03	3.46E-01	1.69E-02	1.00E+00	1.64E-02	8.60E-01	3.36E-01	1.00E+00	7.40E-02	1.00E+00	receptor signaling protein activity	F
GO:0005066	11	4.76E-01	1.00E+00	9.05E-01	1.00E+00	2.98E-01	1.00E+00	6.45E-01	1.00E+00	5.16E-01	1.00E+00	9.74E-01	1.00E+00	6.97E-01	1.00E+00	5.99E-01	1.00E+00	transmembrane receptor protein tyrosine ki	F
GO:0005070	47	5.99E-02	1.00E+00	4.08E-02	1.00E+00	2.68E-01	1.00E+00	1.51E-02	8.18E-01	5.55E-02	1.00E+00	6.92E-02	1.00E+00	1.57E-01	1.00E+00	3.31E-01	1.00E+00	SH3/SH2 adaptor activity	F
GO:0005080	10	4.52E-01	1.00E+00	1.36E-01	1.00E+00	4.96E-01	1.00E+00	5.08E-01	1.00E+00	1.80E-01	1.00E+00	3.06E-02	1.00E+00	1.00E+00	1.00E+00	7.70E-01	1.00E+00	protein kinase C binding	F
GO:0005083	257	1.41E-03	2.02E-01	2.32E-04	4.19E-02	7.19E-04	4.50E-02	1.23E-02	8.18E-01	5.87E-03	5.39E-01	4.11E-03	2.70E-01	2.74E-01	1.00E+00	3.50E-03	1.85E-01	small GTPase regulator activity	F
GO:0005085	150	9.91E-02	1.00E+00	2.62E-02	1.00E+00	1.90E-02	1.00E+00	5.26E-02	1.00E+00	1.10E-01	1.00E+00	3.41E-02	1.00E+00	9.89E-01	1.00E+00	2.82E-01	1.00E+00	guanyl-nucleotide exchange factor activity	F
GO:0005086	17	1.17E-01	1.00E+00	2.91E-01	1.00E+00	9.45E-02	1.00E+00	9.90E-02	1.00E+00	1.86E-01	1.00E+00	3.54E-01	1.00E+00	8.41E-01	1.00E+00	9.47E-01	1.00E+00	ARF guanyl-nucleotide exchange factor act	F
GO:0005088	89	6.70E-01	1.00E+00	1.15E-01	1.00E+00	4.52E-01	1.00E+00	4.86E-01	1.00E+00	5.13E-01	1.00E+00	1.01E-01	1.00E+00	9.99E-01	1.00E+00	1.49E-01	1.00E+00	Ras guanyl-nucleotide exchange factor acti	F
GO:0005089	77	7.61E-01	1.00E+00	2.26E-01	1.00E+00	3.72E-01	1.00E+00	6.25E-01	1.00E+00	6.59E-01	1.00E+00	1.70E-01	1.00E+00	9.98E-01	1.00E+00	2.29E-01	1.00E+00	Rho guanyl-nucleotide exchange factor acti	F
GO:0005095	10	6.75E-03	5.17E-01	1.17E-04	1.50E-02	2.86E-01	1.00E+00	9.60E-02	1.00E+00	7.96E-03	5.39E-01	4.85E-03	2.70E-01	8.41E-02	1.00E+00	3.54E-02	1.00E+00	GTPase inhibitor activity	F
GO:0005096	251	1.11E-02	6.67E-01	4.82E-04	6.90E-02	9.82E-03	4.60E-01	1.30E-02	8.18E-01	3.35E-02	1.00E+00	4.15E-03	2.70E-01	2.43E-01	1.00E+00	1.33E-02	6.47E-01	GTPase activator activity	F
GO:0005097	56	1.37E-01	1.00E+00	8.41E-02	1.00E+00	2.50E-01	1.00E+00	5.04E-01	1.00E+00	2.43E-01	1.00E+00	1.26E-01	1.00E+00	5.74E-02	1.00E+00	1.07E-01	1.00E+00	Rab GTPase activator activity	F
GO:0005099	94	4.98E-02	1.00E+00	3.81E-03	1.97E-01	6.33E-02	1.00E+00	4.05E-02	1.00E+00	1.51E-01	1.00E+00	5.31E-02	1.00E+00	3.48E-02	1.00E+00	8.90E-03	4.81E-01	Ras GTPase activator activity	F
GO:0005100	25	1.35E-01	1.00E+00	3.40E-02	1.00E+00	3.33E-02	1.00E+00	2.03E-02	1.00E+00	3.15E-01	1.00E+00	1.79E-01	1.00E+00	5.05E-01	1.00E+00	6.40E-02	1.00E+00	Rho GTPase activator activity	F
GO:0005102	905	4.20E-01	1.00E+00	3.68E-01	1.00E+00	4.84E-01	1.00E+00	3.27E-01	1.00E+00	3.70E-01	1.00E+00	3.30E-01	1.00E+00	4.30E-01	1.00E+00	6.77E-01	1.00E+00	receptor binding	F
GO:0005104	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.58E-01	1.00E+00	9.99E-01	1.00E+00	fibroblast growth factor receptor binding	F
GO:0005125	258	9.85E-01	1.00E+00	9.97E-01	1.00E+00	8.84E-01	1.00E+00	8.72E-01	1.00E+00	9.83E-01	1.00E+00	9.98E-01	1.00E+00	8.84E-01	1.00E+00	9.71E-01	1.00E+00	cytokine activity	F
GO:0005126	47	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.54E-01	1.00E+00	1.00E+00	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0005149	16	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	9.36E-01	1.00E+00	1.00E+00	1.00E+00	interleukin-1 receptor binding	F
GO:0005154	11	8.63E-01	1.00E+00	8.06E-01	1.00E+00	2.81E-01	1.00E+00	4.10E-01	1.00E+00	9.52E-01	1.00E+00	9.81E-01	1.00E+00	9.97E-01	1.00E+00	1.53E-01	1.00E+00	epidermal growth factor receptor binding	F
GO:0005158	23	9.53E-01	1.00E+00	9.98E-01	1.00E+00	5.45E-01	1.00E+00	8.25E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	9.40E-01	1.00E+00	insulin receptor binding	F
GO:0005159	13	5.59E-01	1.00E+00	7.05E-01	1.00E+00	4.90E-01	1.00E+00	2.24E-01	1.00E+00	6.25E-01	1.00E+00	8.68E-01	1.00E+00	3.98E-01	1.00E+00	8.67E-01	1.00E+00	insulin-like growth factor receptor binding	F
GO:0005160	12	3.32E-01	1.00E+00	3.70E-01	1.00E+00	2.22E-01	1.00E+00	1.65E-01	1.00E+00	3.22E-01	1.00E+00	3.22E-01	1.00E+00	8.09E-01	1.00E+00	9.92E-01	1.00E+00	transforming growth factor beta receptor bir	F
GO:0005164	35	8.26E-02	1.00E+00	2.20E-01	1.00E+00	1.42E-01	1.00E+00	5.68E-01	1.00E+00	5.92E-02	1.00E+00	2.33E-01	1.00E+00	5.60E-01	1.00E+00	1.15E-01	1.00E+00	tumor necrosis factor receptor binding	F
GO:0005178	49	5.39E-01	1.00E+00	4.84E-01	1.00E+00	1.53E-01	1.00E+00	3.61E-01	1.00E+00	7.26E-01	1.00E+00	5.32E-01	1.00E+00	5.67E-01	1.00E+00	6.64E-01	1.00E+00	integrin binding	F
GO:0005179	175	9.53E-02	1.00E+00	3.08E-01	1.00E+00	5.61E-01	1.00E+00	5.48E-01	1.00E+00	1.19E-01	1.00E+00	1.63E-01	1.00E+00	1.12E-02	6.30E-01	6.40E-01	1.00E+00	hormone activity	F
GO:0005184	29	4.71E-01	1.00E+00	4.02E-01	1.00E+00	9.02E-01	1.00E+00	9.57E-02	1.00E+00	6.27E-01	1.00E+00	6.51E-01	1.00E+00	6.80E-02	1.00E+00	2.26E-01	1.00E+00	neuropeptide hormone activity	F
GO:0005198	973	1.68E-04	2.50E-02	3.42E-03	1.97E-01	1.08E-02	5.32E-01	1.99E-01	1.00E+00	1.96E-04	1.70E-02	9.28E-04	5.49E-02	1.37E-02	6.47E-01	4.82E-02	1.00E+00	structural molecule activity	F
GO:0005199	77	2.99E-02	1.00E+00	2.10E-02	1.00E+00	3.02E-01	1.00E+00	1.22E-02	8.18E-01	3.41E-02	1.00E+00	3.95E-02	1.00E+00	2.26E-02	1.00E+00	2.16E-01	1.00E+00	structural constituent of cell wall	F
GO:0005200	81	3.14E-01	1.00E+00	7.79E-02	1.00E+00	3.43E-02	1.00E+00	2.47E-01	1.00E+00	6.23E-01	1.00E+00	2.98E-02	1.00E+00	7.82E-01	1.00E+00	7.38E-01	1.00E+00	structural constituent of cytoskeleton	F
GO:0005201	100	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	9.65E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	extracellular matrix structural constituent	F
GO:0005212	17	1.34E-01	1.00E+00	1.49E-01	1.00E+00	9.64E-03	4.60E-01	8.49E-02	1.00E+00	5.21E-01	1.00E+00	2.51E-01	1.00E+00	2.48E-01	1.00E+00	1.39E-01	1.00E+00	structural constituent of eye lens	F
GO:0005215	1546	3.79E-05	1.00E-02	2.61E-05	9.58E-03	2.91E-02	1.00E+00	8.66E-03	7.13E-01	6.41E-06	2.88E-03	2.72E-06	2.97E-03	1.84E-01	1.00E+00	3.26E-01	1.00E+00	transporter activity	F
GO:0005216	496	2.81E-01	1.00E+00	4.86E-01	1.00E+00	2.72E-01	1.00E+00	4.73E-01	1.00E+00	2.87E-01	1.00E+00	4.19E-01	1.00E+00	4.96E-01	1.00E+00	5.58E-01	1.00E+00	ion channel activity	F
GO:0005217	14	9.24E-01	1.00E+00	8.57E-01	1.00E+00	6.13E-01	1.00E+00	8.26E-01	1.00E+00	8.92E-01	1.00E+00	6.38E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	intracellular ligand-gated ion channel activit	F
GO:0005230	74	8.62E-01	1.00E+00	9.33E-01	1.00E+00	8.88E-01	1.00E+00	6.86E-01	1.00E+00	6.80E-01	1.00E+00	8.94E-01	1.00E+00	9.80E-01	1.00E+00	9.71E-01	1.00E+00	extracellular ligand-gated ion channel activi	F
GO:0005231	48	7.73E-01	1.00E+00	5.38E-01	1.00E+00	5.29E-01	1.00E+00	2.31E-01	1.00E+00	6.24E-01	1.00E+00	5.89E-01	1.00E+00	9.95E-01	1.00E+00	6.25E-01	1.00E+00	excitatory extracellular ligand-gated ion cha	F
GO:0005234	19	8.90E-01	1.00E+00	9.68E-01	1.00E+00	7.87E-01	1.00E+00	9.89E-01	1.00E+00	8.58E-01	1.00E+00	8.08E-01	1.00E+00	8.12E-01	1.00E+00	9.99E-01	1.00E+00	glutamate-gated ion channel activity	F
GO:0005242	23	9.85E-01	1.00E+00	8.08E-01	1.00E+00	9.49E-01	1.00E+00	7.23E-01	1.00E+00	9.85E-01	1.00E+00	8.13E-01	1.00E+00	5.36E-01	1.00E+00	6.16E-01	1.00E+00	inward rectifier potassium channel activity	F
GO:0005244	311	3.44E-01	1.00E+00	5.90E-01	1.00E+00	5.11E-01	1.00E+00	6.41E-01	1.00E+00	3.57E-01	1.00E+00	5.67E-01	1.00E+00	2.64E-01	1.00E+00	4.80E-01	1.00E+00	voltage-gated ion channel activity	F
GO:0005245	50	2.07E-01	1.00E+00	1.86E-01	1.00E+00	6.76E-01	1.00E+00	1.86E-01	1.00E+00	1.59E-01	1.00E+00	2.80E-01	1.00E+00	2.75E-01	1.00E+00	3.10E-01	1.00E+00	voltage-gated calcium channel activity	F
GO:0005246	15	6.65E-01	1.00E+00	4.57E-01	1.00E+00	9.74E-01	1.00E+00	4.37E-01	1.00E+00	5.74E-01	1.00E+00	3.61E-01	1.00E+00	2.73E-01	1.00E+00	6.73E-01	1.00E+00	calcium channel regulator activity	F
GO:0005247	27	3.60E-01	1.00E+00	8.88E-02	1.00E+00	7.13E-01	1.00E+00	1.42E-01	1.00E+00	2.03E-01	1.00E+00	9.19E-02	1.00E+00	4.23E-01	1.00E+00	6.55E-01	1.00E+00	voltage-gated chloride channel activity	F
GO:0005248	17	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.33E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	voltage-gated sodium channel activity	F
GO:0005249	225	5.77E-01	1.00E+00	8.08E-01	1.00E+00	3.03E-01	1.00E+00	8.06E-01	1.00E+00	7.53E-01	1.00E+00	8.12E-01	1.00E+00	3.43E-01	1.00E+00	4.63E-01	1.00E+00	voltage-gated potassium channel activity	F
GO:0005251	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.32E-01	1.00E+00	9.83E-01	1.00E+00	delayed rectifier potassium channel activity	F
GO:0005253	79	6.60E-01	1.00E+00	8.01E-01	1.00E+00	5.51E-01	1.00E+00	4.51E-01	1.00E+00	5.81E-01	1.00E+00	7.41E-01	1.00E+00	8.73E-01	1.00E+00	9.84E-01	1.00E+00	anion channel activity	F
GO:0005254	72	8.56E-01	1.00E+00	9.53E-01	1.00E+00	8.26E-01	1.00E+00	7.80E-01	1.00E+00	7.67E-01	1.00E+00	8.98E-01	1.00E+00	8.61E-01	1.00E+00	9.93E-01	1.00E+00	chloride channel activity	F
GO:0005261	374	3.32E-01	1.00E+00	3.90E-01	1.00E+00	2.00E-01	1.00E+00	5.33E-01	1.00E+00	3.94E-01	1.00E+00	3.36E-01	1.00E+00	5.27E-01	1.00E+00	3.57E-01	1.00E+00	cation channel activity	F
GO:0005262	98	4.00E-01	1.00E+00	8.69E-02	1.00E+00	7.58E-01	1.00E+00	3.82E-01	1.00E+00	3.55E-01	1.00E+00	5.24E-02	1.00E+00	2.58E-01	1.00E+00	3.65E-01	1.00E+00	calcium channel activity	F
GO:0005267	244	6.56E-01	1.00E+00	8.76E-01	1.00E+00	4.95E-01	1.00E+00	8.93E-01	1.00E+00	7.38E-01	1.00E+00	8.60E-01	1.00E+00	4.69E-01	1.00E+00	4.94E-01	1.00E+00	potassium channel activity	F
GO:0005272	34	9.14E-01	1.00E+00	9.99E-01	1.00E+00	4.19E-01	1.00E+00	7.32E-01	1.00E+00	9.85E-01	1.00E+00	9.99E-01	1.00E+00	6.93E-01	1.00E+00	9.98E-01	1.00E+00	sodium channel activity	F
GO:0005275	69	9.81E-01	1.00E+00	2.50E-01	1.00E+00	7.09E-01	1.00E+00	3.50E-01	1.00E+00	9.86E-01	1.00E+00	2.19E-01	1.00E+00	9.85E-01	1.00E+00	5.60E-01	1.00E+00	amine transporter activity	F
GO:0005279	21	1.00E+00	1.00E+00	8.23E-01	1.00E+00	9.58E-01	1.00E+00	7.65E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	9.72E-01	1.00E+00	4.07E-01	1.00E+00	amino acid-polyamine transporter activity	F
GO:0005283	15	1.00E+00	1.00E+00	6.18E-01	1.00E+00	9.31E-01	1.00E+00	5.60E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	9.64E-01	1.00E+00	2.52E-01	1.00E+00	sodium:amino acid symporter activity	F
GO:0005310	64	7.08E-01	1.00E+00	8.65E-01	1.00E+00	9.85E-01	1.00E+00	7.85E-01	1.00E+00	6.22E-01	1.00E+00	8.27E-01	1.00E+00	2.52E-01	1.00E+00	9.45E-01	1.00E+00	dicarboxylic acid transporter activity	F
GO:0005313	10	9.57E-01	1.00E+00	4.15E-01	1.00E+00	7.89E-01	1.00E+00	3.30E-01	1.00E+00	9.48E-01	1.00E+00	4.63E-01	1.00E+00	7.95E-01	1.00E+00	6.49E-01	1.00E+00	L-glutamate transporter activity	F
GO:0005319	79	2.84E-02	1.00E+00	4.82E-02	1.00E+00	1.34E-01	1.00E+00	8.17E-02	1.00E+00	3.27E-02	1.00E+00	4.09E-02	1.00E+00	6.92E-02	1.00E+00	4.90E-01	1.00E+00	lipid transporter activity	F
GO:0005326	28	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	7.79E-01	1.00E+00	neurotransmitter transporter activity	F
GO:0005328	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	7.52E-01	1.00E+00	neurotransmitter:sodium symporter activity	F
GO:0005337	18	1.89E-02	1.00E+00	5.92E-03	3.60E-01	4.00E-03	3.27E-01	3.57E-01	1.00E+00	4.32E-02	1.00E+00	9.63E-04	5.49E-02	2.51E-01	1.00E+00	6.37E-01	1.00E+00	nucleoside transporter activity	F
GO:0005342	130	7.35E-01	1.00E+00	7.51E-01	1.00E+00	9.69E-01	1.00E+00	9.02E-01	1.00E+00	6.15E-01	1.00E+00	5.33E-01	1.00E+00	4.78E-01	1.00E+00	9.25E-01	1.00E+00	organic acid transporter activity	F
GO:0005343	80	8.87E-01	1.00E+00	8.99E-01	1.00E+00	9.66E-01	1.00E+00	8.35E-01	1.00E+00	8.99E-01	1.00E+00	8.89E-01	1.00E+00	5.78E-01	1.00E+00	7.93E-01	1.00E+00	organic acid:sodium symporter activity	F
GO:0005344	15	2.16E-01	1.00E+00	1.00E+00	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	1.44E-01	1.00E+00	1.00E+00	1.00E+00	5.77E-02	1.00E+00	3.47E-01	1.00E+00	oxygen transporter activity	F
GO:0005351	44	6.35E-02	1.00E+00	1.71E-02	1.00E+00	1.97E-01	1.00E+00	3.07E-02	1.00E+00	8.26E-02	1.00E+00	4.79E-02	1.00E+00	1.35E-01	1.00E+00	2.37E-01	1.00E+00	sugar porter activity	F
GO:0005355	15	8.53E-02	1.00E+00	3.87E-02	1.00E+00	1.07E-01	1.00E+00	2.13E-01	1.00E+00	1.31E-01	1.00E+00	5.70E-02	1.00E+00	1.20E-01	1.00E+00	2.92E-01	1.00E+00	glucose transporter activity	F
GO:0005372	11	9.37E-01	1.00E+00	3.08E-01	1.00E+00	5.87E-01	1.00E+00	5.44E-01	1.00E+00	8.74E-01	1.00E+00	2.20E-01	1.00E+00	1.00E+00	1.00E+00	5.93E-01	1.00E+00	water transporter activity	F
GO:0005375	11	4.92E-01	1.00E+00	7.16E-02	1.00E+00	1.00E+00	1.00E+00	8.88E-02	1.00E+00	3.51E-01	1.00E+00	1.17E-01	1.00E+00	8.51E-01	1.00E+00	4.98E-01	1.00E+00	copper ion transporter activity	F
GO:0005385	12	1.51E-02	6.67E-01	4.62E-02	1.00E+00	6.72E-01	1.00E+00	5.62E-01	1.00E+00	9.62E-03	5.39E-01	7.69E-03	5.30E-01	5.61E-01	1.00E+00	4.72E-01	1.00E+00	zinc ion transporter activity	F
GO:0005386	409	4.90E-01	1.00E+00	1.47E-01	1.00E+00	9.39E-01	1.00E+00	5.51E-01	1.00E+00	2.18E-01	1.00E+00	7.34E-02	1.00E+00	8.36E-01	1.00E+00	5.10E-01	1.00E+00	carrier activity	F
GO:0005391	10	5.46E-01	1.00E+00	6.24E-01	1.00E+00	3.39E-01	1.00E+00	1.00E+00	1.00E+00	4.33E-01	1.00E+00	5.29E-01	1.00E+00	9.93E-01	1.00E+00	2.03E-01	1.00E+00	sodium:potassium-exchanging ATPase acti	F

GO:0005416	18	1.00E+00	1.00E+00	7.46E-01	1.00E+00	9.40E-01	1.00E+00	7.42E-01	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	9.73E-01	1.00E+00	3.07E-01	1.00E+00	cation:amino acid symporter activity	F
GO:0005451	14	9.60E-01	1.00E+00	8.71E-01	1.00E+00	9.99E-01	1.00E+00	4.67E-01	1.00E+00	7.01E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	monovalent cation:proton antiporter activity	F
GO:0005452	20	5.09E-01	1.00E+00	3.04E-01	1.00E+00	2.41E-01	1.00E+00	4.29E-01	1.00E+00	5.77E-01	1.00E+00	3.20E-01	1.00E+00	6.81E-01	1.00E+00	5.89E-01	1.00E+00	inorganic anion exchanger activity	F
GO:0005478	29	2.25E-02	1.00E+00	3.94E-04	6.90E-02	3.22E-02	1.00E+00	2.90E-03	1.47E-01	4.21E-02	1.00E+00	7.47E-04	5.49E-02	4.74E-01	1.00E+00	9.40E-02	1.00E+00	intracellular transporter activity	F
GO:0005484	20	8.35E-02	1.00E+00	4.15E-02	1.00E+00	7.99E-02	1.00E+00	3.50E-02	1.00E+00	1.18E-01	1.00E+00	6.00E-02	1.00E+00	4.23E-01	1.00E+00	2.96E-01	1.00E+00	SNAP receptor activity	F
GO:0005488	13036	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.65E-41	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.93E-24	0.00E+00	8.95E-33	0.00E+00	binding	F
GO:0005496	80	5.92E-01	1.00E+00	8.89E-01	1.00E+00	1.11E-01	1.00E+00	7.33E-01	1.00E+00	6.94E-01	1.00E+00	7.99E-01	1.00E+00	8.88E-01	1.00E+00	9.79E-01	1.00E+00	steroid binding	F
GO:0005501	17	8.12E-01	1.00E+00	6.88E-01	1.00E+00	8.78E-01	1.00E+00	8.09E-01	1.00E+00	8.59E-01	1.00E+00	5.44E-01	1.00E+00	2.25E-01	1.00E+00	5.91E-01	1.00E+00	retinoid binding	F
GO:0005504	26	7.15E-02	1.00E+00	8.06E-02	1.00E+00	2.86E-01	1.00E+00	2.45E-01	1.00E+00	9.17E-02	1.00E+00	1.50E-01	1.00E+00	3.55E-02	1.00E+00	6.88E-02	1.00E+00	fatty acid binding	F
GO:0005506	322	4.75E-01	1.00E+00	9.92E-02	1.00E+00	5.63E-01	1.00E+00	7.49E-01	1.00E+00	3.52E-01	1.00E+00	1.44E-02	7.39E-01	6.92E-01	1.00E+00	7.52E-01	1.00E+00	iron ion binding	F
GO:0005507	81	9.88E-01	1.00E+00	7.24E-01	1.00E+00	9.91E-01	1.00E+00	5.87E-01	1.00E+00	9.68E-01	1.00E+00	7.37E-01	1.00E+00	8.04E-01	1.00E+00	6.89E-01	1.00E+00	copper ion binding	F
GO:0005509	1057	1.00E+00	1.00E+00	7.03E-01	1.00E+00	9.45E-01	1.00E+00	6.69E-01	1.00E+00	1.00E+00	1.00E+00	4.99E-01	1.00E+00	9.99E-01	1.00E+00	9.21E-01	1.00E+00	calcium ion binding	F
GO:0005515	7540	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.21E-37	0.00E+00	5.61E-45	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.87E-15	0.00E+00	3.81E-30	0.00E+00	protein binding	F
GO:0005516	147	2.55E-01	1.00E+00	2.74E-02	1.00E+00	7.21E-02	1.00E+00	2.07E-01	1.00E+00	2.60E-01	1.00E+00	7.05E-03	5.30E-01	9.76E-01	1.00E+00	6.73E-01	1.00E+00	calmodulin binding	F
GO:0005518	18	4.05E-01	1.00E+00	5.45E-01	1.00E+00	7.38E-01	1.00E+00	5.66E-01	1.00E+00	3.67E-01	1.00E+00	5.40E-01	1.00E+00	4.31E-01	1.00E+00	3.53E-01	1.00E+00	collagen binding	F
GO:0005520	25	6.02E-01	1.00E+00	9.75E-01	1.00E+00	2.67E-01	1.00E+00	3.45E-01	1.00E+00	7.52E-01	1.00E+00	1.00E+00	1.00E+00	5.11E-01	1.00E+00	7.05E-01	1.00E+00	insulin-like growth factor binding	F
GO:0005523	13	1.50E-01	1.00E+00	3.96E-01	1.00E+00	1.85E-01	1.00E+00	4.10E-01	1.00E+00	1.79E-01	1.00E+00	1.98E-01	1.00E+00	6.44E-01	1.00E+00	9.98E-01	1.00E+00	tropomyosin binding	F
GO:0005524	1567	5.96E-25	0.00E+00	1.78E-35	0.00E+00	1.18E-15	0.00E+00	7.49E-18	0.00E+00	2.91E-21	0.00E+00	6.00E-32	0.00E+00	3.16E-06	1.95E-03	4.52E-09	7.71E-04	ATP binding	F
GO:0005525	404	4.50E-08	1.84E-03	5.28E-07	8.39E-03	6.77E-04	4.50E-02	1.25E-02	8.18E-01	1.34E-07	1.69E-03	1.36E-07	9.20E-04	1.54E-05	5.44E-03	1.23E-02	6.47E-01	GTP binding	F
GO:0005529	204	9.87E-01	1.00E+00	3.05E-01	1.00E+00	9.65E-01	1.00E+00	6.54E-01	1.00E+00	9.87E-01	1.00E+00	1.95E-01	1.00E+00	6.13E-01	1.00E+00	3.78E-01	1.00E+00	sugar binding	F
GO:0005537	13	8.18E-01	1.00E+00	4.04E-01	1.00E+00	6.38E-01	1.00E+00	4.77E-01	1.00E+00	9.35E-01	1.00E+00	3.57E-01	1.00E+00	2.30E-01	1.00E+00	4.57E-01	1.00E+00	mannose binding	F
GO:0005539	105	8.74E-01	1.00E+00	9.48E-01	1.00E+00	3.82E-01	1.00E+00	9.28E-01	1.00E+00	9.07E-01	1.00E+00	8.58E-01	1.00E+00	9.04E-01	1.00E+00	9.38E-01	1.00E+00	glycosaminoglycan binding	F
GO:0005540	17	7.29E-01	1.00E+00	7.65E-01	1.00E+00	5.88E-01	1.00E+00	8.36E-01	1.00E+00	7.86E-01	1.00E+00	6.39E-01	1.00E+00	6.60E-01	1.00E+00	8.45E-01	1.00E+00	hyaluronic acid binding	F
GO:0005542	13	1.92E-01	1.00E+00	1.15E-01	1.00E+00	1.36E-01	1.00E+00	7.05E-01	1.00E+00	2.34E-01	1.00E+00	5.99E-02	1.00E+00	5.84E-01	1.00E+00	3.18E-01	1.00E+00	folic acid binding	F
GO:0005543	147	3.80E-04	3.37E-02	1.06E-06	8.39E-03	1.64E-02	6.93E-01	2.36E-04	2.70E-02	2.08E-03	2.85E-01	2.90E-06	2.97E-03	1.54E-02	6.47E-01	1.30E-02	6.47E-01	phospholipid binding	F
GO:0005544	24	4.13E-01	1.00E+00	3.76E-01	1.00E+00	9.16E-01	1.00E+00	1.58E-01	1.00E+00	4.25E-01	1.00E+00	5.80E-01	1.00E+00	1.33E-01	1.00E+00	4.14E-01	1.00E+00	calcium-dependent phospholipid binding	F
GO:0005545	16	1.87E-01	1.00E+00	1.13E-01	1.00E+00	4.06E-01	1.00E+00	1.28E-01	1.00E+00	1.97E-01	1.00E+00	1.48E-01	1.00E+00	2.56E-01	1.00E+00	4.82E-01	1.00E+00	phosphatidylinositol binding	F
GO:0005548	30	1.06E-01	1.00E+00	2.44E-01	1.00E+00	3.20E-01	1.00E+00	4.82E-01	1.00E+00	1.05E-01	1.00E+00	2.00E-01	1.00E+00	2.54E-01	1.00E+00	5.59E-01	1.00E+00	phospholipid transporter activity	F
GO:0005575	16286	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.69E-29	0.00E+00	3.35E-30	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.63E-19	0.00E+00	5.77E-28	0.00E+00	cellular_component	C
GO:0005576	2040	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	extracellular region	C
GO:0005578	344	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.72E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	extracellular matrix (sensu Metazoa)	C
GO:0005581	35	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	collagen	C
GO:0005604	75	1.00E+00	1.00E+00	9.17E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.86E-01	1.00E+00	9.88E-01	1.00E+00	6.94E-01	1.00E+00	basement membrane	C
GO:0005605	30	9.79E-01	1.00E+00	5.90E-01	1.00E+00	9.91E-01	1.00E+00	9.53E-01	1.00E+00	8.97E-01	1.00E+00	3.91E-01	1.00E+00	9.04E-01	1.00E+00	4.21E-01	1.00E+00	basal lamina	C
GO:0005615	516	9.45E-01	1.00E+00	9.63E-01	1.00E+00	7.39E-01	1.00E+00	9.42E-01	1.00E+00	9.66E-01	1.00E+00	8.52E-01	1.00E+00	5.26E-01	1.00E+00	9.99E-01	1.00E+00	extracellular space	C
GO:0005622	10868	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.10E-39	0.00E+00	0.00E+00	0.00E+00	intracellular	C
GO:0005623	14957	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.10E-35	0.00E+00	1.65E-36	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.18E-22	0.00E+00	2.60E-32	0.00E+00	cell	C
GO:0005624	653	8.79E-02	1.00E+00	1.56E-02	1.00E+00	2.89E-01	1.00E+00	2.41E-01	1.00E+00	7.96E-02	1.00E+00	4.12E-03	2.70E-01	2.01E-01	1.00E+00	5.03E-01	1.00E+00	membrane fraction	C
GO:0005625	222	2.61E-03	2.39E-01	3.05E-03	1.97E-01	7.02E-02	1.00E+00	3.15E-02	1.00E+00	2.92E-03	2.85E-01	9.29E-03	7.39E-01	1.83E-02	9.11E-01	3.74E-02	1.00E+00	soluble fraction	C
GO:0005626	23	5.43E-01	1.00E+00	3.49E-01	1.00E+00	2.70E-01	1.00E+00	2.88E-01	1.00E+00	7.32E-01	1.00E+00	4.69E-01	1.00E+00	3.01E-01	1.00E+00	1.43E-01	1.00E+00	insoluble fraction	C
GO:0005634	4933	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.13E-33	0.00E+00	1.49E-40	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.18E-24	0.00E+00	1.72E-33	0.00E+00	nucleus	C
GO:0005635	194	1.01E-08	8.06E-04	1.68E-10	0.00E+00	3.50E-05	6.00E-03	7.84E-05	1.20E-02	7.53E-08	1.69E-03	4.43E-09	8.37E-04	1.25E-02	6.30E-01	4.78E-05	9.00E-03	nuclear envelope	C
GO:0005637	19	2.51E-02	1.00E+00	3.04E-02	1.00E+00	2.01E-01	1.00E+00	5.29E-01	1.00E+00	5.01E-02	1.00E+00	1.58E-02	7.63E-01	3.32E-01	1.00E+00	2.75E-01	1.00E+00	nuclear inner membrane	C
GO:0005640	15	4.41E-01	1.00E+00	8.22E-02	1.00E+00	2.00E-01	1.00E+00	2.67E-01	1.00E+00	3.15E-01	1.00E+00	4.02E-02	1.00E+00	1.00E+00	1.00E+00	4.37E-01	1.00E+00	nuclear outer membrane	C
GO:0005643	69	2.51E-08	9.77E-04	3.90E-14	0.00E+00	2.34E-03	2.48E-01	5.17E-07	1.96E-03	2.35E-08	9.64E-04	2.72E-12	0.00E+00	2.71E-03	1.95E-01	3.17E-04	2.70E-02	nuclear pore	C
GO:0005654	739	2.08E-26	0.00E+00	1.57E-23	0.00E+00	2.53E-13	0.00E+00	9.91E-13	0.00E+00	8.45E-26	0.00E+00	5.29E-21	0.00E+00	3.48E-06	1.95E-03	1.46E-05	9.00E-03	nucleoplasm	C
GO:0005657	33	6.35E-05	1.10E-02	5.95E-06	8.39E-03	8.16E-03	4.60E-01	4.59E-03	3.46E-01	3.88E-05	5.00E-03	4.19E-06	2.97E-03	1.32E-01	1.00E+00	1.80E-01	1.00E+00	replication fork	C
GO:0005665	14	2.09E-01	1.00E+00	4.86E-02	1.00E+00	4.66E-01	1.00E+00	5.17E-02	1.00E+00	3.74E-01	1.00E+00	4.82E-02	1.00E+00	3.33E-02	1.00E+00	8.66E-01	1.00E+00	DNA-directed RNA polymerase II, core com	C
GO:0005667	224	1.65E-04	2.50E-02	4.67E-04	6.90E-02	4.74E-03	3.27E-01	4.02E-03	2.41E-01	1.36E-04	1.70E-02	1.35E-03	6.40E-02	1.95E-01	1.00E+00	1.28E-01	1.00E+00	transcription factor complex	C
GO:0005669	25	1.62E-03	2.02E-01	4.83E-03	3.60E-01	7.01E-03	4.60E-01	1.25E-01	1.00E+00	1.49E-03	1.76E-01	1.29E-02	7.39E-01	3.41E-01	1.00E+00	8.11E-02	1.00E+00	transcription factor TFIID complex	C
GO:0005680	12	5.82E-02	1.00E+00	3.60E-02	1.00E+00	1.55E-01	1.00E+00	7.66E-02	1.00E+00	3.64E-01	1.00E+00	6.86E-02	1.00E+00	4.42E-04	6.50E-02	7.31E-02	1.00E+00	anaphase-promoting complex	C
GO:0005681	132	1.34E-11	0.00E+00	2.80E-09	4.97E-03	1.81E-06	2.42E-03	1.91E-03	1.24E-01	9.62E-10	9.64E-04	1.19E-08	8.37E-04	3.32E-04	3.40E-02	1.41E-04	2.00E-02	spliceosome complex	C
GO:0005684	10	6.83E-04	3.44E-02	2.04E-03	1.29E-01	3.76E-03	3.27E-01	1.00E-02	7.13E-01	5.41E-03	4.18E-01	2.36E-03	1.64E-01	5.32E-02	1.00E+00	5.14E-01	1.00E+00	major (U2-dependent) spliceosome	C
GO:0005689	11	2.07E-04	2.50E-02	3.25E-02	1.00E+00	6.88E-02	1.00E+00	8.04E-02	1.00E+00	3.51E-04	1.98E-02	3.31E-02	1.00E+00	4.34E-02	1.00E+00	4.34E-01	1.00E+00	minor (U12-dependent) spliceosome compl	C
GO:0005694	526	7.27E-12	0.00E+00	2.84E-11	0.00E+00	4.39E-04	3.60E-02	3.24E-03	1.47E-01	6.46E-12	0.00E+00	1.73E-10	0.00E+00	8.49E-05	2.50E-02	2.70E-06	1.88E-03	chromosome	C
GO:0005720	24	1.94E-01	1.00E+00	5.03E-01	1.00E+00	5.46E-01	1.00E+00	8.05E-01	1.00E+00	1.92E-01	1.00E+00	4.63E-01	1.00E+00	2.14E-01	1.00E+00	3.49E-01	1.00E+00	nuclear heterochromatin	C
GO:0005730	177	2.61E-10	0.00E+00	1.36E-08	4.97E-03	1.38E-05	3.72E-03	1.02E-03	8.30E-02	1.02E-08	9.64E-04	3.58E-07	2.97E-03	1.21E-03	1.68E-01	9.49E-04	9.16E-02	nucleolus	C
GO:0005732	15	3.52E-01	1.00E+00	1.37E-01	1.00E+00	2.44E-01	1.00E+00	7.10E-01	1.00E+00	3.46E-01	1.00E+00	2.23E-01	1.00E+00	5.30E-01	1.00E+00	4.04E-02	1.00E+00	small nucleolar ribonucleoprotein complex	C
GO:0005737	6696	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.24E-42	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.27E-21	0.00E+00	1.17E-26	0.00E+00	cytoplasm	C
GO:0005739	966	2.68E-24	0.00E+00	1.46E-20	0.00E+00	1.55E-15	0.00E+00	1.29E-10	0.00E+00	2.05E-20	0.00E+00	6.68E-19	0.00E+00	7.05E-06	2.00E-03	5.39E-05	9.00E-03	mitochondrion	C
GO:0005740	395	5.89E-16	0.00E+00	2.55E-10	0.00E+00	3.47E-08	9.68E-04	6.36E-06	8.00E-03	2.87E-15	0.00E+00	2.16E-09	0.00E+00	1.90E-03	1.95E-01	2.09E-03	1.40E-01	mitochondrial envelope	C
GO:0005741	76	2.88E-04	3.37E-02	4.96E-05	9.58E-03	1.06E-02	5.32E-01	3.44E-03	2.02E-01	2.02E-04	1.70E-02	3.85E-04	3.07E-02	1.24E-01	1.00E+00	2.77E-03	1.85E-01	mitochondrial outer membrane	C
GO:0005743	285	1.10E-14	0.00E+00	6.25E-07	8.39E-03	1.47E-06	2.42E-03	4.24E-04	4.20E-02	8.11E-15	0.00E+00	7.19E-07	2.97E-03	8.16E-03	6.30E-01	6.45E-02	1.00E+00	mitochondrial inner membrane	C
GO:0005744	12	2.11E-03	2.02E-01	5.66E-02	1.00E+00	1.81E-01	1.00E+00	1.29E-01	1.00E+00	6.90E-04	4.00E-02	3.96E-02	1.00E+00	1.53E-01	1.00E+00	4.85E-01	1.00E+00	mitochondrial inner membrane presequenc	C
GO:0005746	63	1.89E-05	8.00E-03	6.14E-04	6.90E-02	3.45E-03	3.27E-01	2.30E-02	1.00E+00	3.39E-05	5.00E-03	1.26E-03	6.40E-02	5.75E-02	1.00E+00	5.78E-02	1.00E+00	mitochondrial electron transport chain	C
GO:0005747	36	2.28E-04	2.64E-02	6.99E-03	3.60E-01	3.80E-02	1.00E+00	3.32E-02	1.00E+00	6.72E-04	4.00E-02	2.96E-02	1.00E+00	3.27E-02	1.00E+00	5.08E-02	1.00E+00	respiratory chain complex I (sensu Eukaryo	C
GO:0005753	16	4.52E-03	3.28E-01	1.44E-01	1.00E+00	7.76E-03	4.60E-01	1.41E-01	1.00E+00	3.88E-03	2.85E-01	1.85E-01	1.00E+00	1.75E-01	1.00E+00	2.49E-01	1.00E+00	proton-transporting ATP synthase complex	C
GO:0005758	29	1.92E-01	1.00E+00	3.81E-01	1.00E+00	7.08E-01	1.00E+00	4.90E-01	1.00E+00	6.84E-02	1.00E+00	2.62E-01	1.00E+00	4.12E-01	1.00E+00	8.79E-01	1.00E+00	mitochondrial intermembrane space	C
GO:0005759	196	1.41E-04	2.50E-02	4.52E-03	3.60E-01	2.06E-04	2.40E-02	5.56E-03	3.46E-01	2.62E-03	2.85E-01	1.00E-02	7.39E-01	1.97E-02	9.11E-01	3.85E-01	1.00E+00	mitochondrial matrix	C
GO:0005761	48	1.30E-02	6.67E-01	1.19E-01	1.00E+00	3.22E-03	2.48E-01	1.36E-01	1.00E+00	2.57E-01	1.00E+00	2.33E-01	1.00E+00	2.61E-03	1.95E-01	2.71E-01	1.00E+00	mitochondrial ribosome	C
GO:0005762	17	4.74E-01	1.00E+00	1.57E-01	1.00E+00	5.42E-01	1.00E+00	3.42E-02	1.00E+00	5.84E-01	1.00E+00	2.13E-01	1.00E+00	1.32E-01	1.00E+00	3.97E-01	1.00E+00	mitochondrial large ribosomal subunit	C
GO:0005763	18	3.80E-02	1.00E+00	2.41E-01	1.00E+00	1.18E-02	5.32E-01	4.21E-01	1.00E+00	1.64E-01	1.00E+00	2.56E-01	1.00E+00	1.23E-01	1.00E+00	5.15E-01	1.00E+00	mitochondrial small ribosomal subunit	C
GO:0005764	209	1.10E-03	9.60E-02	1.11E-03	9.10E-02	1.95E-01	1.00E+00	3.73E-02	1.00E+00	2.75E-04	1.70E-02	4.42E-03	2.70E-01	1.49E-01	1.00E+00	3.98E-03	1.85E-01	lysosome	C
GO:0005765	57	1.26E-03	2.02E-01	2.08E-02	1.00E+00	3.99E-02	1.00E+00	1.09E-01	1.00E+00	1.86E-03	1.76E-01	8.55E-02	1.00E+00	4.13E-01	1.00E+00	1.63E-02	8.49E-01	lysosomal membrane	C
GO:0005768	231	1.55E-06	1.95E-03	3.50E-05	9.58E-03	1.59E-02	6.93E-01	1.87E-02	1.00E+00	7.87E-06	2.88E-03	1.12E-04	1.70E-02	1.45E-04	2.50E-02	4.77E-03	3.60E-01	endosome	C

GO:0005769	65	1.36E-04	2.50E-02	3.54E-05	9.58E-03	4.22E-02	1.00E+00	1.82E-02	1.00E+00	3.19E-04	1.98E-02	1.61E-04	1.70E-02	8.72E-02	1.00E+00	1.61E-02	8.49E-01	early endosome	C
GO:0005770	58	1.61E-03	2.02E-01	1.72E-03	9.10E-02	8.61E-02	1.00E+00	4.37E-02	1.00E+00	2.50E-03	2.85E-01	1.36E-02	7.39E-01	2.79E-02	1.00E+00	1.26E-02	6.47E-01	late endosome	C
GO:0005773	232	1.34E-04	2.50E-02	1.45E-04	1.50E-02	1.92E-01	1.00E+00	1.94E-02	1.00E+00	3.32E-05	5.00E-03	4.85E-04	4.10E-02	5.44E-02	1.00E+00	3.42E-03	1.85E-01	vacuole	C
GO:0005774	68	1.86E-03	2.02E-01	2.40E-02	1.00E+00	1.15E-01	1.00E+00	1.08E-01	1.00E+00	2.94E-03	2.85E-01	8.95E-02	1.00E+00	2.19E-01	1.00E+00	1.94E-02	1.00E+00	vacuolar membrane	C
GO:0005776	10	6.34E-03	5.17E-01	1.12E-03	9.10E-02	5.38E-02	1.00E+00	3.02E-01	1.00E+00	1.09E-02	5.39E-01	7.70E-04	5.49E-02	1.06E-01	1.00E+00	3.19E-01	1.00E+00	autophagic vacuole	C
GO:0005777	98	6.28E-04	3.44E-02	4.39E-02	1.00E+00	2.23E-02	1.00E+00	3.68E-02	1.00E+00	7.84E-04	4.04E-02	4.26E-02	1.00E+00	2.14E-02	9.11E-01	5.34E-01	1.00E+00	peroxisome	C
GO:0005778	42	2.90E-03	2.39E-01	1.83E-01	1.00E+00	4.91E-02	1.00E+00	1.68E-01	1.00E+00	3.56E-03	2.85E-01	1.62E-01	1.00E+00	4.25E-03	3.57E-01	4.58E-01	1.00E+00	peroxisomal membrane	C
GO:0005779	12	4.28E-02	1.00E+00	4.11E-01	1.00E+00	5.89E-02	1.00E+00	2.28E-01	1.00E+00	8.79E-02	1.00E+00	3.88E-01	1.00E+00	1.25E-01	1.00E+00	9.14E-01	1.00E+00	integral to peroxisomal membrane	C
GO:0005783	856	8.86E-06	7.00E-03	1.71E-08	4.97E-03	3.23E-04	3.60E-02	6.69E-04	4.70E-02	7.93E-05	1.70E-02	1.29E-08	8.37E-04	8.98E-03	6.30E-01	5.73E-03	3.60E-01	endoplasmic reticulum	C
GO:0005788	65	1.64E-02	6.67E-01	2.47E-03	1.77E-01	1.38E-02	6.93E-01	6.44E-02	1.00E+00	3.65E-02	1.00E+00	1.60E-03	1.61E-01	3.47E-01	1.00E+00	1.82E-01	1.00E+00	endoplasmic reticulum lumen	C
GO:0005789	502	2.96E-03	2.39E-01	5.78E-04	6.90E-02	7.20E-02	1.00E+00	1.13E-01	1.00E+00	5.27E-03	4.18E-01	6.06E-04	5.49E-02	2.63E-02	1.00E+00	6.06E-03	3.60E-01	endoplasmic reticulum membrane	C
GO:0005790	10	4.41E-01	1.00E+00	5.51E-01	1.00E+00	3.17E-01	1.00E+00	9.61E-01	1.00E+00	3.28E-01	1.00E+00	3.74E-01	1.00E+00	9.72E-01	1.00E+00	4.34E-01	1.00E+00	smooth endoplasmic reticulum	C
GO:0005791	17	2.19E-01	1.00E+00	7.91E-02	1.00E+00	3.00E-01	1.00E+00	4.31E-01	1.00E+00	2.53E-01	1.00E+00	7.75E-02	1.00E+00	1.04E-01	1.00E+00	3.64E-02	1.00E+00	rough endoplasmic reticulum	C
GO:0005792	182	3.16E-01	1.00E+00	4.78E-01	1.00E+00	4.37E-01	1.00E+00	7.01E-01	1.00E+00	4.00E-01	1.00E+00	3.40E-01	1.00E+00	8.34E-02	1.00E+00	6.93E-01	1.00E+00	microsome	C
GO:0005793	34	9.12E-02	1.00E+00	1.28E-03	9.10E-02	1.12E-01	1.00E+00	1.21E-02	8.18E-01	9.45E-02	1.00E+00	1.57E-03	1.61E-01	4.84E-01	1.00E+00	2.60E-01	1.00E+00	ER-Golgi intermediate compartment	C
GO:0005794	691	9.26E-08	1.85E-03	3.40E-10	0.00E+00	1.82E-06	2.42E-03	3.39E-05	8.00E-03	2.99E-06	2.60E-03	2.68E-10	0.00E+00	1.29E-02	6.30E-01	4.97E-02	1.00E+00	Golgi apparatus	C
GO:0005795	21	2.95E-01	1.00E+00	5.38E-02	1.00E+00	7.73E-02	1.00E+00	1.23E-01	1.00E+00	4.35E-01	1.00E+00	4.89E-02	1.00E+00	7.78E-01	1.00E+00	6.48E-01	1.00E+00	Golgi stack	C
GO:0005798	54	5.00E-04	3.37E-02	1.89E-03	1.29E-01	2.02E-02	1.00E+00	1.13E-01	1.00E+00	4.77E-04	2.20E-02	3.61E-03	2.70E-01	3.28E-02	1.00E+00	4.37E-02	1.00E+00	Golgi-associated vesicle	C
GO:0005801	14	1.84E-04	2.50E-02	9.08E-04	6.90E-02	9.61E-02	1.00E+00	2.47E-03	1.47E-01	3.13E-03	2.85E-01	4.65E-03	2.70E-01	3.98E-01	1.00E+00	1.33E-01	1.00E+00	Golgi cis face	C
GO:0005802	28	5.05E-02	1.00E+00	5.58E-02	1.00E+00	1.46E-01	1.00E+00	1.07E-01	1.00E+00	8.51E-02	1.00E+00	3.56E-02	1.00E+00	6.45E-02	1.00E+00	8.25E-01	1.00E+00	Golgi trans face	C
GO:0005811	13	7.63E-03	6.34E-01	9.84E-02	1.00E+00	5.06E-02	1.00E+00	5.55E-02	1.00E+00	2.09E-02	1.00E+00	1.24E-01	1.00E+00	3.34E-02	1.00E+00	5.04E-01	1.00E+00	lipid particle	C
GO:0005813	143	7.31E-04	6.71E-02	5.07E-03	3.60E-01	3.44E-03	3.27E-01	4.47E-03	3.46E-01	3.75E-03	2.85E-01	2.52E-02	1.00E+00	4.37E-02	1.00E+00	3.77E-02	1.00E+00	centrosome	C
GO:0005814	10	4.73E-02	1.00E+00	1.04E-01	1.00E+00	1.62E-01	1.00E+00	4.64E-02	1.00E+00	2.62E-02	1.00E+00	1.56E-01	1.00E+00	5.76E-01	1.00E+00	6.26E-01	1.00E+00	centriole	C
GO:0005815	162	1.27E-03	2.02E-01	4.66E-03	3.60E-01	7.45E-03	4.60E-01	4.94E-03	3.46E-01	8.99E-03	5.39E-01	1.55E-02	7.63E-01	1.75E-02	9.11E-01	8.60E-02	1.00E+00	microtubule organizing center	C
GO:0005819	90	3.60E-05	1.00E-02	6.37E-04	6.90E-02	4.45E-04	3.60E-02	5.29E-02	1.00E+00	4.05E-04	2.20E-02	5.26E-04	4.10E-02	4.15E-02	1.00E+00	3.54E-02	1.00E+00	spindle	C
GO:0005829	959	5.48E-30	0.00E+00	1.40E-30	0.00E+00	7.86E-12	0.00E+00	4.44E-14	0.00E+00	1.47E-28	0.00E+00	1.83E-26	0.00E+00	1.12E-11	0.00E+00	8.14E-13	0.00E+00	cytosol	C
GO:0005833	14	1.56E-01	1.00E+00	9.88E-01	1.00E+00	9.04E-01	1.00E+00	1.00E+00	1.00E+00	6.50E-02	1.00E+00	9.70E-01	1.00E+00	9.26E-02	1.00E+00	3.64E-01	1.00E+00	hemoglobin complex	C
GO:0005834	29	2.65E-01	1.00E+00	5.92E-01	1.00E+00	5.44E-01	1.00E+00	3.87E-01	1.00E+00	3.16E-01	1.00E+00	4.47E-01	1.00E+00	1.06E-01	1.00E+00	9.18E-01	1.00E+00	heterotrimeric G-protein complex	C
GO:0005839	21	1.77E-01	1.00E+00	2.28E-02	1.00E+00	6.21E-01	1.00E+00	6.47E-02	1.00E+00	1.99E-01	1.00E+00	4.04E-02	1.00E+00	4.18E-02	1.00E+00	3.30E-02	1.00E+00	proteasome core complex (sensu Eukaryot	C
GO:0005840	327	6.57E-12	0.00E+00	9.59E-06	9.58E-03	2.95E-06	2.42E-03	2.22E-02	1.00E+00	6.48E-10	0.00E+00	2.25E-05	7.63E-03	9.60E-06	5.44E-03	2.93E-03	1.85E-01	ribosome	C
GO:0005844	12	1.48E-01	1.00E+00	1.15E-01	1.00E+00	4.89E-02	1.00E+00	8.26E-02	1.00E+00	3.22E-01	1.00E+00	8.56E-02	1.00E+00	3.09E-01	1.00E+00	5.96E-01	1.00E+00	polysome	C
GO:0005852	12	7.58E-05	1.24E-02	1.01E-02	5.18E-01	7.38E-03	4.60E-01	5.79E-01	1.00E+00	2.80E-05	5.00E-03	6.66E-03	5.30E-01	1.93E-02	9.11E-01	3.05E-01	1.00E+00	eukaryotic translation initiation factor 3 com	C
GO:0005856	1227	3.94E-04	3.37E-02	3.87E-05	9.58E-03	6.00E-03	4.60E-01	2.39E-02	1.00E+00	1.43E-04	1.70E-02	8.83E-06	4.88E-03	4.34E-01	1.00E+00	4.26E-02	1.00E+00	cytoskeleton	C
GO:0005858	13	3.59E-01	1.00E+00	9.71E-01	1.00E+00	1.48E-01	1.00E+00	7.36E-01	1.00E+00	5.32E-01	1.00E+00	7.72E-01	1.00E+00	5.19E-01	1.00E+00	9.81E-01	1.00E+00	axonemal dynein complex	C
GO:0005863	18	9.89E-01	1.00E+00	4.65E-01	1.00E+00	9.33E-01	1.00E+00	3.36E-01	1.00E+00	9.51E-01	1.00E+00	3.44E-01	1.00E+00	9.87E-01	1.00E+00	9.36E-01	1.00E+00	striated muscle thick filament	C
GO:0005865	13	4.13E-02	1.00E+00	1.09E-01	1.00E+00	2.29E-02	1.00E+00	5.38E-01	1.00E+00	1.02E-01	1.00E+00	3.26E-02	1.00E+00	4.24E-01	1.00E+00	4.65E-01	1.00E+00	striated muscle thin filament	C
GO:0005871	18	3.63E-02	1.00E+00	4.97E-02	1.00E+00	5.78E-03	4.60E-01	6.20E-02	1.00E+00	4.15E-02	1.00E+00	6.29E-02	1.00E+00	5.63E-01	1.00E+00	2.47E-01	1.00E+00	kinesin complex	C
GO:0005874	247	1.51E-07	1.85E-03	2.68E-06	8.39E-03	4.77E-05	1.20E-02	2.92E-03	1.47E-01	1.06E-06	2.60E-03	8.42E-06	4.88E-03	6.13E-03	3.57E-01	4.70E-03	3.60E-01	microtubule	C
GO:0005875	117	6.00E-04	3.37E-02	1.05E-03	9.10E-02	7.04E-05	1.20E-02	1.88E-04	2.70E-02	3.64E-03	2.85E-01	6.84E-03	5.30E-01	2.01E-01	1.00E+00	2.58E-01	1.00E+00	microtubule associated complex	C
GO:0005876	19	1.84E-03	2.02E-01	2.72E-02	1.00E+00	3.31E-02	1.00E+00	1.90E-01	1.00E+00	1.00E-03	4.40E-02	5.54E-02	1.00E+00	1.77E-01	1.00E+00	4.35E-02	1.00E+00	spindle microtubule	C
GO:0005882	182	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	intermediate filament	C
GO:0005884	30	1.66E-02	6.67E-01	3.12E-02	1.00E+00	9.85E-04	9.80E-02	6.85E-03	4.53E-01	6.02E-02	1.00E+00	1.55E-01	1.00E+00	3.79E-01	1.00E+00	5.03E-01	1.00E+00	actin filament	C
GO:0005886	3358	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	plasma membrane	C
GO:0005887	1228	9.98E-01	1.00E+00	9.42E-01	1.00E+00	9.88E-01	1.00E+00	9.96E-01	1.00E+00	9.76E-01	1.00E+00	7.45E-01	1.00E+00	9.99E-01	1.00E+00	8.55E-01	1.00E+00	integral to plasma membrane	C
GO:0005891	32	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.29E-01	1.00E+00	6.48E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	8.03E-01	1.00E+00	9.00E-01	1.00E+00	voltage-gated calcium channel complex	C
GO:0005892	14	6.30E-01	1.00E+00	4.16E-01	1.00E+00	6.27E-01	1.00E+00	2.37E-01	1.00E+00	4.44E-01	1.00E+00	6.28E-01	1.00E+00	9.74E-01	1.00E+00	1.66E-01	1.00E+00	nicotinic acetylcholine-gated receptor-chan	C
GO:0005901	34	1.25E-01	1.00E+00	5.38E-01	1.00E+00	3.10E-02	1.00E+00	5.81E-01	1.00E+00	2.98E-01	1.00E+00	6.78E-01	1.00E+00	8.86E-02	1.00E+00	2.70E-01	1.00E+00	caveola	C
GO:0005902	17	8.86E-01	1.00E+00	4.38E-01	1.00E+00	3.59E-01	1.00E+00	6.88E-01	1.00E+00	9.81E-01	1.00E+00	3.26E-01	1.00E+00	5.43E-01	1.00E+00	6.43E-01	1.00E+00	microvillus	C
GO:0005903	27	8.25E-01	1.00E+00	3.16E-01	1.00E+00	4.03E-01	1.00E+00	9.47E-01	1.00E+00	9.41E-01	1.00E+00	2.59E-01	1.00E+00	3.45E-01	1.00E+00	2.07E-01	1.00E+00	brush border	C
GO:0005905	38	1.73E-03	2.02E-01	1.30E-04	1.50E-02	8.86E-03	4.60E-01	4.56E-02	1.00E+00	2.52E-03	2.85E-01	3.67E-05	1.20E-02	4.01E-02	1.00E+00	3.86E-01	1.00E+00	coated pit	C
GO:0005911	176	6.64E-02	1.00E+00	2.53E-02	1.00E+00	5.38E-02	1.00E+00	1.54E-02	8.18E-01	2.90E-02	1.00E+00	4.58E-02	1.00E+00	6.48E-01	1.00E+00	1.98E-01	1.00E+00	intercellular junction	C
GO:0005912	72	1.04E-01	1.00E+00	5.34E-02	1.00E+00	1.21E-02	5.32E-01	1.09E-02	8.18E-01	1.77E-01	1.00E+00	9.74E-02	1.00E+00	6.65E-01	1.00E+00	6.63E-01	1.00E+00	adherens junction	C
GO:0005913	26	2.42E-01	1.00E+00	8.16E-02	1.00E+00	1.43E-01	1.00E+00	4.61E-02	1.00E+00	4.16E-01	1.00E+00	1.69E-01	1.00E+00	1.47E-01	1.00E+00	2.17E-01	1.00E+00	cell-cell adherens junction	C
GO:0005921	30	7.44E-01	1.00E+00	4.10E-01	1.00E+00	6.73E-01	1.00E+00	1.67E-01	1.00E+00	7.03E-01	1.00E+00	4.96E-01	1.00E+00	5.94E-01	1.00E+00	4.60E-01	1.00E+00	gap junction	C
GO:0005922	24	5.98E-01	1.00E+00	5.43E-01	1.00E+00	7.36E-01	1.00E+00	2.83E-01	1.00E+00	5.41E-01	1.00E+00	5.75E-01	1.00E+00	3.66E-01	1.00E+00	6.62E-01	1.00E+00	connexon complex	C
GO:0005923	88	1.78E-03	2.02E-01	1.76E-03	9.10E-02	1.58E-02	6.93E-01	5.52E-03	3.46E-01	2.77E-04	1.70E-02	3.71E-03	2.70E-01	3.56E-01	1.00E+00	1.50E-01	1.00E+00	tight junction	C
GO:0005924	44	3.30E-01	1.00E+00	2.18E-01	1.00E+00	1.33E-02	5.53E-01	9.02E-02	1.00E+00	4.34E-01	1.00E+00	1.63E-01	1.00E+00	9.89E-01	1.00E+00	9.96E-01	1.00E+00	cell-substrate adherens junction	C
GO:0005925	40	4.12E-01	1.00E+00	2.52E-01	1.00E+00	2.74E-02	1.00E+00	1.31E-01	1.00E+00	4.56E-01	1.00E+00	1.92E-01	1.00E+00	9.85E-01	1.00E+00	9.90E-01	1.00E+00	focal adhesion	C
GO:0005929	88	5.39E-01	1.00E+00	1.37E-01	1.00E+00	3.42E-01	1.00E+00	3.99E-01	1.00E+00	6.66E-01	1.00E+00	4.97E-02	1.00E+00	4.25E-01	1.00E+00	6.96E-01	1.00E+00	cilium	C
GO:0005930	22	5.26E-01	1.00E+00	8.24E-01	1.00E+00	5.08E-01	1.00E+00	7.50E-01	1.00E+00	7.31E-01	1.00E+00	5.81E-01	1.00E+00	2.04E-01	1.00E+00	9.86E-01	1.00E+00	axoneme	C
GO:0005932	13	7.72E-01	1.00E+00	4.46E-01	1.00E+00	7.33E-01	1.00E+00	2.47E-01	1.00E+00	8.95E-01	1.00E+00	3.39E-01	1.00E+00	3.52E-01	1.00E+00	9.48E-01	1.00E+00	basal body	C
GO:0005938	82	8.80E-05	1.24E-02	5.84E-05	9.58E-03	1.67E-04	1.50E-02	1.24E-02	8.18E-01	1.48E-03	1.76E-01	3.73E-04	3.07E-02	3.14E-03	1.95E-01	1.21E-02	6.47E-01	cell cortex	C
GO:0005941	52	8.47E-01	1.00E+00	2.93E-01	1.00E+00	9.36E-01	1.00E+00	5.65E-01	1.00E+00	8.04E-01	1.00E+00	2.70E-01	1.00E+00	7.17E-01	1.00E+00	2.83E-01	1.00E+00	unlocalized protein complex	C
GO:0005942	18	4.61E-02	1.00E+00	1.00E-01	1.00E+00	2.54E-02	1.00E+00	3.33E-02	1.00E+00	1.04E-01	1.00E+00	2.09E-01	1.00E+00	9.82E-02	1.00E+00	1.02E-01	1.00E+00	phosphoinositide 3-kinase complex	C
GO:0005952	23	9.72E-01	1.00E+00	9.92E-01	1.00E+00	9.08E-01	1.00E+00	9.83E-01	1.00E+00	9.83E-01	1.00E+00	9.29E-01	1.00E+00	7.54E-01	1.00E+00	9.98E-01	1.00E+00	cAMP-dependent protein kinase complex	C
GO:0005964	19	6.45E-01	1.00E+00	3.88E-01	1.00E+00	9.26E-01	1.00E+00	7.24E-01	1.00E+00	4.79E-01	1.00E+00	3.79E-01	1.00E+00	9.29E-01	1.00E+00	1.97E-01	1.00E+00	phosphorylase kinase complex	C
GO:0005975	560	2.96E-03	2.39E-01	2.54E-03	1.77E-01	5.04E-02	1.00E+00	5.57E-02	1.00E+00	2.15E-03	2.85E-01	4.21E-03	2.70E-01	2.41E-01	1.00E+00	3.08E-02	1.00E+00	carbohydrate metabolism	P
GO:0005976	89	7.13E-01	1.00E+00	4.75E-01	1.00E+00	7.19E-01	1.00E+00	7.82E-01	1.00E+00	6.28E-01	1.00E+00	2.23E-01	1.00E+00	6.70E-01	1.00E+00	8.31E-01	1.00E+00	polysaccharide metabolism	P
GO:0005977	56	7.71E-01	1.00E+00	5.96E-01	1.00E+00	8.33E-01	1.00E+00	6.96E-01	1.00E+00	6.42E-01	1.00E+00	3.29E-01	1.00E+00	7.75E-01	1.00E+00	8.86E-01	1.00E+00	glycogen metabolism	P
GO:0005978	30	8.40E-01	1.00E+00	5.21E-01	1.00E+00	9.62E-01	1.00E+00	7.69E-01	1.00E+00	6.35E-01	1.00E+00	4.31E-01	1.00E+00	8.84E-01	1.00E+00	3.48E-01	1.00E+00	glycogen biosynthesis	P
GO:0005996	187	1.40E-04	2.50E-02	1.33E-03	9.10E-02	2.81E-03	2.48E-01	1.08E-02	8.18E-01	2.13E-04	1.70E-02	1.14E-02	7.39E-01	1.11E-01	1.00E+00	3.96E-03	1.85E-01	monosaccharide metabolism	P
GO:0006000	13	6.06E-01	1.00E+00	6.06E-01	1.00E+00	9.08E-01	1.00E+00	3.57E-01	1.00E+00	5.58E-01	1.00E+00	7.87E-01	1.00E+00	3.46E-01	1.00E+00	2.29E-01	1.00E+00	fructose metabolism	P
GO:0006004	15	1.39E-01	1.00E+00	1.63E-01	1.00E+00	5.24E-01	1.00E+00	2.89E-01	1.00E+00	8.11E-02	1.00E+00	1.90E-01	1.00E+00	3.00E-01	1.00E+00	7.28E-02	1.00E+00	fucose metabolism	P
GO:0006006	134	5.58E-05	1.10E-02	7.94E-04	6.90E-02	1.53E-04	1.50E-02	8.67E-03	7.13E-01	4.62E-04	2.20E-02	8.08E-03	7.39E-01	4.11E-02	1.00E+00	5.58E-03	3.60E-01	glucose metabolism	P
GO:0006007	78	3.78E-04	3.37E-02	2.08E-03	1.29E-01	4.07E-05	1.20E-02	5.24E-03	3.46E-01	3.77E-03	2.85E-01	1.14E-02	7.39E-01	1.79E-01	1.00E+00	8.48E-02	1.00E+00	glucose catabolism	P

GO:0006022	47	6.26E-01	1.00E+00	3.64E-01	1.00E+00	4.12E-01	1.00E+00	2.44E-01	1.00E+00	6.49E-01	1.00E+00	5.84E-01	1.00E+00	7.12E-01	1.00E+00	1.69E-01	1.00E+00	aminoglycan metabolism	P
GO:0006023	21	7.69E-01	1.00E+00	2.58E-01	1.00E+00	1.90E-01	1.00E+00	6.03E-02	1.00E+00	9.30E-01	1.00E+00	4.68E-01	1.00E+00	7.20E-01	1.00E+00	7.30E-01	1.00E+00	aminoglycan biosynthesis	P
GO:0006024	21	7.69E-01	1.00E+00	2.58E-01	1.00E+00	1.90E-01	1.00E+00	6.03E-02	1.00E+00	9.30E-01	1.00E+00	4.68E-01	1.00E+00	7.20E-01	1.00E+00	7.30E-01	1.00E+00	glycosaminoglycan biosynthesis	P
GO:0006029	34	9.81E-01	1.00E+00	9.68E-01	1.00E+00	3.29E-01	1.00E+00	5.51E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	9.34E-01	1.00E+00	6.55E-01	1.00E+00	proteoglycan metabolism	P
GO:0006030	10	1.00E+00	1.00E+00	8.65E-01	1.00E+00	9.93E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	8.34E-01	1.00E+00	5.84E-01	1.00E+00	8.60E-01	1.00E+00	chitin metabolism	P
GO:0006040	33	8.54E-01	1.00E+00	2.12E-01	1.00E+00	7.93E-01	1.00E+00	3.48E-01	1.00E+00	7.72E-01	1.00E+00	2.18E-01	1.00E+00	7.10E-01	1.00E+00	3.01E-01	1.00E+00	amino sugar metabolism	P
GO:0006041	27	9.52E-01	1.00E+00	4.59E-01	1.00E+00	7.30E-01	1.00E+00	5.01E-01	1.00E+00	9.63E-01	1.00E+00	5.17E-01	1.00E+00	6.29E-01	1.00E+00	4.32E-01	1.00E+00	glucosamine metabolism	P
GO:0006044	27	9.52E-01	1.00E+00	4.59E-01	1.00E+00	7.30E-01	1.00E+00	5.01E-01	1.00E+00	9.63E-01	1.00E+00	5.17E-01	1.00E+00	6.29E-01	1.00E+00	4.32E-01	1.00E+00	N-acetylglucosamine metabolism	P
GO:0006066	400	1.27E-04	2.50E-02	2.41E-03	1.77E-01	4.15E-04	3.60E-02	2.49E-03	1.47E-01	4.05E-04	2.20E-02	2.77E-02	1.00E+00	2.19E-01	1.00E+00	3.23E-03	1.85E-01	alcohol metabolism	P
GO:0006071	36	2.51E-02	1.00E+00	2.70E-02	1.00E+00	4.78E-02	1.00E+00	5.14E-02	1.00E+00	6.72E-02	1.00E+00	8.89E-02	1.00E+00	1.19E-01	1.00E+00	1.28E-01	1.00E+00	glycerol metabolism	P
GO:0006072	19	2.71E-01	1.00E+00	2.74E-02	1.00E+00	4.46E-01	1.00E+00	1.03E-01	1.00E+00	4.22E-01	1.00E+00	1.25E-01	1.00E+00	1.80E-01	1.00E+00	7.21E-02	1.00E+00	glycerol-3-phosphate metabolism	P
GO:0006073	57	8.07E-01	1.00E+00	6.00E-01	1.00E+00	8.63E-01	1.00E+00	6.97E-01	1.00E+00	6.75E-01	1.00E+00	3.28E-01	1.00E+00	7.99E-01	1.00E+00	9.03E-01	1.00E+00	glucan metabolism	P
GO:0006081	18	4.96E-02	1.00E+00	3.00E-01	1.00E+00	1.27E-02	5.32E-01	6.42E-01	1.00E+00	1.77E-01	1.00E+00	2.08E-01	1.00E+00	6.28E-01	1.00E+00	7.20E-01	1.00E+00	aldehyde metabolism	P
GO:0006082	670	4.23E-05	1.00E-02	1.89E-06	8.39E-03	4.37E-04	3.60E-02	8.25E-05	1.20E-02	1.20E-04	1.70E-02	3.49E-05	1.20E-02	1.26E-01	1.00E+00	5.15E-03	3.60E-01	organic acid metabolism	P
GO:0006084	28	1.37E-01	1.00E+00	2.43E-01	1.00E+00	3.86E-02	1.00E+00	1.43E-01	1.00E+00	1.80E-01	1.00E+00	3.79E-01	1.00E+00	6.94E-01	1.00E+00	2.90E-01	1.00E+00	acetyl-CoA metabolism	P
GO:0006090	29	3.86E-01	1.00E+00	3.27E-01	1.00E+00	5.10E-01	1.00E+00	5.41E-01	1.00E+00	3.62E-01	1.00E+00	4.79E-01	1.00E+00	3.89E-01	1.00E+00	9.52E-02	1.00E+00	pyruvate metabolism	P
GO:0006091	324	3.58E-09	8.06E-04	9.89E-07	8.39E-03	2.38E-06	2.42E-03	8.33E-04	5.90E-02	2.03E-08	9.64E-04	5.86E-06	4.00E-03	1.52E-02	6.47E-01	4.98E-03	3.60E-01	generation of precursor metabolites and en	P
GO:0006092	128	6.89E-05	1.24E-02	2.60E-04	4.19E-02	3.45E-05	6.00E-03	1.40E-03	1.15E-01	5.25E-04	2.20E-02	3.80E-03	2.70E-01	1.06E-01	1.00E+00	2.04E-02	1.00E+00	main pathways of carbohydrate metabolism	P
GO:0006094	26	2.68E-01	1.00E+00	1.38E-01	1.00E+00	3.92E-01	1.00E+00	3.81E-01	1.00E+00	2.80E-01	1.00E+00	3.01E-01	1.00E+00	2.81E-01	1.00E+00	4.38E-02	1.00E+00	gluconeogenesis	P
GO:0006096	67	3.38E-03	2.73E-01	1.53E-02	1.00E+00	4.11E-04	3.60E-02	2.07E-02	1.00E+00	2.25E-02	1.00E+00	3.64E-02	1.00E+00	2.58E-01	1.00E+00	2.44E-01	1.00E+00	glycolysis	P
GO:0006098	10	2.02E-02	1.00E+00	1.13E-02	6.77E-01	1.66E-02	6.93E-01	7.05E-02	1.00E+00	5.05E-02	1.00E+00	8.43E-02	1.00E+00	1.25E-01	1.00E+00	7.32E-02	1.00E+00	pentose-phosphate shunt	P
GO:0006099	24	6.17E-02	1.00E+00	1.65E-01	1.00E+00	1.33E-02	5.53E-01	8.30E-02	1.00E+00	1.08E-01	1.00E+00	2.70E-01	1.00E+00	4.90E-01	1.00E+00	2.67E-01	1.00E+00	tricarboxylic acid cycle	P
GO:0006100	22	4.30E-02	1.00E+00	1.48E-01	1.00E+00	7.06E-02	1.00E+00	3.83E-02	1.00E+00	3.54E-02	1.00E+00	2.12E-01	1.00E+00	7.06E-01	1.00E+00	6.97E-01	1.00E+00	tricarboxylic acid cycle intermediate metabc	P
GO:0006109	18	2.67E-01	1.00E+00	4.32E-01	1.00E+00	2.01E-01	1.00E+00	3.72E-01	1.00E+00	2.31E-01	1.00E+00	2.82E-01	1.00E+00	6.19E-01	1.00E+00	9.95E-01	1.00E+00	regulation of carbohydrate metabolism	P
GO:0006110	10	6.34E-02	1.00E+00	2.28E-01	1.00E+00	6.18E-02	1.00E+00	1.64E-01	1.00E+00	8.58E-02	1.00E+00	2.46E-01	1.00E+00	1.02E-01	1.00E+00	8.30E-01	1.00E+00	regulation of glycolysis	P
GO:0006112	63	5.96E-01	1.00E+00	5.70E-01	1.00E+00	6.33E-01	1.00E+00	6.75E-01	1.00E+00	4.33E-01	1.00E+00	3.16E-01	1.00E+00	8.73E-01	1.00E+00	9.16E-01	1.00E+00	energy reserve metabolism	P
GO:0006118	59	5.53E-04	3.37E-02	3.74E-02	1.00E+00	4.44E-02	1.00E+00	3.12E-01	1.00E+00	1.21E-03	7.80E-02	5.05E-02	1.00E+00	3.13E-02	1.00E+00	7.47E-02	1.00E+00	electron transport	P
GO:0006119	77	1.93E-06	1.95E-03	1.17E-02	6.77E-01	4.38E-03	3.27E-01	5.67E-02	1.00E+00	7.62E-06	2.88E-03	2.54E-02	1.00E+00	4.20E-03	3.57E-01	1.19E-01	1.00E+00	oxidative phosphorylation	P
GO:0006120	37	1.78E-04	2.50E-02	1.99E-02	1.00E+00	3.99E-02	1.00E+00	1.09E-01	1.00E+00	8.28E-04	4.40E-02	4.29E-02	1.00E+00	1.62E-02	6.63E-01	6.51E-02	1.00E+00	mitochondrial electron transport, NADH to u	P
GO:0006139	4139	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.22E-25	0.00E+00	7.05E-33	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.75E-23	0.00E+00	4.72E-26	0.00E+00	nucleobase, nucleoside, nucleotide and nuc	P
GO:0006140	16	1.04E-01	1.00E+00	9.05E-02	1.00E+00	2.83E-01	1.00E+00	1.08E-01	1.00E+00	8.42E-02	1.00E+00	1.28E-01	1.00E+00	4.06E-01	1.00E+00	3.13E-01	1.00E+00	regulation of nucleotide metabolism	P
GO:0006144	10	2.27E-02	1.00E+00	8.23E-02	1.00E+00	7.15E-01	1.00E+00	1.92E-01	1.00E+00	2.91E-02	1.00E+00	3.74E-02	1.00E+00	1.71E-02	9.11E-01	5.46E-01	1.00E+00	purine base metabolism	P
GO:0006163	80	5.56E-04	3.37E-02	8.89E-03	5.03E-01	2.79E-02	1.00E+00	4.13E-02	1.00E+00	4.27E-04	2.20E-02	7.04E-03	5.30E-01	1.17E-01	1.00E+00	3.14E-01	1.00E+00	purine nucleotide metabolism	P
GO:0006164	65	3.66E-04	3.37E-02	4.36E-02	1.00E+00	2.23E-02	1.00E+00	7.23E-02	1.00E+00	6.49E-04	4.00E-02	3.88E-02	1.00E+00	2.54E-02	1.00E+00	5.38E-01	1.00E+00	purine nucleotide biosynthesis	P
GO:0006171	20	5.77E-01	1.00E+00	4.21E-01	1.00E+00	7.38E-01	1.00E+00	4.55E-01	1.00E+00	3.85E-01	1.00E+00	3.55E-01	1.00E+00	7.71E-01	1.00E+00	5.52E-01	1.00E+00	cAMP biosynthesis	P
GO:0006182	13	9.56E-01	1.00E+00	7.09E-01	1.00E+00	9.50E-01	1.00E+00	6.23E-01	1.00E+00	9.61E-01	1.00E+00	6.93E-01	1.00E+00	3.91E-01	1.00E+00	8.99E-01	1.00E+00	cGMP biosynthesis	P
GO:0006183	11	2.48E-02	1.00E+00	1.66E-01	1.00E+00	2.36E-02	1.00E+00	1.63E-01	1.00E+00	3.63E-02	1.00E+00	2.35E-01	1.00E+00	1.88E-01	1.00E+00	2.38E-01	1.00E+00	GTP biosynthesis	P
GO:0006206	10	1.05E-01	1.00E+00	1.35E-01	1.00E+00	2.70E-01	1.00E+00	2.46E-01	1.00E+00	1.01E-01	1.00E+00	1.99E-01	1.00E+00	2.63E-01	1.00E+00	4.84E-02	1.00E+00	pyrimidine base metabolism	P
GO:0006213	12	4.67E-01	1.00E+00	3.76E-01	1.00E+00	9.84E-01	1.00E+00	1.23E-01	1.00E+00	3.53E-01	1.00E+00	8.81E-01	1.00E+00	2.75E-01	1.00E+00	4.97E-02	1.00E+00	pyrimidine nucleoside metabolism	P
GO:0006220	31	4.26E-02	1.00E+00	1.30E-02	7.47E-01	4.64E-01	1.00E+00	2.54E-02	1.00E+00	2.26E-02	1.00E+00	3.05E-02	1.00E+00	9.71E-02	1.00E+00	2.73E-02	1.00E+00	pyrimidine nucleotide metabolism	P
GO:0006221	22	2.66E-02	1.00E+00	4.05E-02	1.00E+00	3.55E-01	1.00E+00	4.92E-02	1.00E+00	1.57E-02	1.00E+00	7.98E-02	1.00E+00	9.04E-02	1.00E+00	1.12E-01	1.00E+00	pyrimidine nucleotide biosynthesis	P
GO:0006228	11	2.48E-02	1.00E+00	1.66E-01	1.00E+00	2.36E-02	1.00E+00	1.63E-01	1.00E+00	3.63E-02	1.00E+00	2.35E-01	1.00E+00	1.88E-01	1.00E+00	2.38E-01	1.00E+00	UTP biosynthesis	P
GO:0006241	12	2.15E-02	1.00E+00	1.03E-01	1.00E+00	5.38E-02	1.00E+00	8.83E-02	1.00E+00	2.46E-02	1.00E+00	1.88E-01	1.00E+00	1.70E-01	1.00E+00	1.59E-01	1.00E+00	CTP biosynthesis	P
GO:0006259	905	4.15E-22	0.00E+00	2.26E-23	0.00E+00	1.12E-09	9.34E-04	2.88E-11	0.00E+00	9.28E-21	0.00E+00	2.95E-21	0.00E+00	4.64E-06	2.00E-03	8.19E-07	1.88E-03	DNA metabolism	P
GO:0006260	222	3.33E-12	0.00E+00	3.88E-10	0.00E+00	2.53E-06	2.42E-03	5.93E-07	1.96E-03	1.42E-10	0.00E+00	6.06E-10	0.00E+00	1.61E-04	2.50E-02	4.99E-02	1.00E+00	DNA replication	P
GO:0006261	119	4.50E-08	1.84E-03	3.03E-07	8.39E-03	5.39E-04	3.60E-02	5.35E-05	8.00E-03	9.06E-08	1.69E-03	5.83E-07	2.97E-03	4.13E-03	3.57E-01	3.48E-01	1.00E+00	DNA-dependent DNA replication	P
GO:0006265	24	5.71E-02	1.00E+00	5.60E-01	1.00E+00	1.53E-01	1.00E+00	1.35E-01	1.00E+00	1.61E-01	1.00E+00	7.24E-01	1.00E+00	1.08E-01	1.00E+00	8.23E-01	1.00E+00	DNA topological change	P
GO:0006268	13	9.33E-03	6.67E-01	2.02E-01	1.00E+00	1.19E-01	1.00E+00	1.88E-01	1.00E+00	8.96E-04	4.40E-02	2.01E-01	1.00E+00	2.41E-01	1.00E+00	9.06E-01	1.00E+00	DNA unwinding during replication	P
GO:0006270	28	4.79E-03	3.28E-01	2.59E-03	1.77E-01	1.48E-02	6.93E-01	2.18E-01	1.00E+00	2.54E-02	1.00E+00	1.32E-03	6.40E-02	3.75E-02	1.00E+00	2.78E-02	1.00E+00	DNA replication initiation	P
GO:0006275	46	3.30E-04	3.37E-02	2.35E-03	1.77E-01	1.25E-03	9.80E-02	7.07E-03	4.53E-01	8.94E-04	4.40E-02	4.64E-03	2.70E-01	1.17E-01	1.00E+00	1.29E-01	1.00E+00	regulation of DNA replication	P
GO:0006281	296	1.59E-08	9.77E-04	6.73E-08	4.97E-03	1.38E-04	1.50E-02	1.37E-06	2.00E-03	9.67E-08	1.69E-03	3.25E-07	2.97E-03	1.15E-02	6.30E-01	1.99E-01	1.00E+00	DNA repair	P
GO:0006284	27	1.18E-02	6.67E-01	7.21E-02	1.00E+00	1.25E-01	1.00E+00	1.22E-02	8.18E-01	8.48E-03	5.39E-01	6.49E-02	1.00E+00	5.18E-01	1.00E+00	9.91E-01	1.00E+00	base-excision repair	P
GO:0006289	57	5.30E-04	3.37E-02	4.13E-02	1.00E+00	5.88E-02	1.00E+00	6.78E-02	1.00E+00	4.99E-04	2.20E-02	2.90E-02	1.00E+00	4.92E-02	1.00E+00	9.39E-01	1.00E+00	nucleotide-excision repair	P
GO:0006297	17	1.30E-04	2.50E-02	1.95E-02	1.00E+00	1.29E-01	1.00E+00	1.90E-01	1.00E+00	8.10E-06	2.88E-03	3.59E-03	2.70E-01	9.27E-02	1.00E+00	5.36E-01	1.00E+00	nucleotide-excision repair, DNA gap filling	P
GO:0006298	29	1.43E-03	2.02E-01	1.62E-04	1.50E-02	1.55E-01	1.00E+00	3.05E-03	1.47E-01	6.26E-04	4.00E-02	8.03E-05	1.70E-02	7.89E-02	1.00E+00	8.76E-01	1.00E+00	mismatch repair	P
GO:0006302	40	2.22E-02	1.00E+00	1.56E-03	9.10E-02	6.33E-03	4.60E-01	1.28E-01	1.00E+00	1.19E-01	1.00E+00	4.66E-04	4.10E-02	8.92E-02	1.00E+00	3.15E-01	1.00E+00	double-strand break repair	P
GO:0006303	10	4.31E-01	1.00E+00	6.05E-01	1.00E+00	3.17E-01	1.00E+00	1.00E+00	1.00E+00	4.31E-01	1.00E+00	5.42E-02	1.00E+00	3.95E-01	1.00E+00	9.99E-01	1.00E+00	double-strand break repair via nonhomologo	P
GO:0006304	30	1.28E-01	1.00E+00	4.03E-02	1.00E+00	2.32E-01	1.00E+00	5.93E-02	1.00E+00	9.57E-02	1.00E+00	1.68E-02	8.60E-01	5.89E-01	1.00E+00	5.59E-01	1.00E+00	DNA modification	P
GO:0006305	20	2.80E-02	1.00E+00	1.19E-02	6.77E-01	6.82E-02	1.00E+00	5.14E-02	1.00E+00	4.85E-02	1.00E+00	5.19E-03	2.70E-01	3.85E-01	1.00E+00	2.46E-01	1.00E+00	DNA alkylation	P
GO:0006306	20	2.80E-02	1.00E+00	1.19E-02	6.77E-01	6.82E-02	1.00E+00	5.14E-02	1.00E+00	4.85E-02	1.00E+00	5.19E-03	2.70E-01	3.85E-01	1.00E+00	2.46E-01	1.00E+00	DNA methylation	P
GO:0006308	24	5.58E-02	1.00E+00	2.63E-02	1.00E+00	1.18E-01	1.00E+00	6.33E-03	3.64E-01	1.29E-01	1.00E+00	2.41E-01	1.00E+00	1.20E-01	1.00E+00	2.07E-01	1.00E+00	DNA catabolism	P
GO:0006309	16	2.03E-01	1.00E+00	2.14E-01	1.00E+00	2.67E-01	1.00E+00	2.36E-02	1.00E+00	2.68E-01	1.00E+00	5.30E-01	1.00E+00	2.73E-01	1.00E+00	8.28E-01	1.00E+00	DNA fragmentation during apoptosis	P
GO:0006310	110	5.09E-04	3.37E-02	1.19E-04	1.50E-02	1.85E-02	1.00E+00	1.20E-03	1.15E-01	6.09E-04	4.00E-02	1.24E-04	1.70E-02	2.82E-01	1.00E+00	5.46E-01	1.00E+00	DNA recombination	P
GO:0006323	413	1.49E-10	0.00E+00	1.09E-13	0.00E+00	3.50E-03	3.27E-01	1.45E-03	1.15E-01	7.48E-12	0.00E+00	2.73E-13	0.00E+00	2.72E-03	1.95E-01	1.20E-07	1.88E-03	DNA packaging	P
GO:0006325	409	4.91E-10	8.06E-04	2.61E-13	0.00E+00	4.98E-03	4.19E-01	2.53E-03	1.47E-01	2.96E-11	0.00E+00	2.86E-13	0.00E+00	2.61E-03	1.95E-01	3.25E-07	1.88E-03	establishment and/or maintenance of chron	P
GO:0006333	234	1.52E-03	2.02E-01	3.24E-03	1.97E-01	7.92E-01	1.00E+00	8.49E-01	1.00E+00	6.64E-05	1.70E-02	1.99E-03	1.61E-01	2.95E-02	1.00E+00	2.52E-04	2.70E-02	chromatin assembly or disassembly	P
GO:0006334	179	3.85E-02	1.00E+00	9.08E-02	1.00E+00	9.97E-01	1.00E+00	9.62E-01	1.00E+00	1.48E-03	1.76E-01	5.42E-02	1.00E+00	9.84E-02	1.00E+00	1.06E-02	4.81E-01	nucleosome assembly	P
GO:0006338	55	9.95E-06	7.00E-03	1.16E-06	8.39E-03	4.09E-03	3.27E-01	4.70E-04	4.70E-02	3.09E-06	2.60E-03	1.63E-05	7.63E-03	3.39E-02	1.00E+00	2.91E-04	2.70E-02	chromatin remodeling	P
GO:0006342	13	7.22E-03	6.34E-01	2.29E-02	1.00E+00	1.38E-01	1.00E+00	7.05E-02	1.00E+00	1.79E-03	1.76E-01	4.10E-02	1.00E+00	8.64E-02	1.00E+00	1.34E-02	6.47E-01	chromatin silencing	P
GO:0006350	2793	7.29E-32	0.00E+00	3.75E-41	0.00E+00	3.68E-13	0.00E+00	3.28E-17	0.00E+00	7.88E-31	0.00E+00	1.57E-36	0.00E+00	1.36E-10	0.00E+00	1.21E-15	0.00E+00	transcription	P
GO:0006351	2589	2.79E-28	0.00E+00	2.14E-35	0.00E+00	8.62E-11	9.34E-04	1.30E-13	0.00E+00	2.08E-28	0.00E+00	9.83E-32	0.00E+00	3.67E-09	0.00E+00	1.93E-15	0.00E+00	transcription, DNA-dependent	P
GO:0006352	106	1.09E-09	8.06E-04	4.23E-06	8.39E-03	5.04E-05	1.20E-02	1.09E-02	8.18E-01	9.26E-08	1.69E-03	7.39E-06	4.88E-03	1.52E-03	1.68E-01	6.78E-03	4.81E-01	transcription initiation	P
GO:0006354	50	4.92E-06	7.00E-03	1.51E-05	9.58E-03	6.00E-04	3.60E-02	8.79E-03	7.13E-01	5.55E-05	6.35E-03	5.64E-05	1.70E-02	4.36E-03	3.57E-01	7.10E-03	4.81E-01	RNA elongation	P
GO:0006355	2516	1.98E-26	0.00E+00	9.48E-34	0.00E+00	3.57E-10	9.34E-04	2.43E-13	0.00E+00	1.65E-26	0.00E+00	2.44E-30	0.00E+00	1.21E-08	8.55E-04	1.90E-14	0.00E+00	regulation of transcription, DNA-dependent	P
GO:0006357	563	1.24E-04	2.50E-02	5.19E-03	3.60E-01	9.88E-04	9.80E-02	7.30E-03	4.55E-01	5.16E-04	2.20E-02	2.18E-02	1.00E+00	3.38E-02	1.00E+00	8.41E-02	1.00E+00	regulation of transcription from RNA polyme	P

GO:0006360	11	1.38E-01	1.00E+00	5.41E-01	1.00E+00	2.96E-01	1.00E+00	4.49E-01	1.00E+00	1.66E-01	1.00E+00	5.90E-01	1.00E+00	9.18E-02	1.00E+00	7.11E-01	1.00E+00	transcription from RNA polymerase I promo	P
GO:0006364	71	5.64E-03	3.50E-01	1.06E-01	1.00E+00	8.87E-02	1.00E+00	3.25E-01	1.00E+00	4.41E-03	3.60E-01	2.28E-01	1.00E+00	1.39E-01	1.00E+00	1.08E-01	1.00E+00	rRNA processing	P
GO:0006366	728	5.44E-08	1.84E-03	6.17E-06	8.39E-03	2.27E-05	6.00E-03	2.71E-04	2.70E-02	4.12E-07	1.69E-03	6.56E-05	1.70E-02	5.43E-03	3.57E-01	1.48E-02	8.49E-01	transcription from RNA polymerase II promo	P
GO:0006367	68	6.95E-08	1.84E-03	1.02E-05	9.58E-03	5.27E-05	1.20E-02	4.34E-03	3.46E-01	5.72E-06	2.88E-03	8.63E-06	4.88E-03	3.71E-03	3.57E-01	1.82E-01	1.00E+00	transcription initiation from RNA polymerase	P
GO:0006368	47	1.28E-05	7.00E-03	1.41E-05	9.58E-03	7.80E-04	4.50E-02	1.15E-02	8.18E-01	1.21E-04	1.70E-02	3.90E-05	1.20E-02	6.16E-03	3.57E-01	8.59E-03	4.81E-01	RNA elongation from RNA polymerase II pr	P
GO:0006376	16	5.99E-02	1.00E+00	2.70E-02	1.00E+00	5.90E-02	1.00E+00	1.15E-02	8.18E-01	1.51E-01	1.00E+00	4.79E-02	1.00E+00	1.31E-01	1.00E+00	5.65E-01	1.00E+00	mRNA splice site selection	P
GO:0006383	28	7.58E-03	6.34E-01	2.91E-02	1.00E+00	1.75E-01	1.00E+00	2.60E-01	1.00E+00	1.29E-02	1.00E+00	3.18E-02	1.00E+00	2.81E-02	1.00E+00	1.20E-01	1.00E+00	transcription from RNA polymerase III prom	P
GO:0006396	497	3.31E-27	0.00E+00	1.24E-25	0.00E+00	4.47E-12	0.00E+00	2.28E-11	0.00E+00	7.07E-24	0.00E+00	8.18E-22	0.00E+00	3.84E-09	0.00E+00	6.20E-10	7.71E-04	RNA processing	P
GO:0006397	301	4.43E-18	0.00E+00	1.37E-20	0.00E+00	2.99E-09	9.34E-04	7.37E-09	9.71E-04	2.90E-15	0.00E+00	1.25E-18	0.00E+00	1.36E-06	1.95E-03	5.47E-08	1.88E-03	mRNA processing	P
GO:0006399	136	3.98E-05	1.00E-02	1.16E-04	1.50E-02	5.04E-03	4.19E-01	1.49E-02	8.18E-01	5.17E-05	6.35E-03	2.44E-04	2.60E-02	3.79E-02	1.00E+00	3.85E-02	1.00E+00	tRNA metabolism	P
GO:0006400	12	3.87E-01	1.00E+00	2.40E-01	1.00E+00	5.27E-01	1.00E+00	8.67E-01	1.00E+00	3.78E-01	1.00E+00	5.18E-02	1.00E+00	2.00E-01	1.00E+00	7.53E-01	1.00E+00	tRNA modification	P
GO:0006401	48	4.59E-08	1.84E-03	2.74E-06	8.39E-03	1.04E-03	9.80E-02	5.10E-03	3.46E-01	3.66E-06	2.60E-03	1.01E-05	4.88E-03	8.07E-05	2.50E-02	3.50E-03	1.85E-01	RNA catabolism	P
GO:0006402	31	9.96E-09	8.06E-04	4.85E-05	9.58E-03	1.84E-04	2.40E-02	6.68E-03	4.53E-01	3.68E-07	1.69E-03	2.11E-04	2.60E-02	2.97E-04	3.40E-02	4.02E-03	1.85E-01	mRNA catabolism	P
GO:0006403	90	1.83E-07	1.95E-03	8.44E-11	0.00E+00	1.96E-04	2.40E-02	4.90E-06	8.00E-03	7.26E-07	2.45E-03	7.25E-10	0.00E+00	2.30E-02	1.00E+00	1.95E-04	2.00E-02	RNA localization	P
GO:0006405	33	1.47E-06	1.95E-03	7.06E-05	1.00E-02	2.23E-04	2.40E-02	6.77E-03	4.53E-01	6.79E-05	1.70E-02	2.73E-05	1.20E-02	2.05E-02	9.11E-01	4.92E-03	3.60E-01	RNA export from nucleus	P
GO:0006406	25	6.87E-05	1.24E-02	8.81E-04	6.90E-02	2.41E-03	2.48E-01	1.60E-02	8.18E-01	7.01E-04	4.00E-02	3.31E-04	3.07E-02	1.37E-02	6.47E-01	9.71E-03	4.81E-01	mRNA export from nucleus	P
GO:0006412	805	2.67E-20	0.00E+00	8.12E-15	0.00E+00	1.62E-09	9.34E-04	6.54E-05	1.20E-02	5.80E-18	0.00E+00	6.99E-15	0.00E+00	1.86E-08	8.55E-04	3.09E-06	1.88E-03	protein biosynthesis	P
GO:0006413	67	2.26E-07	1.95E-03	2.59E-07	8.39E-03	1.04E-04	1.20E-02	5.24E-04	4.70E-02	3.26E-07	1.69E-03	1.22E-06	2.97E-03	2.20E-02	1.00E+00	4.56E-03	3.60E-01	translational initiation	P
GO:0006414	105	9.43E-11	0.00E+00	5.79E-10	0.00E+00	1.84E-03	2.48E-01	3.99E-03	2.41E-01	1.10E-10	0.00E+00	1.32E-07	9.20E-04	2.31E-04	3.40E-02	2.31E-06	1.88E-03	translational elongation	P
GO:0006415	11	1.44E-02	6.67E-01	6.28E-02	1.00E+00	5.56E-02	1.00E+00	3.93E-02	1.00E+00	6.36E-02	1.00E+00	1.55E-01	1.00E+00	1.25E-02	6.30E-01	5.14E-02	1.00E+00	translational termination	P
GO:0006417	183	2.21E-04	2.64E-02	1.62E-05	9.58E-03	4.13E-05	1.20E-02	5.47E-04	4.70E-02	5.16E-03	4.18E-01	7.56E-05	1.70E-02	2.32E-02	1.00E+00	5.13E-03	3.60E-01	regulation of protein biosynthesis	P
GO:0006418	72	3.30E-03	2.73E-01	6.83E-03	3.60E-01	2.18E-02	1.00E+00	1.04E-01	1.00E+00	4.97E-03	4.18E-01	8.80E-03	7.39E-01	1.50E-01	1.00E+00	1.12E-01	1.00E+00	tRNA aminoacylation for protein translation	P
GO:0006445	58	2.08E-06	1.95E-03	9.98E-07	8.39E-03	1.38E-04	1.50E-02	7.32E-04	4.70E-02	2.18E-05	5.00E-03	1.42E-05	7.63E-03	8.51E-03	6.30E-01	6.90E-04	9.16E-02	regulation of translation	P
GO:0006446	42	4.14E-07	1.95E-03	2.52E-06	8.39E-03	1.99E-04	2.40E-02	2.38E-03	1.47E-01	3.85E-06	2.60E-03	1.59E-05	7.63E-03	3.98E-02	1.00E+00	5.54E-03	3.60E-01	regulation of translational initiation	P
GO:0006457	200	2.95E-08	9.77E-04	7.39E-08	4.97E-03	5.02E-05	1.20E-02	3.11E-04	4.20E-02	1.10E-07	1.69E-03	2.89E-08	8.37E-04	1.29E-02	6.30E-01	4.35E-01	1.00E+00	protein folding	P
GO:0006461	474	4.21E-04	3.37E-02	1.31E-06	8.39E-03	4.45E-01	1.00E+00	8.78E-04	5.90E-02	7.17E-05	1.70E-02	1.93E-05	7.63E-03	1.15E-02	6.30E-01	1.61E-03	9.16E-02	protein complex assembly	P
GO:0006464	1894	4.99E-20	0.00E+00	2.80E-35	0.00E+00	1.13E-09	9.34E-04	4.74E-21	0.00E+00	1.10E-19	0.00E+00	5.85E-31	0.00E+00	2.46E-04	3.40E-02	1.07E-11	0.00E+00	protein modification	P
GO:0006468	721	1.44E-04	2.50E-02	3.01E-10	0.00E+00	1.83E-03	2.48E-01	2.11E-08	9.71E-04	1.34E-04	1.70E-02	6.49E-08	8.37E-04	2.00E-01	1.00E+00	2.92E-04	2.70E-02	protein amino acid phosphorylation	P
GO:0006469	64	1.60E-02	6.67E-01	3.67E-03	1.97E-01	1.14E-01	1.00E+00	8.00E-02	1.00E+00	1.12E-02	5.39E-01	4.61E-03	2.70E-01	3.49E-01	1.00E+00	1.33E-01	1.00E+00	negative regulation of protein kinase activity	P
GO:0006470	149	1.25E-01	1.00E+00	2.13E-03	1.29E-01	3.62E-01	1.00E+00	1.09E-02	8.18E-01	1.07E-01	1.00E+00	4.53E-03	2.70E-01	2.76E-01	1.00E+00	4.91E-02	1.00E+00	protein amino acid dephosphorylation	P
GO:0006471	20	2.52E-02	1.00E+00	3.12E-02	1.00E+00	2.12E-01	1.00E+00	3.45E-03	2.02E-01	1.79E-02	1.00E+00	6.00E-02	1.00E+00	1.59E-01	1.00E+00	1.41E-01	1.00E+00	protein amino acid ADP-ribosylation	P
GO:0006473	22	6.57E-04	3.44E-02	9.97E-06	9.58E-03	8.59E-03	4.60E-01	3.55E-02	1.00E+00	1.61E-03	1.76E-01	1.16E-04	1.70E-02	1.54E-01	1.00E+00	5.53E-04	9.16E-02	protein amino acid acetylation	P
GO:0006476	19	9.82E-02	1.00E+00	2.06E-01	1.00E+00	9.31E-02	1.00E+00	2.96E-01	1.00E+00	1.08E-01	1.00E+00	1.16E-01	1.00E+00	3.48E-01	1.00E+00	6.33E-01	1.00E+00	protein amino acid deacetylation	P
GO:0006479	28	4.32E-03	3.28E-01	4.93E-04	6.90E-02	4.55E-01	1.00E+00	1.39E-02	8.18E-01	1.34E-03	7.80E-02	1.11E-03	5.49E-02	1.49E-01	1.00E+00	3.11E-02	1.00E+00	protein amino acid methylation	P
GO:0006486	121	1.82E-01	1.00E+00	6.46E-03	3.60E-01	5.32E-01	1.00E+00	4.44E-01	1.00E+00	9.06E-02	1.00E+00	1.30E-03	6.40E-02	4.75E-01	1.00E+00	5.11E-02	1.00E+00	protein amino acid glycosylation	P
GO:0006487	42	3.68E-01	1.00E+00	1.62E-01	1.00E+00	5.47E-01	1.00E+00	5.85E-01	1.00E+00	2.53E-01	1.00E+00	9.66E-02	1.00E+00	5.76E-01	1.00E+00	2.55E-01	1.00E+00	protein amino acid N-linked glycosylation	P
GO:0006493	24	2.58E-01	1.00E+00	2.17E-01	1.00E+00	1.47E-01	1.00E+00	6.99E-01	1.00E+00	4.09E-01	1.00E+00	1.40E-01	1.00E+00	2.99E-01	1.00E+00	2.08E-01	1.00E+00	protein amino acid O-linked glycosylation	P
GO:0006497	51	1.43E-03	2.02E-01	1.37E-01	1.00E+00	9.91E-02	1.00E+00	3.94E-01	1.00E+00	6.79E-04	4.00E-02	8.70E-02	1.00E+00	1.58E-01	1.00E+00	3.35E-01	1.00E+00	protein amino acid lipidation	P
GO:0006505	34	1.19E-02	6.67E-01	1.61E-01	1.00E+00	4.57E-02	1.00E+00	3.33E-01	1.00E+00	1.39E-02	1.00E+00	1.09E-01	1.00E+00	1.74E-01	1.00E+00	5.46E-01	1.00E+00	GPI anchor metabolism	P
GO:0006506	31	1.53E-02	6.67E-01	1.82E-01	1.00E+00	7.95E-02	1.00E+00	2.69E-01	1.00E+00	1.44E-02	1.00E+00	1.58E-01	1.00E+00	2.84E-01	1.00E+00	4.93E-01	1.00E+00	GPI anchor biosynthesis	P
GO:0006508	852	1.06E-03	9.60E-02	3.81E-08	4.97E-03	1.20E-02	5.32E-01	3.94E-04	4.20E-02	2.39E-03	2.85E-01	2.94E-07	9.41E-04	5.43E-02	1.00E+00	4.21E-05	9.00E-03	proteolysis	P
GO:0006509	12	2.37E-01	1.00E+00	1.58E-01	1.00E+00	5.27E-01	1.00E+00	3.87E-01	1.00E+00	1.40E-01	1.00E+00	1.24E-01	1.00E+00	6.40E-01	1.00E+00	3.17E-01	1.00E+00	membrane protein ectodomain proteolysis	P
GO:0006511	230	5.01E-06	7.00E-03	1.07E-09	0.00E+00	1.23E-02	5.32E-01	1.03E-05	8.00E-03	2.36E-05	5.00E-03	2.24E-08	8.37E-04	8.30E-04	6.50E-02	2.35E-04	2.70E-02	ubiquitin-dependent protein catabolism	P
GO:0006512	594	3.46E-14	0.00E+00	1.79E-17	0.00E+00	2.59E-07	2.42E-03	3.52E-11	0.00E+00	1.34E-12	0.00E+00	3.44E-15	0.00E+00	1.03E-04	2.50E-02	9.23E-07	1.88E-03	ubiquitin cycle	P
GO:0006515	18	2.10E-02	1.00E+00	2.66E-06	8.39E-03	7.48E-02	1.00E+00	4.69E-02	1.00E+00	7.63E-02	1.00E+00	5.44E-05	1.70E-02	3.98E-02	1.00E+00	8.88E-03	4.81E-01	misfolded or incompletely synthesized prote	P
GO:0006516	17	5.11E-01	1.00E+00	1.04E-01	1.00E+00	7.64E-01	1.00E+00	4.58E-01	1.00E+00	3.00E-01	1.00E+00	1.66E-01	1.00E+00	5.94E-01	1.00E+00	4.92E-02	1.00E+00	glycoprotein catabolism	P
GO:0006518	23	2.53E-01	1.00E+00	9.88E-01	1.00E+00	3.60E-01	1.00E+00	9.66E-01	1.00E+00	1.79E-01	1.00E+00	9.36E-01	1.00E+00	7.50E-01	1.00E+00	9.99E-01	1.00E+00	peptide metabolism	P
GO:0006519	478	1.47E-03	2.02E-01	5.67E-04	6.90E-02	1.40E-03	9.80E-02	1.04E-03	8.30E-02	3.02E-03	2.85E-01	1.29E-03	6.40E-02	2.39E-01	1.00E+00	2.60E-01	1.00E+00	amino acid and derivative metabolism	P
GO:0006520	393	4.51E-03	3.28E-01	1.11E-03	9.10E-02	3.56E-03	3.27E-01	3.29E-03	1.47E-01	7.22E-03	5.39E-01	2.26E-03	1.64E-01	4.21E-01	1.00E+00	3.22E-01	1.00E+00	amino acid metabolism	P
GO:0006521	91	8.89E-01	1.00E+00	9.37E-01	1.00E+00	4.29E-01	1.00E+00	4.50E-01	1.00E+00	8.66E-01	1.00E+00	9.59E-01	1.00E+00	9.83E-01	1.00E+00	9.61E-01	1.00E+00	regulation of amino acid metabolism	P
GO:0006525	13	2.74E-01	1.00E+00	5.62E-02	1.00E+00	3.43E-01	1.00E+00	2.32E-01	1.00E+00	3.06E-01	1.00E+00	3.33E-02	1.00E+00	2.86E-01	1.00E+00	2.20E-01	1.00E+00	arginine metabolism	P
GO:0006536	14	1.51E-01	1.00E+00	3.45E-01	1.00E+00	3.10E-01	1.00E+00	1.73E-01	1.00E+00	1.43E-01	1.00E+00	4.43E-01	1.00E+00	1.51E-01	1.00E+00	5.69E-01	1.00E+00	glutamate metabolism	P
GO:0006541	18	4.50E-02	1.00E+00	2.86E-01	1.00E+00	6.15E-01	1.00E+00	9.73E-01	1.00E+00	1.36E-02	1.00E+00	4.56E-02	1.00E+00	5.64E-01	1.00E+00	7.01E-01	1.00E+00	glutamine metabolism	P
GO:0006544	14	3.30E-01	1.00E+00	7.45E-02	1.00E+00	9.09E-01	1.00E+00	9.85E-02	1.00E+00	1.75E-01	1.00E+00	4.96E-02	1.00E+00	4.54E-01	1.00E+00	5.04E-01	1.00E+00	glycine metabolism	P
GO:0006547	12	6.77E-01	1.00E+00	9.65E-01	1.00E+00	3.41E-01	1.00E+00	8.26E-01	1.00E+00	6.47E-01	1.00E+00	9.35E-01	1.00E+00	9.54E-01	1.00E+00	9.51E-01	1.00E+00	histidine metabolism	P
GO:0006555	10	6.76E-01	1.00E+00	4.12E-01	1.00E+00	5.82E-01	1.00E+00	5.29E-01	1.00E+00	4.95E-01	1.00E+00	2.99E-01	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	methionine metabolism	P
GO:0006560	10	1.94E-02	1.00E+00	3.22E-02	1.00E+00	8.00E-02	1.00E+00	9.06E-03	7.13E-01	4.97E-02	1.00E+00	9.43E-02	1.00E+00	6.34E-02	1.00E+00	6.65E-02	1.00E+00	proline metabolism	P
GO:0006570	13	8.02E-01	1.00E+00	5.00E-01	1.00E+00	8.68E-01	1.00E+00	5.92E-01	1.00E+00	6.00E-01	1.00E+00	6.68E-01	1.00E+00	9.83E-01	1.00E+00	1.12E-01	1.00E+00	tyrosine metabolism	P
GO:0006575	146	1.44E-01	1.00E+00	1.23E-01	1.00E+00	7.00E-02	1.00E+00	4.33E-02	1.00E+00	3.00E-01	1.00E+00	1.86E-01	1.00E+00	1.28E-01	1.00E+00	2.34E-01	1.00E+00	amino acid derivative metabolism	P
GO:0006576	79	5.80E-01	1.00E+00	4.62E-01	1.00E+00	3.61E-01	1.00E+00	1.61E-01	1.00E+00	6.43E-01	1.00E+00	4.81E-01	1.00E+00	4.92E-01	1.00E+00	7.05E-01	1.00E+00	biogenic amine metabolism	P
GO:0006582	10	8.69E-01	1.00E+00	7.80E-01	1.00E+00	8.50E-01	1.00E+00	2.10E-01	1.00E+00	6.54E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.13E-01	1.00E+00	melanin metabolism	P
GO:0006584	32	8.24E-01	1.00E+00	5.88E-01	1.00E+00	3.88E-01	1.00E+00	1.25E-01	1.00E+00	9.06E-01	1.00E+00	7.27E-01	1.00E+00	8.37E-01	1.00E+00	4.49E-01	1.00E+00	catecholamine metabolism	P
GO:0006586	11	2.45E-01	1.00E+00	4.27E-01	1.00E+00	1.96E-01	1.00E+00	7.02E-01	1.00E+00	6.42E-01	1.00E+00	2.32E-01	1.00E+00	7.19E-02	1.00E+00	7.27E-01	1.00E+00	indolalkylamine metabolism	P
GO:0006595	15	2.58E-02	1.00E+00	5.82E-04	6.90E-02	1.18E-01	1.00E+00	6.11E-03	3.46E-01	1.85E-02	1.00E+00	1.53E-03	1.61E-01	1.73E-01	1.00E+00	1.11E-02	5.11E-01	polyamine metabolism	P
GO:0006596	10	1.07E-01	1.00E+00	1.69E-03	9.10E-02	1.98E-01	1.00E+00	3.01E-03	1.47E-01	1.09E-01	1.00E+00	1.65E-02	8.60E-01	2.41E-01	1.00E+00	5.27E-06	1.88E-03	polyamine biosynthesis	P
GO:0006605	215	9.68E-09	8.06E-04	3.60E-10	0.00E+00	3.43E-05	6.00E-03	1.43E-03	1.15E-01	4.95E-08	9.64E-04	2.50E-10	0.00E+00	3.22E-03	1.95E-01	3.28E-04	2.70E-02	protein targeting	P
GO:0006606	98	5.76E-05	1.10E-02	3.99E-08	4.97E-03	5.03E-02	1.00E+00	3.65E-03	2.02E-01	4.42E-05	6.35E-03	1.80E-07	9.20E-04	4.76E-03	3.57E-01	2.75E-03	1.85E-01	protein import into nucleus	P
GO:0006607	13	1.81E-01	1.00E+00	5.83E-03	3.60E-01	3.57E-01	1.00E+00	2.67E-02	1.00E+00	1.70E-01	1.00E+00	1.36E-02	7.39E-01	9.54E-02	1.00E+00	1.56E-01	1.00E+00	NLS-bearing substrate import into nucleus	P
GO:0006611	20	1.62E-03	2.02E-01	6.50E-04	6.90E-02	3.20E-02	1.00E+00	2.00E-02	1.00E+00	1.24E-03	7.80E-02	4.07E-04	4.10E-02	2.29E-01	1.00E+00	5.23E-03	3.60E-01	protein export from nucleus	P
GO:0006612	30	3.47E-02	1.00E+00	3.03E-01	1.00E+00	5.38E-02	1.00E+00	7.76E-01	1.00E+00	7.20E-02	1.00E+00	4.21E-01	1.00E+00	3.26E-02	1.00E+00	6.07E-02	1.00E+00	protein targeting to membrane	P
GO:0006613	17	2.30E-01	1.00E+00	5.87E-01	1.00E+00	1.47E-01	1.00E+00	9.66E-01	1.00E+00	3.45E-01	1.00E+00	5.75E-01	1.00E+00	1.91E-01	1.00E+00	1.78E-01	1.00E+00	cotranslational protein targeting to membrai	P
GO:0006614	11	3.25E-01	1.00E+00	4.08E-01	1.00E+00	2.42E-01	1.00E+00	8.44E-01	1.00E+00	3.76E-01	1.00E+00	4.66E-01	1.00E+00	4.03E-01	1.00E+00	1.07E-01	1.00E+00	SRP-dependent cotranslational protein targ	P
GO:0006625	13	1.99E-01	1.00E+00	2.75E-01	1.00E+00	5.38E-01	1.00E+00	5.72E-01	1.00E+00	1.60E-01	1.00E+00	1.83E-01	1.00E+00	3.07E-01	1.00E+00	3.18E-01	1.00E+00	protein targeting to peroxisome	P
GO:0006626	20	4.17E-03	3.28E-01	7.79E-02	1.00E+00	1.27E-02	5.32E-01	2.38E-01	1.00E+00	1.71E-02	1.00E+00	4.88E-02	1.00E+00	2.61E-01	1.00E+00	4.63E-01	1.00E+00	protein targeting to mitochondrion	P
GO:0006629	825	1.79E-03	2.02E-01	2.87E-04	4.19E-02	5.59E-02	1.00E+00	5.07E-03	3.46E-01	4.72E-03	4.18E-01	1.34E-03	6.40E-02	4.11E-03	3.57E-01	1.57E-03	9.16E-02	lipid metabolism	P

GO:0006631	190	7.09E-02	1.00E+00	6.22E-03	3.60E-01	3.76E-01	1.00E+00	9.34E-02	1.00E+00	1.01E-01	1.00E+00	2.15E-02	1.00E+00	2.81E-02	1.00E+00	2.05E-03	1.40E-01	fatty acid metabolism	P
GO:0006633	77	1.17E-01	1.00E+00	2.33E-03	1.77E-01	1.75E-01	1.00E+00	2.52E-02	1.00E+00	2.86E-01	1.00E+00	7.25E-03	5.30E-01	8.33E-02	1.00E+00	7.85E-02	1.00E+00	fatty acid biosynthesis	P
GO:0006635	22	2.25E-01	1.00E+00	1.83E-01	1.00E+00	1.92E-01	1.00E+00	6.48E-01	1.00E+00	1.79E-01	1.00E+00	1.06E-01	1.00E+00	4.42E-01	1.00E+00	2.84E-01	1.00E+00	fatty acid beta-oxidation	P
GO:0006637	11	7.78E-02	1.00E+00	8.05E-02	1.00E+00	2.53E-01	1.00E+00	9.25E-03	7.13E-01	2.74E-02	1.00E+00	2.11E-01	1.00E+00	9.01E-01	1.00E+00	3.61E-01	1.00E+00	acyl-CoA metabolism	P
GO:0006638	35	3.24E-01	1.00E+00	8.87E-02	1.00E+00	2.93E-01	1.00E+00	3.21E-01	1.00E+00	4.33E-01	1.00E+00	7.13E-02	1.00E+00	1.62E-01	1.00E+00	8.84E-02	1.00E+00	neutral lipid metabolism	P
GO:0006639	35	3.24E-01	1.00E+00	8.87E-02	1.00E+00	2.93E-01	1.00E+00	3.21E-01	1.00E+00	4.33E-01	1.00E+00	7.13E-02	1.00E+00	1.62E-01	1.00E+00	8.84E-02	1.00E+00	acylglycerol metabolism	P
GO:0006641	30	2.26E-01	1.00E+00	7.33E-02	1.00E+00	2.36E-01	1.00E+00	2.34E-01	1.00E+00	3.68E-01	1.00E+00	6.29E-02	1.00E+00	8.06E-02	1.00E+00	1.16E-01	1.00E+00	triacylglycerol metabolism	P
GO:0006643	238	2.22E-04	2.64E-02	1.73E-04	1.50E-02	1.89E-02	1.00E+00	8.41E-03	7.13E-01	5.86E-04	4.00E-02	6.89E-04	5.49E-02	1.78E-02	9.11E-01	1.06E-02	4.81E-01	membrane lipid metabolism	P
GO:0006644	181	2.35E-03	2.02E-01	3.41E-03	1.97E-01	2.84E-02	1.00E+00	2.42E-02	1.00E+00	7.32E-03	5.39E-01	6.70E-03	5.30E-01	3.39E-02	1.00E+00	6.17E-02	1.00E+00	phospholipid metabolism	P
GO:0006650	91	1.67E-03	2.02E-01	3.00E-04	4.19E-02	6.44E-02	1.00E+00	1.09E-02	8.18E-01	1.51E-03	1.76E-01	7.62E-04	5.49E-02	9.97E-02	1.00E+00	1.09E-02	5.11E-01	glycerophospholipid metabolism	P
GO:0006662	37	2.17E-01	1.00E+00	7.42E-02	1.00E+00	3.03E-01	1.00E+00	3.52E-01	1.00E+00	2.71E-01	1.00E+00	4.65E-02	1.00E+00	1.35E-01	1.00E+00	9.31E-02	1.00E+00	glycerol ether metabolism	P
GO:0006664	27	1.61E-01	1.00E+00	1.26E-01	1.00E+00	6.25E-01	1.00E+00	6.04E-01	1.00E+00	8.77E-02	1.00E+00	1.29E-01	1.00E+00	3.64E-01	1.00E+00	7.31E-02	1.00E+00	glycolipid metabolism	P
GO:0006665	65	3.75E-03	3.28E-01	4.13E-03	1.97E-01	6.92E-02	1.00E+00	1.75E-01	1.00E+00	4.34E-03	3.60E-01	5.49E-03	2.70E-01	9.50E-02	1.00E+00	4.02E-02	1.00E+00	sphingolipid metabolism	P
GO:0006672	33	8.68E-03	6.34E-01	4.98E-03	3.60E-01	9.09E-02	1.00E+00	1.96E-01	1.00E+00	7.06E-03	5.39E-01	2.04E-02	1.00E+00	1.24E-01	1.00E+00	1.08E-03	9.16E-02	ceramide metabolism	P
GO:0006684	11	4.34E-02	1.00E+00	3.08E-01	1.00E+00	2.38E-02	1.00E+00	4.29E-01	1.00E+00	1.88E-01	1.00E+00	1.82E-01	1.00E+00	1.97E-01	1.00E+00	9.84E-01	1.00E+00	sphingomyelin metabolism	P
GO:0006687	18	3.06E-01	1.00E+00	1.14E-01	1.00E+00	7.18E-01	1.00E+00	6.30E-01	1.00E+00	1.46E-01	1.00E+00	1.17E-01	1.00E+00	8.10E-01	1.00E+00	2.82E-02	1.00E+00	glycosphingolipid metabolism	P
GO:0006690	42	2.46E-01	1.00E+00	6.32E-02	1.00E+00	2.27E-01	1.00E+00	2.02E-01	1.00E+00	3.75E-01	1.00E+00	1.25E-01	1.00E+00	1.56E-01	1.00E+00	1.15E-02	6.47E-01	icosanoid metabolism	P
GO:0006691	23	2.09E-01	1.00E+00	2.80E-01	1.00E+00	2.95E-01	1.00E+00	3.68E-01	1.00E+00	2.90E-01	1.00E+00	3.84E-01	1.00E+00	2.62E-01	1.00E+00	1.19E-01	1.00E+00	leukotriene metabolism	P
GO:0006692	17	3.33E-01	1.00E+00	5.76E-02	1.00E+00	1.63E-01	1.00E+00	1.04E-01	1.00E+00	4.50E-01	1.00E+00	1.19E-01	1.00E+00	2.66E-01	1.00E+00	3.61E-02	1.00E+00	prostanoid metabolism	P
GO:0006693	17	3.33E-01	1.00E+00	5.76E-02	1.00E+00	1.63E-01	1.00E+00	1.04E-01	1.00E+00	4.50E-01	1.00E+00	1.19E-01	1.00E+00	2.66E-01	1.00E+00	3.61E-02	1.00E+00	prostaglandin metabolism	P
GO:0006694	99	7.25E-01	1.00E+00	9.27E-01	1.00E+00	2.50E-01	1.00E+00	5.80E-01	1.00E+00	8.53E-01	1.00E+00	9.49E-01	1.00E+00	6.88E-01	1.00E+00	7.41E-01	1.00E+00	steroid biosynthesis	P
GO:0006695	27	1.57E-01	1.00E+00	1.58E-01	1.00E+00	2.36E-01	1.00E+00	9.85E-02	1.00E+00	1.99E-01	1.00E+00	3.35E-01	1.00E+00	1.81E-01	1.00E+00	2.24E-01	1.00E+00	cholesterol biosynthesis	P
GO:0006700	12	6.23E-01	1.00E+00	9.72E-01	1.00E+00	7.95E-01	1.00E+00	9.89E-01	1.00E+00	4.52E-01	1.00E+00	8.97E-01	1.00E+00	8.47E-01	1.00E+00	9.98E-01	1.00E+00	C21-steroid hormone biosynthesis	P
GO:0006706	18	6.44E-02	1.00E+00	4.19E-01	1.00E+00	3.45E-02	1.00E+00	1.19E-01	1.00E+00	1.39E-01	1.00E+00	6.66E-01	1.00E+00	2.97E-01	1.00E+00	2.15E-01	1.00E+00	steroid catabolism	P
GO:0006707	10	1.89E-01	1.00E+00	5.22E-01	1.00E+00	1.96E-02	1.00E+00	1.09E-01	1.00E+00	5.67E-01	1.00E+00	9.44E-01	1.00E+00	4.47E-01	1.00E+00	2.10E-01	1.00E+00	cholesterol catabolism	P
GO:0006720	30	9.76E-01	1.00E+00	6.70E-01	1.00E+00	5.79E-01	1.00E+00	2.40E-01	1.00E+00	9.99E-01	1.00E+00	7.11E-01	1.00E+00	4.07E-01	1.00E+00	8.99E-01	1.00E+00	isoprenoid metabolism	P
GO:0006725	170	1.58E-01	1.00E+00	6.93E-02	1.00E+00	1.95E-01	1.00E+00	2.00E-02	1.00E+00	1.88E-01	1.00E+00	1.71E-01	1.00E+00	3.12E-01	1.00E+00	1.40E-01	1.00E+00	aromatic compound metabolism	P
GO:0006730	112	7.49E-04	6.71E-02	3.25E-06	8.39E-03	1.06E-01	1.00E+00	3.14E-05	8.00E-03	2.00E-04	1.70E-02	2.58E-05	1.20E-02	2.73E-01	1.00E+00	2.78E-02	1.00E+00	one-carbon compound metabolism	P
GO:0006732	175	3.76E-06	7.00E-03	1.66E-04	1.50E-02	6.26E-06	2.66E-03	2.23E-04	2.70E-02	5.65E-05	6.35E-03	5.76E-03	3.51E-01	5.74E-02	1.00E+00	6.83E-03	4.81E-01	coenzyme metabolism	P
GO:0006733	40	7.39E-03	6.34E-01	1.07E-03	9.10E-02	8.55E-03	4.60E-01	2.61E-03	1.47E-01	5.03E-02	1.00E+00	1.20E-02	7.39E-01	1.82E-02	9.11E-01	5.80E-02	1.00E+00	oxidoreduction coenzyme metabolism	P
GO:0006739	14	2.71E-02	1.00E+00	6.93E-03	3.60E-01	5.55E-02	1.00E+00	8.62E-02	1.00E+00	8.82E-02	1.00E+00	4.84E-02	1.00E+00	2.99E-02	1.00E+00	7.90E-02	1.00E+00	NADP metabolism	P
GO:0006740	10	2.02E-02	1.00E+00	1.13E-02	6.77E-01	1.66E-02	6.93E-01	7.05E-02	1.00E+00	5.05E-02	1.00E+00	8.43E-02	1.00E+00	1.25E-01	1.00E+00	7.32E-02	1.00E+00	NADPH regeneration	P
GO:0006749	28	3.89E-03	3.28E-01	9.88E-02	1.00E+00	3.09E-02	1.00E+00	1.96E-01	1.00E+00	1.87E-02	1.00E+00	2.38E-01	1.00E+00	1.54E-01	1.00E+00	4.87E-02	1.00E+00	glutathione metabolism	P
GO:0006750	10	1.48E-01	1.00E+00	5.38E-01	1.00E+00	2.81E-01	1.00E+00	3.16E-01	1.00E+00	1.47E-01	1.00E+00	6.91E-01	1.00E+00	6.56E-01	1.00E+00	4.76E-01	1.00E+00	glutathione biosynthesis	P
GO:0006752	62	2.63E-03	2.39E-01	8.84E-02	1.00E+00	3.43E-03	3.27E-01	1.30E-01	1.00E+00	4.77E-03	4.18E-01	1.00E-01	1.00E+00	2.18E-01	1.00E+00	3.58E-01	1.00E+00	group transfer coenzyme metabolism	P
GO:0006753	28	6.66E-03	5.17E-01	4.22E-01	1.00E+00	2.03E-02	1.00E+00	3.45E-01	1.00E+00	9.91E-03	5.39E-01	5.45E-01	1.00E+00	1.33E-01	1.00E+00	3.44E-01	1.00E+00	nucleoside phosphate metabolism	P
GO:0006754	28	6.66E-03	5.17E-01	4.22E-01	1.00E+00	2.03E-02	1.00E+00	3.45E-01	1.00E+00	9.91E-03	5.39E-01	5.45E-01	1.00E+00	1.33E-01	1.00E+00	3.44E-01	1.00E+00	ATP biosynthesis	P
GO:0006760	18	7.93E-02	1.00E+00	1.47E-02	1.00E+00	1.02E-01	1.00E+00	1.01E-02	7.13E-01	5.16E-02	1.00E+00	2.56E-02	1.00E+00	8.39E-01	1.00E+00	3.51E-01	1.00E+00	folic acid and derivative metabolism	P
GO:0006766	84	1.79E-01	1.00E+00	1.70E-01	1.00E+00	4.86E-02	1.00E+00	2.96E-01	1.00E+00	4.14E-01	1.00E+00	1.71E-01	1.00E+00	1.81E-01	1.00E+00	2.59E-01	1.00E+00	vitamin metabolism	P
GO:0006767	57	2.44E-02	1.00E+00	8.89E-03	5.03E-01	6.06E-03	4.60E-01	8.29E-02	1.00E+00	1.18E-01	1.00E+00	9.67E-03	7.39E-01	8.77E-02	1.00E+00	8.70E-02	1.00E+00	water-soluble vitamin metabolism	P
GO:0006769	28	4.45E-02	1.00E+00	4.47E-02	1.00E+00	2.04E-02	1.00E+00	1.32E-01	1.00E+00	1.79E-01	1.00E+00	9.07E-02	1.00E+00	4.57E-02	1.00E+00	1.21E-01	1.00E+00	nicotinamide metabolism	P
GO:0006775	24	9.57E-01	1.00E+00	9.93E-01	1.00E+00	9.60E-01	1.00E+00	9.29E-01	1.00E+00	9.60E-01	1.00E+00	9.93E-01	1.00E+00	5.47E-01	1.00E+00	9.35E-01	1.00E+00	fat-soluble vitamin metabolism	P
GO:0006776	19	9.16E-01	1.00E+00	9.86E-01	1.00E+00	8.25E-01	1.00E+00	8.73E-01	1.00E+00	9.64E-01	1.00E+00	9.89E-01	1.00E+00	3.46E-01	1.00E+00	8.10E-01	1.00E+00	vitamin A metabolism	P
GO:0006778	28	1.26E-02	6.67E-01	8.92E-04	6.90E-02	3.86E-04	3.60E-02	1.73E-01	1.00E+00	6.37E-02	1.00E+00	6.94E-04	5.49E-02	6.02E-01	1.00E+00	9.89E-02	1.00E+00	porphyrin metabolism	P
GO:0006779	22	3.91E-02	1.00E+00	1.59E-03	9.10E-02	2.01E-03	2.48E-01	8.89E-02	1.00E+00	1.65E-01	1.00E+00	2.99E-03	2.39E-01	8.01E-01	1.00E+00	1.71E-01	1.00E+00	porphyrin biosynthesis	P
GO:0006783	15	3.51E-02	1.00E+00	1.39E-02	7.47E-01	1.98E-02	1.00E+00	1.54E-02	8.18E-01	9.33E-02	1.00E+00	4.23E-02	1.00E+00	6.14E-01	1.00E+00	5.68E-01	1.00E+00	heme biosynthesis	P
GO:0006790	90	9.71E-02	1.00E+00	8.49E-02	1.00E+00	1.75E-02	6.93E-01	1.41E-01	1.00E+00	1.89E-01	1.00E+00	1.53E-01	1.00E+00	6.50E-01	1.00E+00	2.62E-01	1.00E+00	sulfur metabolism	P
GO:0006793	1037	9.48E-08	1.85E-03	7.01E-17	0.00E+00	2.90E-04	3.60E-02	4.97E-12	0.00E+00	2.16E-07	1.69E-03	6.42E-13	0.00E+00	8.00E-03	6.30E-01	2.30E-07	1.88E-03	phosphorus metabolism	P
GO:0006796	1037	9.48E-08	1.85E-03	7.01E-17	0.00E+00	2.90E-04	3.60E-02	4.97E-12	0.00E+00	2.16E-07	1.69E-03	6.42E-13	0.00E+00	8.00E-03	6.30E-01	2.30E-07	1.88E-03	phosphate metabolism	P
GO:0006800	160	1.61E-01	1.00E+00	7.41E-02	1.00E+00	2.42E-01	1.00E+00	4.10E-02	1.00E+00	8.23E-02	1.00E+00	1.85E-01	1.00E+00	8.04E-01	1.00E+00	1.64E-01	1.00E+00	oxygen and reactive oxygen species metab	P
GO:0006801	22	6.05E-01	1.00E+00	2.26E-01	1.00E+00	7.79E-01	1.00E+00	1.08E-01	1.00E+00	4.92E-01	1.00E+00	2.63E-01	1.00E+00	8.48E-01	1.00E+00	6.91E-01	1.00E+00	superoxide metabolism	P
GO:0006805	30	9.74E-01	1.00E+00	9.87E-01	1.00E+00	7.26E-01	1.00E+00	9.65E-01	1.00E+00	9.77E-01	1.00E+00	9.74E-01	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	xenobiotic metabolism	P
GO:0006807	599	2.39E-03	2.02E-01	1.38E-04	1.50E-02	1.16E-03	9.80E-02	2.27E-04	2.70E-02	3.56E-03	2.85E-01	9.57E-04	5.49E-02	5.21E-01	1.00E+00	8.52E-02	1.00E+00	nitrogen compound metabolism	P
GO:0006809	26	2.22E-01	1.00E+00	1.10E-01	1.00E+00	5.19E-02	1.00E+00	2.82E-02	1.00E+00	3.43E-01	1.00E+00	1.44E-01	1.00E+00	3.89E-01	1.00E+00	6.26E-01	1.00E+00	nitric oxide biosynthesis	P
GO:0006810	3017	1.13E-22	0.00E+00	3.47E-21	0.00E+00	3.27E-11	0.00E+00	1.88E-10	0.00E+00	1.35E-22	0.00E+00	1.09E-21	0.00E+00	2.97E-04	3.40E-02	1.21E-03	9.16E-02	transport	P
GO:0006811	989	3.94E-01	1.00E+00	7.32E-01	1.00E+00	5.31E-01	1.00E+00	5.46E-01	1.00E+00	2.68E-01	1.00E+00	5.32E-01	1.00E+00	8.37E-01	1.00E+00	9.86E-01	1.00E+00	ion transport	P
GO:0006812	690	1.21E-01	1.00E+00	1.58E-01	1.00E+00	3.00E-01	1.00E+00	2.27E-01	1.00E+00	8.99E-02	1.00E+00	1.01E-01	1.00E+00	6.27E-01	1.00E+00	7.03E-01	1.00E+00	cation transport	P
GO:0006813	296	5.70E-01	1.00E+00	8.37E-01	1.00E+00	4.52E-01	1.00E+00	8.65E-01	1.00E+00	5.37E-01	1.00E+00	8.48E-01	1.00E+00	7.56E-01	1.00E+00	3.44E-01	1.00E+00	potassium ion transport	P
GO:0006814	142	9.97E-01	1.00E+00	8.77E-01	1.00E+00	8.83E-01	1.00E+00	7.45E-01	1.00E+00	9.91E-01	1.00E+00	8.48E-01	1.00E+00	1.00E+00	1.00E+00	8.99E-01	1.00E+00	sodium ion transport	P
GO:0006816	166	5.53E-01	1.00E+00	1.04E-01	1.00E+00	5.44E-01	1.00E+00	4.33E-01	1.00E+00	6.22E-01	1.00E+00	2.75E-02	1.00E+00	3.38E-01	1.00E+00	8.37E-01	1.00E+00	calcium ion transport	P
GO:0006817	96	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	phosphate transport	P
GO:0006818	73	3.41E-03	2.73E-01	5.18E-02	1.00E+00	1.56E-01	1.00E+00	4.67E-02	1.00E+00	2.49E-03	2.85E-01	5.65E-02	1.00E+00	1.15E-01	1.00E+00	6.81E-01	1.00E+00	hydrogen transport	P
GO:0006820	232	9.95E-01	1.00E+00	9.98E-01	1.00E+00	7.56E-01	1.00E+00	9.57E-01	1.00E+00	9.92E-01	1.00E+00	9.79E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	anion transport	P
GO:0006821	79	7.87E-01	1.00E+00	9.60E-01	1.00E+00	5.79E-01	1.00E+00	8.43E-01	1.00E+00	8.35E-01	1.00E+00	9.22E-01	1.00E+00	4.37E-01	1.00E+00	9.61E-01	1.00E+00	chloride transport	P
GO:0006825	14	6.06E-01	1.00E+00	1.11E-01	1.00E+00	6.06E-01	1.00E+00	3.35E-01	1.00E+00	7.36E-01	1.00E+00	1.19E-01	1.00E+00	5.66E-01	1.00E+00	4.58E-01	1.00E+00	copper ion transport	P
GO:0006826	34	5.06E-01	1.00E+00	2.43E-01	1.00E+00	7.06E-01	1.00E+00	6.46E-02	1.00E+00	6.69E-01	1.00E+00	2.54E-01	1.00E+00	8.98E-02	1.00E+00	8.89E-01	1.00E+00	iron ion transport	P
GO:0006829	24	8.94E-03	6.34E-01	1.11E-01	1.00E+00	4.54E-01	1.00E+00	4.80E-01	1.00E+00	3.17E-03	2.85E-01	3.99E-02	1.00E+00	8.12E-01	1.00E+00	5.36E-01	1.00E+00	zinc ion transport	P
GO:0006833	11	2.56E-01	1.00E+00	1.20E-01	1.00E+00	1.81E-01	1.00E+00	2.40E-01	1.00E+00	1.60E-01	1.00E+00	9.59E-02	1.00E+00	9.65E-01	1.00E+00	2.77E-01	1.00E+00	water transport	P
GO:0006835	63	6.90E-01	1.00E+00	8.73E-01	1.00E+00	9.83E-01	1.00E+00	7.58E-01	1.00E+00	6.13E-01	1.00E+00	8.51E-01	1.00E+00	2.27E-01	1.00E+00	9.55E-01	1.00E+00	dicarboxylic acid transport	P
GO:0006836	58	9.66E-01	1.00E+00	9.37E-01	1.00E+00	9.86E-01	1.00E+00	7.74E-01	1.00E+00	8.89E-01	1.00E+00	9.23E-01	1.00E+00	9.74E-01	1.00E+00	8.89E-01	1.00E+00	neurotransmitter transport	P
GO:0006839	60	2.91E-05	1.00E-02	1.01E-03	9.10E-02	1.90E-03	2.48E-01	2.11E-03	1.24E-01	5.71E-05	6.35E-03	1.92E-03	1.61E-01	3.60E-01	1.00E+00	1.80E-01	1.00E+00	mitochondrial transport	P
GO:0006865	75	1.96E-01	1.00E+00	1.88E-02	1.00E+00	3.22E-01	1.00E+00	2.49E-01	1.00E+00	1.23E-01	1.00E+00	4.12E-03	2.70E-01	8.75E-01	1.00E+00	4.75E-01	1.00E+00	amino acid transport	P
GO:0006869	108	1.42E-03	2.02E-01	5.61E-04	6.90E-02	8.60E-03	4.60E-01	2.80E-04	2.70E-02	1.16E-03	7.80E-02	3.66E-03	2.70E-01	2.30E-01	1.00E+00	8.18E-02	1.00E+00	lipid transport	P
GO:0006873	208	4.53E-01	1.00E+00	5.05E-01	1.00E+00	3.34E-01	1.00E+00	2.56E-01	1.00E+00	6.25E-01	1.00E+00	3.34E-01	1.00E+00	1.37E-01	1.00E+00	9.98E-01	1.00E+00	cell ion homeostasis	P
GO:0006874	129	5.89E-01	1.00E+00	7.24E-01	1.00E+00	5.16E-01	1.00E+00	6.64E-01	1.00E+00	6.39E-01	1.00E+00	5.10E-01	1.00E+00	3.03E-01	1.00E+00	9.85E-01	1.00E+00	calcium ion homeostasis	P

GO:0006875	183	4.73E-01	1.00E+00	5.62E-01	1.00E+00	3.55E-01	1.00E+00	2.49E-01	1.00E+00	6.36E-01	1.00E+00	4.17E-01	1.00E+00	1.66E-01	1.00E+00	9.98E-01	1.00E+00	metal ion homeostasis	P
GO:0006878	10	2.36E-01	1.00E+00	9.70E-02	1.00E+00	1.99E-01	1.00E+00	8.60E-02	1.00E+00	4.62E-01	1.00E+00	2.21E-01	1.00E+00	5.28E-01	1.00E+00	6.41E-01	1.00E+00	copper ion homeostasis	P
GO:0006879	33	4.08E-01	1.00E+00	4.57E-01	1.00E+00	3.79E-01	1.00E+00	4.64E-02	1.00E+00	6.22E-01	1.00E+00	5.80E-01	1.00E+00	9.02E-02	1.00E+00	9.13E-01	1.00E+00	iron ion homeostasis	P
GO:0006884	11	1.68E-01	1.00E+00	2.31E-02	1.00E+00	9.22E-02	1.00E+00	2.37E-01	1.00E+00	4.09E-01	1.00E+00	7.50E-02	1.00E+00	2.88E-01	1.00E+00	3.43E-02	1.00E+00	regulation of cell volume	P
GO:0006885	35	9.38E-01	1.00E+00	8.05E-01	1.00E+00	9.86E-01	1.00E+00	7.09E-01	1.00E+00	8.21E-01	1.00E+00	6.90E-01	1.00E+00	8.30E-01	1.00E+00	9.98E-01	1.00E+00	regulation of pH	P
GO:0006886	517	1.57E-17	0.00E+00	2.20E-16	0.00E+00	2.66E-10	9.34E-04	4.99E-06	8.00E-03	2.34E-15	0.00E+00	3.95E-16	0.00E+00	2.55E-05	5.44E-03	8.07E-06	1.88E-03	intracellular protein transport	P
GO:0006887	100	1.88E-02	1.00E+00	7.65E-02	1.00E+00	1.63E-02	6.93E-01	6.48E-02	1.00E+00	6.46E-02	1.00E+00	1.70E-01	1.00E+00	6.30E-02	1.00E+00	1.24E-01	1.00E+00	exocytosis	P
GO:0006888	36	8.05E-02	1.00E+00	1.41E-02	7.47E-01	1.15E-01	1.00E+00	9.52E-02	1.00E+00	9.60E-02	1.00E+00	1.74E-02	8.81E-01	7.21E-01	1.00E+00	1.90E-01	1.00E+00	ER to Golgi vesicle-mediated transport	P
GO:0006890	16	2.67E-02	1.00E+00	9.81E-02	1.00E+00	2.20E-01	1.00E+00	3.72E-01	1.00E+00	1.11E-02	5.39E-01	6.30E-02	1.00E+00	4.67E-01	1.00E+00	2.02E-01	1.00E+00	retrograde vesicle-mediated transport, Golg	P
GO:0006891	17	9.47E-02	1.00E+00	7.55E-02	1.00E+00	2.75E-01	1.00E+00	6.74E-01	1.00E+00	6.61E-02	1.00E+00	1.37E-02	7.39E-01	8.75E-01	1.00E+00	4.97E-01	1.00E+00	intra-Golgi vesicle-mediated transport	P
GO:0006892	23	7.23E-02	1.00E+00	1.74E-01	1.00E+00	1.57E-01	1.00E+00	4.00E-01	1.00E+00	5.21E-02	1.00E+00	6.91E-02	1.00E+00	4.04E-01	1.00E+00	9.99E-01	1.00E+00	post-Golgi vesicle-mediated transport	P
GO:0006895	10	5.66E-02	1.00E+00	2.76E-01	1.00E+00	9.06E-02	1.00E+00	6.14E-01	1.00E+00	4.27E-02	1.00E+00	1.07E-01	1.00E+00	2.71E-01	1.00E+00	1.00E+00	1.00E+00	Golgi to endosome transport	P
GO:0006897	217	1.86E-05	8.00E-03	1.07E-07	4.97E-03	1.20E-03	9.80E-02	4.52E-03	3.46E-01	2.85E-05	5.00E-03	2.93E-07	9.41E-04	6.98E-02	1.00E+00	7.41E-04	9.16E-02	endocytosis	P
GO:0006898	52	4.97E-02	1.00E+00	3.28E-02	1.00E+00	7.15E-02	1.00E+00	1.25E-01	1.00E+00	2.40E-02	1.00E+00	4.67E-02	1.00E+00	5.86E-01	1.00E+00	2.21E-01	1.00E+00	receptor mediated endocytosis	P
GO:0006900	12	2.97E-02	1.00E+00	1.33E-01	1.00E+00	2.25E-01	1.00E+00	1.34E-01	1.00E+00	1.74E-02	1.00E+00	2.02E-01	1.00E+00	1.52E-01	1.00E+00	1.61E-01	1.00E+00	vesicle budding	P
GO:0006901	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	vesicle coating	P
GO:0006903	21	1.50E-02	6.67E-01	5.76E-02	1.00E+00	1.44E-01	1.00E+00	2.04E-01	1.00E+00	5.13E-03	4.18E-01	6.00E-02	1.00E+00	1.36E-01	1.00E+00	1.44E-01	1.00E+00	vesicle targeting	P
GO:0006904	20	3.65E-02	1.00E+00	2.10E-01	1.00E+00	5.79E-02	1.00E+00	8.38E-02	1.00E+00	1.06E-01	1.00E+00	2.24E-01	1.00E+00	4.67E-02	1.00E+00	6.65E-01	1.00E+00	vesicle docking during exocytosis	P
GO:0006909	46	2.07E-01	1.00E+00	2.24E-02	1.00E+00	1.69E-01	1.00E+00	4.02E-02	1.00E+00	1.67E-01	1.00E+00	2.67E-02	1.00E+00	7.76E-01	1.00E+00	2.38E-01	1.00E+00	phagocytosis	P
GO:0006913	266	6.09E-10	8.06E-04	2.85E-10	0.00E+00	5.96E-05	1.20E-02	5.56E-04	4.70E-02	4.69E-09	9.64E-04	2.62E-10	0.00E+00	6.73E-05	2.50E-02	3.00E-05	9.00E-03	nucleocytoplasmic transport	P
GO:0006914	28	9.54E-04	8.30E-02	6.17E-03	3.60E-01	1.84E-02	1.00E+00	1.30E-01	1.00E+00	1.31E-03	7.80E-02	2.04E-03	1.61E-01	5.94E-02	1.00E+00	3.24E-01	1.00E+00	autophagy	P
GO:0006915	872	4.34E-10	8.06E-04	8.81E-14	0.00E+00	4.79E-08	9.68E-04	4.69E-08	9.71E-04	4.56E-08	9.64E-04	5.25E-11	0.00E+00	1.36E-04	2.50E-02	4.88E-07	1.88E-03	apoptosis	P
GO:0006916	171	5.83E-05	1.10E-02	5.21E-04	6.90E-02	2.22E-03	2.48E-01	7.66E-03	4.55E-01	7.09E-05	1.70E-02	5.50E-03	2.70E-01	1.00E-02	6.30E-01	7.56E-04	9.16E-02	anti-apoptosis	P
GO:0006917	244	3.12E-05	1.00E-02	2.39E-06	8.39E-03	1.53E-04	1.50E-02	2.15E-05	8.00E-03	1.82E-04	1.70E-02	8.06E-05	1.70E-02	3.72E-02	1.00E+00	5.56E-03	3.60E-01	induction of apoptosis	P
GO:0006919	44	4.77E-05	1.00E-02	3.76E-04	6.90E-02	2.67E-03	2.48E-01	1.01E-01	1.00E+00	1.83E-04	1.70E-02	1.01E-04	1.70E-02	5.56E-03	3.57E-01	1.43E-02	8.49E-01	caspase activation	P
GO:0006921	21	9.02E-02	1.00E+00	1.48E-01	1.00E+00	2.13E-01	1.00E+00	1.58E-02	8.18E-01	1.11E-01	1.00E+00	4.11E-01	1.00E+00	2.64E-01	1.00E+00	6.37E-01	1.00E+00	disassembly of cell structures during apopto	P
GO:0006928	513	6.78E-01	1.00E+00	3.90E-01	1.00E+00	1.82E-01	1.00E+00	1.88E-01	1.00E+00	8.01E-01	1.00E+00	6.07E-01	1.00E+00	6.16E-01	1.00E+00	2.43E-01	1.00E+00	cell motility	P
GO:0006929	12	4.02E-01	1.00E+00	1.32E-01	1.00E+00	4.37E-01	1.00E+00	3.51E-02	1.00E+00	4.20E-01	1.00E+00	3.83E-01	1.00E+00	3.08E-01	1.00E+00	1.23E-01	1.00E+00	substrate-bound cell migration	P
GO:0006935	198	6.58E-01	1.00E+00	1.97E-01	1.00E+00	5.20E-01	1.00E+00	1.79E-01	1.00E+00	6.79E-01	1.00E+00	1.83E-01	1.00E+00	5.72E-01	1.00E+00	5.42E-01	1.00E+00	chemotaxis	P
GO:0006936	149	7.64E-01	1.00E+00	7.78E-01	1.00E+00	2.00E-01	1.00E+00	7.23E-01	1.00E+00	8.85E-01	1.00E+00	5.55E-01	1.00E+00	6.86E-01	1.00E+00	9.65E-01	1.00E+00	muscle contraction	P
GO:0006937	42	7.13E-01	1.00E+00	7.88E-01	1.00E+00	1.59E-01	1.00E+00	9.40E-01	1.00E+00	9.50E-01	1.00E+00	5.85E-01	1.00E+00	3.76E-01	1.00E+00	5.28E-01	1.00E+00	regulation of muscle contraction	P
GO:0006939	32	9.22E-01	1.00E+00	8.96E-01	1.00E+00	2.67E-01	1.00E+00	7.31E-01	1.00E+00	9.95E-01	1.00E+00	9.09E-01	1.00E+00	6.22E-01	1.00E+00	5.65E-01	1.00E+00	smooth muscle contraction	P
GO:0006940	20	7.63E-01	1.00E+00	9.33E-01	1.00E+00	1.15E-01	1.00E+00	9.77E-01	1.00E+00	9.63E-01	1.00E+00	8.84E-01	1.00E+00	6.82E-01	1.00E+00	4.10E-01	1.00E+00	regulation of smooth muscle contraction	P
GO:0006941	39	9.77E-01	1.00E+00	5.56E-01	1.00E+00	7.94E-01	1.00E+00	2.48E-01	1.00E+00	9.75E-01	1.00E+00	4.53E-01	1.00E+00	9.09E-01	1.00E+00	9.80E-01	1.00E+00	striated muscle contraction	P
GO:0006942	11	9.94E-01	1.00E+00	5.99E-01	1.00E+00	9.44E-01	1.00E+00	2.53E-01	1.00E+00	9.60E-01	1.00E+00	6.06E-01	1.00E+00	8.96E-01	1.00E+00	8.76E-01	1.00E+00	regulation of striated muscle contraction	P
GO:0006944	42	3.95E-02	1.00E+00	1.55E-01	1.00E+00	1.60E-01	1.00E+00	2.23E-01	1.00E+00	1.17E-01	1.00E+00	2.66E-01	1.00E+00	2.57E-02	1.00E+00	8.58E-02	1.00E+00	membrane fusion	P
GO:0006950	1460	1.72E-07	1.95E-03	3.39E-08	4.97E-03	2.42E-06	2.42E-03	1.34E-07	1.96E-03	8.25E-07	2.45E-03	6.84E-07	2.97E-03	6.89E-02	1.00E+00	3.56E-02	1.00E+00	response to stress	P
GO:0006952	710	9.98E-01	1.00E+00	7.86E-01	1.00E+00	9.99E-01	1.00E+00	8.78E-01	1.00E+00	9.96E-01	1.00E+00	5.93E-01	1.00E+00	6.51E-01	1.00E+00	7.81E-01	1.00E+00	defense response	P
GO:0006953	31	9.79E-01	1.00E+00	9.98E-01	1.00E+00	9.70E-01	1.00E+00	8.73E-01	1.00E+00	9.93E-01	1.00E+00	9.95E-01	1.00E+00	2.18E-01	1.00E+00	9.90E-01	1.00E+00	acute-phase response	P
GO:0006954	374	9.95E-01	1.00E+00	6.13E-01	1.00E+00	9.34E-01	1.00E+00	5.98E-01	1.00E+00	9.98E-01	1.00E+00	5.44E-01	1.00E+00	6.74E-01	1.00E+00	6.99E-01	1.00E+00	inflammatory response	P
GO:0006955	736	9.96E-01	1.00E+00	9.69E-01	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	9.88E-01	1.00E+00	9.33E-01	1.00E+00	7.18E-01	1.00E+00	8.33E-01	1.00E+00	immune response	P
GO:0006956	36	9.93E-01	1.00E+00	8.64E-01	1.00E+00	9.91E-01	1.00E+00	8.52E-01	1.00E+00	9.73E-01	1.00E+00	7.80E-01	1.00E+00	9.20E-01	1.00E+00	6.29E-01	1.00E+00	complement activation	P
GO:0006957	14	5.87E-01	1.00E+00	3.44E-01	1.00E+00	4.90E-01	1.00E+00	7.03E-01	1.00E+00	5.08E-01	1.00E+00	2.29E-01	1.00E+00	9.79E-01	1.00E+00	6.28E-01	1.00E+00	complement activation, alternative pathway	P
GO:0006958	27	9.89E-01	1.00E+00	8.27E-01	1.00E+00	9.95E-01	1.00E+00	6.84E-01	1.00E+00	9.56E-01	1.00E+00	7.31E-01	1.00E+00	8.38E-01	1.00E+00	8.26E-01	1.00E+00	complement activation, classical pathway	P
GO:0006959	76	9.62E-01	1.00E+00	9.44E-01	1.00E+00	9.78E-01	1.00E+00	9.91E-01	1.00E+00	8.62E-01	1.00E+00	8.94E-01	1.00E+00	9.81E-01	1.00E+00	4.49E-01	1.00E+00	humoral immune response	P
GO:0006968	60	7.35E-01	1.00E+00	1.24E-01	1.00E+00	3.85E-01	1.00E+00	2.22E-01	1.00E+00	9.01E-01	1.00E+00	2.04E-01	1.00E+00	5.98E-01	1.00E+00	1.39E-01	1.00E+00	cellular defense response	P
GO:0006970	13	2.09E-01	1.00E+00	1.13E-01	1.00E+00	2.53E-01	1.00E+00	6.12E-02	1.00E+00	2.41E-01	1.00E+00	2.74E-01	1.00E+00	1.16E-01	1.00E+00	5.05E-02	1.00E+00	response to osmotic stress	P
GO:0006974	365	3.93E-11	0.00E+00	9.90E-10	0.00E+00	2.36E-06	2.42E-03	8.67E-08	9.71E-04	1.18E-09	9.64E-04	1.21E-08	8.37E-04	2.60E-03	1.95E-01	5.09E-02	1.00E+00	response to DNA damage stimulus	P
GO:0006979	122	3.83E-02	1.00E+00	3.44E-02	1.00E+00	9.47E-02	1.00E+00	3.89E-02	1.00E+00	1.76E-02	1.00E+00	1.04E-01	1.00E+00	5.90E-01	1.00E+00	5.78E-02	1.00E+00	response to oxidative stress	P
GO:0006984	26	2.98E-02	1.00E+00	7.35E-04	6.90E-02	3.59E-02	1.00E+00	4.47E-02	1.00E+00	3.78E-02	1.00E+00	7.63E-04	5.49E-02	3.17E-01	1.00E+00	3.47E-01	1.00E+00	ER-nuclear signaling pathway	P
GO:0006986	74	9.34E-05	1.24E-02	2.89E-05	9.58E-03	2.95E-02	1.00E+00	1.36E-01	1.00E+00	4.32E-05	6.35E-03	4.50E-06	4.00E-03	6.21E-02	1.00E+00	1.14E-01	1.00E+00	response to unfolded protein	P
GO:0006996	1247	7.19E-22	0.00E+00	1.39E-21	0.00E+00	7.48E-11	9.34E-04	1.42E-07	1.96E-03	5.29E-21	0.00E+00	1.22E-19	0.00E+00	1.21E-05	5.44E-03	1.57E-09	7.71E-04	organelle organization and biogenesis	P
GO:0006997	13	3.04E-03	2.39E-01	1.16E-01	1.00E+00	1.17E-01	1.00E+00	9.69E-02	1.00E+00	7.97E-03	5.39E-01	2.94E-01	1.00E+00	8.28E-03	6.30E-01	2.01E-01	1.00E+00	nuclear organization and biogenesis	P
GO:0007001	437	7.37E-11	0.00E+00	1.70E-13	0.00E+00	8.94E-04	7.56E-02	4.75E-03	3.46E-01	1.23E-11	0.00E+00	8.70E-14	0.00E+00	1.81E-03	1.95E-01	3.85E-07	1.88E-03	chromosome organization and biogenesis (	P
GO:0007004	13	2.79E-01	1.00E+00	8.60E-01	1.00E+00	3.17E-01	1.00E+00	8.79E-01	1.00E+00	3.26E-01	1.00E+00	8.89E-01	1.00E+00	4.59E-01	1.00E+00	4.70E-01	1.00E+00	telomere maintenance via telomerase	P
GO:0007005	44	2.22E-03	2.02E-01	1.23E-05	9.58E-03	2.54E-02	1.00E+00	1.21E-03	1.15E-01	4.82E-04	2.20E-02	8.75E-05	1.70E-02	5.24E-01	1.00E+00	3.15E-02	1.00E+00	mitochondrion organization and biogenesis	P
GO:0007006	21	2.37E-02	1.00E+00	2.07E-03	1.29E-01	2.17E-01	1.00E+00	3.90E-02	1.00E+00	4.76E-03	4.18E-01	3.75E-03	2.70E-01	5.53E-01	1.00E+00	3.52E-01	1.00E+00	mitochondrial membrane organization and b	P
GO:0007009	19	7.67E-01	1.00E+00	3.10E-01	1.00E+00	7.18E-01	1.00E+00	7.88E-01	1.00E+00	8.82E-01	1.00E+00	1.18E-01	1.00E+00	2.12E-01	1.00E+00	8.64E-01	1.00E+00	plasma membrane organization and biogen	P
GO:0007010	540	5.67E-06	7.00E-03	3.67E-05	9.58E-03	5.66E-05	1.20E-02	2.02E-03	1.24E-01	1.68E-05	4.19E-03	1.07E-04	1.70E-02	5.26E-02	1.00E+00	2.25E-02	1.00E+00	cytoskeleton organization and biogenesis	P
GO:0007015	50	4.23E-02	1.00E+00	1.55E-01	1.00E+00	9.45E-03	4.60E-01	6.44E-01	1.00E+00	9.03E-02	1.00E+00	6.93E-02	1.00E+00	2.46E-01	1.00E+00	2.68E-01	1.00E+00	actin filament organization	P
GO:0007017	220	1.50E-05	8.00E-03	7.19E-03	3.60E-01	4.72E-04	3.60E-02	4.41E-02	1.00E+00	8.61E-05	1.70E-02	1.22E-02	7.39E-01	4.29E-03	3.57E-01	1.65E-01	1.00E+00	microtubule-based process	P
GO:0007018	112	1.93E-04	2.50E-02	2.90E-02	1.00E+00	1.43E-02	6.93E-01	4.09E-02	1.00E+00	1.40E-04	1.70E-02	2.87E-02	1.00E+00	1.50E-02	6.47E-01	7.63E-01	1.00E+00	microtubule-based movement	P
GO:0007019	17	9.60E-02	1.00E+00	7.02E-01	1.00E+00	6.54E-03	4.60E-01	5.70E-01	1.00E+00	1.50E-01	1.00E+00	5.53E-01	1.00E+00	6.74E-01	1.00E+00	8.40E-01	1.00E+00	microtubule depolymerization	P
GO:0007026	16	1.29E-01	1.00E+00	7.33E-01	1.00E+00	5.44E-03	4.19E-01	5.44E-01	1.00E+00	2.27E-01	1.00E+00	5.09E-01	1.00E+00	5.93E-01	1.00E+00	9.99E-01	1.00E+00	negative regulation of microtubule depolym	P
GO:0007028	133	3.35E-05	1.00E-02	9.47E-03	5.18E-01	2.43E-03	2.48E-01	7.16E-02	1.00E+00	6.79E-05	1.70E-02	4.54E-02	1.00E+00	3.93E-02	1.00E+00	3.25E-02	1.00E+00	cytoplasm organization and biogenesis	P
GO:0007030	14	1.28E-01	1.00E+00	2.90E-01	1.00E+00	1.85E-02	1.00E+00	1.11E-02	8.18E-01	3.86E-01	1.00E+00	3.79E-01	1.00E+00	3.84E-01	1.00E+00	8.23E-01	1.00E+00	Golgi organization and biogenesis	P
GO:0007031	22	1.76E-02	1.00E+00	1.30E-01	1.00E+00	4.95E-02	1.00E+00	2.67E-01	1.00E+00	3.51E-02	1.00E+00	7.23E-02	1.00E+00	1.01E-01	1.00E+00	3.06E-01	1.00E+00	peroxisome organization and biogenesis	P
GO:0007033	35	7.92E-02	1.00E+00	3.01E-01	1.00E+00	6.95E-02	1.00E+00	5.85E-01	1.00E+00	6.62E-02	1.00E+00	2.93E-01	1.00E+00	8.86E-01	1.00E+00	5.06E-01	1.00E+00	vacuole organization and biogenesis	P
GO:0007034	23	1.21E-01	1.00E+00	1.24E-01	1.00E+00	8.47E-02	1.00E+00	3.41E-02	1.00E+00	1.37E-01	1.00E+00	4.49E-01	1.00E+00	6.25E-01	1.00E+00	4.50E-01	1.00E+00	vacuolar transport	P
GO:0007040	33	3.06E-02	1.00E+00	2.02E-01	1.00E+00	3.52E-02	1.00E+00	5.73E-01	1.00E+00	2.51E-02	1.00E+00	1.92E-01	1.00E+00	8.88E-01	1.00E+00	4.01E-01	1.00E+00	lysosome organization and biogenesis	P
GO:0007041	15	2.30E-01	1.00E+00	5.45E-01	1.00E+00	7.50E-02	1.00E+00	2.03E-01	1.00E+00	2.98E-01	1.00E+00	7.50E-01	1.00E+00	8.75E-01	1.00E+00	6.90E-01	1.00E+00	lysosomal transport	P
GO:0007043	14	3.36E-01	1.00E+00	2.50E-01	1.00E+00	2.32E-01	1.00E+00	3.44E-01	1.00E+00	4.04E-01	1.00E+00	3.23E-01	1.00E+00	3.99E-01	1.00E+00	1.07E-01	1.00E+00	intercellular junction assembly	P
GO:0007046	71	5.64E-03	3.50E-01	1.06E-01	1.00E+00	8.87E-02	1.00E+00	3.25E-01	1.00E+00	4.41E-03	3.60E-01	2.28E-01	1.00E+00	1.39E-01	1.00E+00	1.08E-01	1.00E+00	ribosome biogenesis	P
GO:0007049	850	3.39E-22	0.00E+00	1.79E-25	0.00E+00	4.02E-08	9.68E-04	9.10E-15	0.00E+00	1.18E-21	0.00E+00	2.29E-20	0.00E+00	2.12E-06	1.95E-03	2.91E-10	7.71E-04	cell cycle	P
GO:0007050	92	5.15E-02	1.00E+00	3.93E-03	1.97E-01	8.37E-02	1.00E+00	4.77E-02	1.00E+00	1.07E-01	1.00E+00	3.04E-03	2.39E-01	9.26E-02	1.00E+00	8.54E-02	1.00E+00	cell cycle arrest	P

GO:0007051	30	2.82E-03	2.39E-01	2.41E-02	1.00E+00	1.76E-02	6.93E-01	4.14E-01	1.00E+00	3.89E-03	2.85E-01	1.32E-02	7.39E-01	6.61E-02	1.00E+00	9.60E-02	1.00E+00	spindle organization and biogenesis	P
GO:0007052	12	6.84E-03	5.17E-01	1.81E-02	1.00E+00	2.14E-02	1.00E+00	5.97E-02	1.00E+00	7.03E-03	5.39E-01	4.54E-02	1.00E+00	5.35E-01	1.00E+00	1.60E-01	1.00E+00	mitotic spindle organization and biogenesis	P
GO:0007059	66	1.13E-02	6.67E-01	5.92E-04	6.90E-02	2.05E-01	1.00E+00	8.75E-03	7.13E-01	1.90E-02	1.00E+00	1.59E-02	7.63E-01	1.14E-01	1.00E+00	2.18E-04	2.70E-02	chromosome segregation	P
GO:0007062	10	9.29E-01	1.00E+00	1.65E-01	1.00E+00	9.31E-01	1.00E+00	9.38E-02	1.00E+00	7.44E-01	1.00E+00	1.85E-01	1.00E+00	9.98E-01	1.00E+00	4.35E-01	1.00E+00	sister chromatid cohesion	P
GO:0007067	220	3.92E-09	8.06E-04	5.60E-12	0.00E+00	1.36E-03	9.80E-02	1.60E-10	0.00E+00	2.07E-08	9.64E-04	3.72E-08	8.37E-04	6.34E-04	6.50E-02	4.01E-06	1.88E-03	mitosis	P
GO:0007076	17	7.73E-03	6.34E-01	1.38E-02	7.47E-01	3.66E-01	1.00E+00	6.65E-03	4.53E-01	1.81E-02	1.00E+00	2.02E-01	1.00E+00	2.21E-02	1.00E+00	7.95E-03	4.81E-01	mitotic chromosome condensation	P
GO:0007088	65	8.54E-03	6.34E-01	1.63E-03	9.10E-02	5.60E-02	1.00E+00	6.80E-03	4.53E-01	6.03E-03	5.39E-01	8.20E-03	7.39E-01	6.20E-01	1.00E+00	4.75E-03	3.60E-01	regulation of mitosis	P
GO:0007090	10	2.82E-01	1.00E+00	2.88E-01	1.00E+00	4.31E-01	1.00E+00	5.47E-01	1.00E+00	2.61E-01	1.00E+00	3.53E-01	1.00E+00	4.75E-01	1.00E+00	6.50E-02	1.00E+00	regulation of S phase of mitotic cell cycle	P
GO:0007091	10	2.68E-02	1.00E+00	2.84E-02	1.00E+00	1.10E-01	1.00E+00	4.53E-02	1.00E+00	1.68E-01	1.00E+00	5.03E-02	1.00E+00	6.31E-04	6.50E-02	4.74E-02	1.00E+00	mitotic metaphase/anaphase transition	P
GO:0007093	20	4.69E-01	1.00E+00	3.45E-01	1.00E+00	3.73E-01	1.00E+00	3.49E-01	1.00E+00	4.77E-01	1.00E+00	4.86E-01	1.00E+00	9.47E-01	1.00E+00	4.19E-01	1.00E+00	mitotic checkpoint	P
GO:0007096	12	2.68E-03	2.39E-01	9.19E-02	1.00E+00	3.83E-02	1.00E+00	6.42E-02	1.00E+00	3.80E-04	2.20E-02	1.67E-01	1.00E+00	7.59E-01	1.00E+00	6.60E-02	1.00E+00	regulation of exit from mitosis	P
GO:0007098	14	6.99E-02	1.00E+00	1.12E-01	1.00E+00	1.56E-01	1.00E+00	1.69E-01	1.00E+00	5.62E-02	1.00E+00	1.45E-01	1.00E+00	3.73E-01	1.00E+00	1.73E-01	1.00E+00	centrosome cycle	P
GO:0007126	86	3.10E-02	1.00E+00	1.13E-03	9.10E-02	7.51E-02	1.00E+00	1.38E-02	8.18E-01	3.04E-02	1.00E+00	2.35E-03	1.64E-01	5.52E-01	1.00E+00	6.21E-02	1.00E+00	meiosis	P
GO:0007127	37	4.42E-02	1.00E+00	2.23E-03	1.77E-01	3.84E-02	1.00E+00	4.71E-02	1.00E+00	4.59E-02	1.00E+00	1.77E-03	1.61E-01	7.52E-01	1.00E+00	1.19E-01	1.00E+00	meiosis I	P
GO:0007131	20	1.31E-01	1.00E+00	1.04E-02	5.18E-01	1.28E-01	1.00E+00	1.29E-01	1.00E+00	9.23E-02	1.00E+00	2.90E-02	1.00E+00	9.60E-01	1.00E+00	2.82E-01	1.00E+00	meiotic recombination	P
GO:0007154	4345	9.83E-01	1.00E+00	8.10E-02	1.00E+00	7.68E-01	1.00E+00	2.46E-01	1.00E+00	9.67E-01	1.00E+00	3.35E-02	1.00E+00	9.86E-01	1.00E+00	4.58E-01	1.00E+00	cell communication	P
GO:0007155	849	9.96E-01	1.00E+00	4.09E-01	1.00E+00	9.48E-01	1.00E+00	6.55E-01	1.00E+00	9.95E-01	1.00E+00	3.39E-01	1.00E+00	8.80E-01	1.00E+00	3.14E-01	1.00E+00	cell adhesion	P
GO:0007156	122	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.78E-01	1.00E+00	homophilic cell adhesion	P
GO:0007157	44	3.39E-01	1.00E+00	2.90E-01	1.00E+00	4.68E-01	1.00E+00	6.75E-01	1.00E+00	3.42E-01	1.00E+00	1.14E-01	1.00E+00	1.86E-01	1.00E+00	8.74E-01	1.00E+00	heterophilic cell adhesion	P
GO:0007159	24	1.72E-01	1.00E+00	2.21E-01	1.00E+00	3.48E-01	1.00E+00	9.23E-01	1.00E+00	1.44E-01	1.00E+00	9.50E-02	1.00E+00	1.75E-01	1.00E+00	6.88E-01	1.00E+00	leukocyte adhesion	P
GO:0007160	117	3.60E-01	1.00E+00	9.90E-02	1.00E+00	3.56E-01	1.00E+00	1.59E-01	1.00E+00	3.39E-01	1.00E+00	1.24E-01	1.00E+00	5.78E-01	1.00E+00	2.73E-01	1.00E+00	cell-matrix adhesion	P
GO:0007162	19	1.79E-01	1.00E+00	6.31E-02	1.00E+00	2.69E-01	1.00E+00	2.09E-01	1.00E+00	1.74E-01	1.00E+00	6.39E-02	1.00E+00	3.76E-01	1.00E+00	1.33E-01	1.00E+00	negative regulation of cell adhesion	P
GO:0007163	37	6.52E-02	1.00E+00	7.96E-03	3.60E-01	2.66E-02	1.00E+00	2.17E-02	1.00E+00	1.47E-01	1.00E+00	3.17E-02	1.00E+00	1.73E-01	1.00E+00	1.66E-02	8.49E-01	establishment and/or maintenance of cell p	P
GO:0007165	3953	9.74E-01	1.00E+00	1.64E-01	1.00E+00	6.78E-01	1.00E+00	3.46E-01	1.00E+00	9.63E-01	1.00E+00	1.24E-01	1.00E+00	9.71E-01	1.00E+00	2.43E-01	1.00E+00	signal transduction	P
GO:0007166	2173	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	cell surface receptor linked signal transduct	P
GO:0007167	353	3.68E-01	1.00E+00	1.43E-01	1.00E+00	1.43E-01	1.00E+00	9.80E-02	1.00E+00	4.00E-01	1.00E+00	3.16E-01	1.00E+00	7.41E-01	1.00E+00	2.07E-01	1.00E+00	enzyme linked receptor protein signaling pa	P
GO:0007169	232	3.01E-01	1.00E+00	5.96E-02	1.00E+00	9.13E-02	1.00E+00	1.79E-01	1.00E+00	4.03E-01	1.00E+00	1.26E-01	1.00E+00	6.59E-01	1.00E+00	7.43E-02	1.00E+00	transmembrane receptor protein tyrosine ki	P
GO:0007172	16	2.07E-01	1.00E+00	7.07E-02	1.00E+00	3.71E-02	1.00E+00	1.47E-01	1.00E+00	3.30E-01	1.00E+00	5.61E-02	1.00E+00	9.30E-01	1.00E+00	5.39E-01	1.00E+00	signal complex formation	P
GO:0007173	34	2.27E-01	1.00E+00	3.88E-04	6.90E-02	1.11E-02	5.32E-01	1.02E-02	7.13E-01	7.11E-01	1.00E+00	2.01E-03	1.61E-01	5.36E-01	1.00E+00	2.68E-03	1.85E-01	epidermal growth factor receptor signaling p	P
GO:0007178	109	4.73E-01	1.00E+00	5.05E-01	1.00E+00	5.58E-01	1.00E+00	8.04E-02	1.00E+00	3.58E-01	1.00E+00	7.82E-01	1.00E+00	6.91E-01	1.00E+00	4.55E-01	1.00E+00	transmembrane receptor protein serine/thre	P
GO:0007179	65	1.75E-01	1.00E+00	1.08E-01	1.00E+00	4.57E-01	1.00E+00	5.59E-03	3.46E-01	7.78E-02	1.00E+00	3.47E-01	1.00E+00	6.66E-01	1.00E+00	4.34E-01	1.00E+00	transforming growth factor beta receptor sig	P
GO:0007186	1459	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor protein signaling	P
GO:0007187	127	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	8.70E-01	1.00E+00	G-protein signaling, coupled to cyclic nucle	P
GO:0007188	96	9.98E-01	1.00E+00	9.73E-01	1.00E+00	9.99E-01	1.00E+00	9.25E-01	1.00E+00	9.79E-01	1.00E+00	9.85E-01	1.00E+00	9.81E-01	1.00E+00	5.53E-01	1.00E+00	G-protein signaling, coupled to cAMP nucle	P
GO:0007189	44	9.71E-01	1.00E+00	8.31E-01	1.00E+00	8.07E-01	1.00E+00	4.45E-01	1.00E+00	9.81E-01	1.00E+00	9.56E-01	1.00E+00	7.99E-01	1.00E+00	2.04E-01	1.00E+00	G-protein signaling, adenylate cyclase activ	P
GO:0007190	25	6.39E-01	1.00E+00	6.01E-01	1.00E+00	5.18E-01	1.00E+00	2.31E-01	1.00E+00	7.21E-01	1.00E+00	8.32E-01	1.00E+00	4.08E-01	1.00E+00	2.11E-01	1.00E+00	adenylate cyclase activation	P
GO:0007193	21	9.58E-01	1.00E+00	5.69E-01	1.00E+00	1.00E+00	1.00E+00	7.28E-01	1.00E+00	7.77E-01	1.00E+00	5.64E-01	1.00E+00	6.83E-01	1.00E+00	2.82E-01	1.00E+00	G-protein signaling, adenylate cyclase inhib	P
GO:0007194	16	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	negative regulation of adenylate cyclase ac	P
GO:0007200	80	9.46E-01	1.00E+00	9.83E-01	1.00E+00	4.87E-01	1.00E+00	9.94E-01	1.00E+00	9.83E-01	1.00E+00	9.24E-01	1.00E+00	6.61E-01	1.00E+00	9.00E-01	1.00E+00	G-protein signaling, coupled to IP3 second	P
GO:0007202	16	4.93E-01	1.00E+00	1.89E-01	1.00E+00	2.41E-01	1.00E+00	3.00E-01	1.00E+00	8.09E-01	1.00E+00	1.63E-01	1.00E+00	1.08E-01	1.00E+00	3.59E-01	1.00E+00	phospholipase C activation	P
GO:0007204	76	6.54E-01	1.00E+00	7.31E-01	1.00E+00	5.75E-01	1.00E+00	7.74E-01	1.00E+00	6.21E-01	1.00E+00	5.55E-01	1.00E+00	5.11E-01	1.00E+00	9.36E-01	1.00E+00	elevation of cytosolic calcium ion concentra	P
GO:0007205	28	7.42E-01	1.00E+00	6.53E-01	1.00E+00	1.91E-01	1.00E+00	9.59E-01	1.00E+00	7.56E-01	1.00E+00	3.33E-01	1.00E+00	9.74E-01	1.00E+00	7.63E-01	1.00E+00	protein kinase C activation	P
GO:0007212	11	9.56E-01	1.00E+00	2.80E-01	1.00E+00	1.00E+00	1.00E+00	4.12E-01	1.00E+00	6.31E-01	1.00E+00	3.45E-01	1.00E+00	9.06E-01	1.00E+00	1.51E-01	1.00E+00	dopamine receptor signaling pathway	P
GO:0007214	30	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.94E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	8.98E-01	1.00E+00	9.99E-01	1.00E+00	gamma-aminobutyric acid signaling pathwa	P
GO:0007215	22	8.93E-01	1.00E+00	8.81E-01	1.00E+00	5.68E-01	1.00E+00	8.44E-01	1.00E+00	9.22E-01	1.00E+00	8.40E-01	1.00E+00	6.94E-01	1.00E+00	7.05E-01	1.00E+00	glutamate signaling pathway	P
GO:0007218	96	9.05E-01	1.00E+00	6.41E-01	1.00E+00	9.43E-01	1.00E+00	3.11E-01	1.00E+00	8.28E-01	1.00E+00	4.91E-01	1.00E+00	8.56E-01	1.00E+00	9.58E-01	1.00E+00	neuropeptide signaling pathway	P
GO:0007219	53	3.68E-01	1.00E+00	1.29E-01	1.00E+00	1.41E-01	1.00E+00	2.72E-01	1.00E+00	3.58E-01	1.00E+00	1.61E-01	1.00E+00	9.86E-01	1.00E+00	1.17E-01	1.00E+00	Notch signaling pathway	P
GO:0007223	21	8.75E-01	1.00E+00	7.87E-01	1.00E+00	9.35E-01	1.00E+00	7.73E-01	1.00E+00	5.81E-01	1.00E+00	6.74E-01	1.00E+00	1.00E+00	1.00E+00	6.95E-01	1.00E+00	frizzled-2 signaling pathway	P
GO:0007224	25	5.52E-01	1.00E+00	3.85E-01	1.00E+00	6.16E-01	1.00E+00	7.05E-01	1.00E+00	5.49E-01	1.00E+00	4.11E-01	1.00E+00	5.06E-01	1.00E+00	2.45E-01	1.00E+00	smoothened signaling pathway	P
GO:0007229	62	4.46E-01	1.00E+00	2.00E-01	1.00E+00	4.87E-01	1.00E+00	2.39E-01	1.00E+00	5.08E-01	1.00E+00	2.38E-01	1.00E+00	3.11E-01	1.00E+00	8.10E-01	1.00E+00	integrin-mediated signaling pathway	P
GO:0007242	1451	2.10E-07	1.95E-03	2.08E-11	0.00E+00	3.69E-06	2.66E-03	1.01E-06	2.00E-03	1.56E-06	2.60E-03	1.63E-10	0.00E+00	1.79E-02	9.11E-01	5.57E-04	9.16E-02	intracellular signaling cascade	P
GO:0007243	450	3.39E-05	1.00E-02	6.45E-08	4.97E-03	4.13E-03	3.27E-01	5.27E-05	8.00E-03	3.61E-05	5.00E-03	5.12E-07	2.97E-03	2.05E-02	9.11E-01	2.09E-03	1.40E-01	protein kinase cascade	P
GO:0007249	149	1.78E-03	2.02E-01	4.57E-04	6.90E-02	3.47E-02	1.00E+00	1.50E-02	8.18E-01	5.09E-03	4.18E-01	4.99E-04	4.10E-02	4.21E-03	3.57E-01	1.36E-01	1.00E+00	I-kappaB kinase/NF-kappaB cascade	P
GO:0007250	13	4.53E-01	1.00E+00	2.41E-01	1.00E+00	8.72E-01	1.00E+00	2.36E-01	1.00E+00	5.53E-01	1.00E+00	2.51E-01	1.00E+00	5.35E-02	1.00E+00	3.69E-01	1.00E+00	activation of NF-kappaB-inducing kinase	P
GO:0007254	76	1.40E-02	6.67E-01	4.19E-02	1.00E+00	4.54E-02	1.00E+00	3.04E-02	1.00E+00	1.04E-02	5.39E-01	1.91E-01	1.00E+00	3.85E-01	1.00E+00	6.07E-03	3.60E-01	JNK cascade	P
GO:0007257	22	1.67E-01	1.00E+00	5.10E-02	1.00E+00	8.11E-02	1.00E+00	3.85E-02	1.00E+00	1.82E-01	1.00E+00	7.76E-02	1.00E+00	9.55E-01	1.00E+00	2.24E-01	1.00E+00	activation of JNK activity	P
GO:0007259	53	5.81E-02	1.00E+00	7.67E-02	1.00E+00	9.38E-02	1.00E+00	1.58E-01	1.00E+00	1.26E-01	1.00E+00	7.11E-02	1.00E+00	4.45E-02	1.00E+00	3.50E-01	1.00E+00	JAK-STAT cascade	P
GO:0007260	25	1.42E-01	1.00E+00	3.34E-01	1.00E+00	5.24E-02	1.00E+00	1.19E-01	1.00E+00	2.12E-01	1.00E+00	5.01E-01	1.00E+00	3.30E-01	1.00E+00	6.65E-01	1.00E+00	tyrosine phosphorylation of STAT protein	P
GO:0007263	12	9.36E-01	1.00E+00	9.86E-01	1.00E+00	8.52E-01	1.00E+00	9.01E-01	1.00E+00	9.11E-01	1.00E+00	9.80E-01	1.00E+00	3.12E-01	1.00E+00	9.34E-01	1.00E+00	nitric oxide mediated signal transduction	P
GO:0007264	458	3.95E-06	7.00E-03	7.76E-08	4.97E-03	4.81E-06	2.66E-03	1.21E-04	1.30E-02	4.29E-05	6.35E-03	9.13E-07	2.97E-03	4.53E-02	1.00E+00	3.32E-04	2.70E-02	small GTPase mediated signal transduction	P
GO:0007265	66	1.30E-02	6.67E-01	1.02E-03	9.10E-02	3.51E-02	1.00E+00	8.69E-03	7.13E-01	1.49E-02	1.00E+00	1.59E-03	1.61E-01	1.40E-01	1.00E+00	2.27E-02	1.00E+00	Ras protein signal transduction	P
GO:0007266	110	1.40E-01	1.00E+00	6.58E-02	1.00E+00	1.55E-01	1.00E+00	2.67E-01	1.00E+00	1.05E-01	1.00E+00	1.20E-01	1.00E+00	6.39E-01	1.00E+00	3.88E-02	1.00E+00	Rho protein signal transduction	P
GO:0007267	651	9.94E-01	1.00E+00	9.66E-01	1.00E+00	8.82E-01	1.00E+00	6.82E-01	1.00E+00	9.89E-01	1.00E+00	9.34E-01	1.00E+00	9.69E-01	1.00E+00	9.98E-01	1.00E+00	cell-cell signaling	P
GO:0007268	316	9.38E-01	1.00E+00	6.82E-01	1.00E+00	8.84E-01	1.00E+00	1.64E-01	1.00E+00	8.14E-01	1.00E+00	7.25E-01	1.00E+00	9.69E-01	1.00E+00	9.52E-01	1.00E+00	synaptic transmission	P
GO:0007269	60	9.83E-01	1.00E+00	9.86E-01	1.00E+00	9.16E-01	1.00E+00	9.10E-01	1.00E+00	9.83E-01	1.00E+00	9.91E-01	1.00E+00	9.13E-01	1.00E+00	8.79E-01	1.00E+00	neurotransmitter secretion	P
GO:0007270	48	7.49E-01	1.00E+00	9.28E-01	1.00E+00	6.30E-01	1.00E+00	7.64E-01	1.00E+00	6.34E-01	1.00E+00	9.44E-01	1.00E+00	8.45E-01	1.00E+00	8.05E-01	1.00E+00	nerve-nerve synaptic transmission	P
GO:0007271	19	4.03E-01	1.00E+00	4.31E-01	1.00E+00	2.82E-01	1.00E+00	3.38E-01	1.00E+00	3.59E-01	1.00E+00	4.79E-01	1.00E+00	9.32E-01	1.00E+00	4.76E-01	1.00E+00	synaptic transmission, cholinergic	P
GO:0007272	39	8.87E-02	1.00E+00	2.49E-01	1.00E+00	1.87E-02	1.00E+00	1.91E-01	1.00E+00	3.36E-01	1.00E+00	2.44E-01	1.00E+00	1.46E-01	1.00E+00	6.86E-01	1.00E+00	ensheathment of neurons	P
GO:0007274	15	7.43E-01	1.00E+00	8.11E-01	1.00E+00	5.27E-01	1.00E+00	8.01E-01	1.00E+00	6.97E-01	1.00E+00	7.42E-01	1.00E+00	9.12E-01	1.00E+00	9.17E-01	1.00E+00	neuromuscular synaptic transmission	P
GO:0007275	2975	6.14E-01	1.00E+00	3.84E-01	1.00E+00	2.95E-01	1.00E+00	1.99E-01	1.00E+00	5.96E-01	1.00E+00	4.58E-01	1.00E+00	8.32E-01	1.00E+00	4.08E-01	1.00E+00	development	P
GO:0007276	336	6.62E-02	1.00E+00	2.64E-02	1.00E+00	5.42E-01	1.00E+00	6.40E-02	1.00E+00	1.05E-01	1.00E+00	1.08E-02	7.39E-01	2.74E-03	1.95E-01	7.15E-01	1.00E+00	gametogenesis	P
GO:0007281	40	2.78E-01	1.00E+00	1.76E-01	1.00E+00	4.14E-01	1.00E+00	1.48E-01	1.00E+00	3.22E-01	1.00E+00	1.17E-01	1.00E+00	2.28E-01	1.00E+00	7.23E-01	1.00E+00	germ cell development	P
GO:0007283	265	2.17E-02	1.00E+00	2.14E-02	1.00E+00	2.15E-01	1.00E+00	2.72E-02	1.00E+00	4.38E-02	1.00E+00	1.43E-02	7.39E-01	5.04E-03	3.57E-01	7.41E-01	1.00E+00	spermatogenesis	P
GO:0007286	40	8.77E-02	1.00E+00	4.14E-02	1.00E+00	1.75E-01	1.00E+00	5.37E-02	1.00E+00	8.53E-02	1.00E+00	9.10E-02	1.00E+00	4.31E-01	1.00E+00	1.59E-01	1.00E+00	spermatid development	P
GO:0007292	47	1.58E-01	1.00E+00	2.18E-01	1.00E+00	5.30E-01	1.00E+00	3.37E-01	1.00E+00	1.71E-01	1.00E+00	2.79E-01	1.00E+00	5.73E-02	1.00E+00	1.54E-01	1.00E+00	female gamete generation	P

GO:0007338	68	5.27E-01	1.00E+00	9.27E-01	1.00E+00	6.06E-01	1.00E+00	8.69E-01	1.00E+00	6.18E-01	1.00E+00	9.59E-01	1.00E+00	3.05E-01	1.00E+00	4.01E-01	1.00E+00	fertilization (sensu Metazoa)	P
GO:0007339	17	3.40E-01	1.00E+00	2.03E-01	1.00E+00	2.49E-01	1.00E+00	5.33E-02	1.00E+00	4.60E-01	1.00E+00	3.22E-01	1.00E+00	4.55E-01	1.00E+00	8.15E-01	1.00E+00	binding of sperm to zona pellucida	P
GO:0007340	14	5.66E-01	1.00E+00	5.25E-01	1.00E+00	5.46E-01	1.00E+00	4.93E-01	1.00E+00	6.04E-01	1.00E+00	6.32E-01	1.00E+00	5.54E-01	1.00E+00	3.59E-01	1.00E+00	acrosome reaction	P
GO:0007342	10	7.91E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	6.91E-01	1.00E+00	9.91E-01	1.00E+00	4.28E-01	1.00E+00	8.37E-02	1.00E+00	fusion of sperm to egg plasma membrane	P
GO:0007346	42	8.11E-02	1.00E+00	3.08E-02	1.00E+00	3.83E-01	1.00E+00	5.29E-01	1.00E+00	6.94E-02	1.00E+00	2.31E-02	1.00E+00	3.26E-01	1.00E+00	7.10E-02	1.00E+00	regulation of progression through mitotic ce	P
GO:0007368	33	7.97E-01	1.00E+00	2.09E-01	1.00E+00	9.87E-01	1.00E+00	4.41E-01	1.00E+00	7.05E-01	1.00E+00	1.99E-01	1.00E+00	4.46E-01	1.00E+00	1.69E-01	1.00E+00	determination of left/right symmetry	P
GO:0007369	55	8.79E-02	1.00E+00	2.53E-01	1.00E+00	1.44E-01	1.00E+00	9.07E-01	1.00E+00	1.04E-01	1.00E+00	2.51E-01	1.00E+00	4.26E-01	1.00E+00	4.87E-02	1.00E+00	gastrulation	P
GO:0007379	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	segment specification	P
GO:0007389	217	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	pattern specification	P
GO:0007398	198	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	ectoderm development	P
GO:0007399	888	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	nervous system development	P
GO:0007405	23	2.82E-01	1.00E+00	1.22E-01	1.00E+00	2.92E-01	1.00E+00	1.16E-01	1.00E+00	2.53E-01	1.00E+00	1.29E-01	1.00E+00	4.58E-01	1.00E+00	5.84E-01	1.00E+00	neuroblast proliferation	P
GO:0007409	174	9.93E-01	1.00E+00	9.29E-01	1.00E+00	8.52E-01	1.00E+00	9.53E-01	1.00E+00	9.87E-01	1.00E+00	9.16E-01	1.00E+00	9.86E-01	1.00E+00	4.58E-01	1.00E+00	axonogenesis	P
GO:0007411	91	9.99E-01	1.00E+00	9.89E-01	1.00E+00	9.15E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.77E-01	1.00E+00	9.97E-01	1.00E+00	7.62E-01	1.00E+00	axon guidance	P
GO:0007416	35	6.31E-01	1.00E+00	3.46E-01	1.00E+00	4.45E-01	1.00E+00	5.46E-02	1.00E+00	6.51E-01	1.00E+00	4.71E-01	1.00E+00	6.37E-01	1.00E+00	7.60E-01	1.00E+00	synaptogenesis	P
GO:0007417	342	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	central nervous system development	P
GO:0007420	226	9.75E-01	1.00E+00	9.97E-01	1.00E+00	7.15E-01	1.00E+00	9.52E-01	1.00E+00	9.75E-01	1.00E+00	9.92E-01	1.00E+00	9.86E-01	1.00E+00	9.99E-01	1.00E+00	brain development	P
GO:0007422	36	5.90E-01	1.00E+00	9.93E-01	1.00E+00	3.82E-01	1.00E+00	9.67E-01	1.00E+00	6.27E-01	1.00E+00	9.80E-01	1.00E+00	4.02E-01	1.00E+00	9.94E-01	1.00E+00	peripheral nervous system development	P
GO:0007423	141	9.83E-01	1.00E+00	1.00E+00	1.00E+00	8.80E-01	1.00E+00	9.54E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.11E-01	1.00E+00	sensory organ development	P
GO:0007431	11	7.22E-01	1.00E+00	9.98E-01	1.00E+00	9.88E-01	1.00E+00	9.74E-01	1.00E+00	4.13E-01	1.00E+00	9.91E-01	1.00E+00	8.75E-01	1.00E+00	7.67E-01	1.00E+00	salivary gland development	P
GO:0007492	12	9.93E-01	1.00E+00	9.89E-01	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	9.90E-01	1.00E+00	9.85E-01	1.00E+00	9.83E-01	1.00E+00	7.80E-01	1.00E+00	endoderm development	P
GO:0007498	64	2.26E-01	1.00E+00	5.55E-01	1.00E+00	3.22E-01	1.00E+00	9.24E-01	1.00E+00	1.69E-01	1.00E+00	5.15E-01	1.00E+00	8.03E-01	1.00E+00	2.35E-01	1.00E+00	mesoderm development	P
GO:0007507	139	3.84E-01	1.00E+00	3.68E-01	1.00E+00	6.50E-01	1.00E+00	2.09E-01	1.00E+00	3.89E-01	1.00E+00	4.39E-01	1.00E+00	1.05E-01	1.00E+00	3.04E-01	1.00E+00	heart development	P
GO:0007512	13	9.59E-01	1.00E+00	9.88E-01	1.00E+00	9.02E-01	1.00E+00	9.35E-01	1.00E+00	9.78E-01	1.00E+00	9.48E-01	1.00E+00	5.35E-01	1.00E+00	9.84E-01	1.00E+00	adult heart development	P
GO:0007517	238	2.65E-01	1.00E+00	2.12E-01	1.00E+00	1.42E-01	1.00E+00	1.47E-01	1.00E+00	3.46E-01	1.00E+00	1.81E-01	1.00E+00	3.55E-01	1.00E+00	5.90E-01	1.00E+00	muscle development	P
GO:0007519	147	2.16E-01	1.00E+00	1.43E-01	1.00E+00	1.21E-01	1.00E+00	2.54E-01	1.00E+00	3.15E-01	1.00E+00	8.89E-02	1.00E+00	3.89E-01	1.00E+00	4.55E-01	1.00E+00	striated muscle development	P
GO:0007528	25	1.28E-01	1.00E+00	4.34E-02	1.00E+00	1.32E-01	1.00E+00	4.76E-02	1.00E+00	2.01E-01	1.00E+00	4.57E-02	1.00E+00	2.87E-01	1.00E+00	2.46E-01	1.00E+00	neuromuscular junction development	P
GO:0007530	25	3.61E-01	1.00E+00	8.43E-01	1.00E+00	3.66E-01	1.00E+00	6.92E-01	1.00E+00	4.20E-01	1.00E+00	8.08E-01	1.00E+00	2.62E-01	1.00E+00	6.50E-01	1.00E+00	sex determination	P
GO:0007548	104	7.07E-01	1.00E+00	7.49E-01	1.00E+00	5.28E-01	1.00E+00	7.61E-01	1.00E+00	6.42E-01	1.00E+00	5.91E-01	1.00E+00	8.91E-01	1.00E+00	8.25E-01	1.00E+00	sex differentiation	P
GO:0007565	73	8.73E-01	1.00E+00	1.00E+00	1.00E+00	6.42E-01	1.00E+00	9.82E-01	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	1.91E-01	1.00E+00	8.87E-01	1.00E+00	pregnancy	P
GO:0007566	16	7.32E-02	1.00E+00	5.71E-01	1.00E+00	1.03E-01	1.00E+00	7.22E-01	1.00E+00	1.81E-01	1.00E+00	4.91E-01	1.00E+00	1.42E-01	1.00E+00	4.52E-01	1.00E+00	embryo implantation	P
GO:0007568	44	9.36E-02	1.00E+00	9.86E-02	1.00E+00	2.66E-01	1.00E+00	3.46E-01	1.00E+00	5.93E-02	1.00E+00	6.34E-02	1.00E+00	3.29E-01	1.00E+00	1.92E-01	1.00E+00	aging	P
GO:0007569	20	1.48E-01	1.00E+00	7.07E-02	1.00E+00	2.31E-01	1.00E+00	1.91E-01	1.00E+00	1.13E-01	1.00E+00	5.19E-02	1.00E+00	2.30E-01	1.00E+00	2.26E-01	1.00E+00	cell aging	P
GO:0007582	13042	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.17E-34	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.22E-21	0.00E+00	1.89E-31	0.00E+00	physiological process	P
GO:0007584	55	2.77E-02	1.00E+00	1.81E-03	9.10E-02	7.53E-01	1.00E+00	3.09E-01	1.00E+00	6.36E-03	5.39E-01	6.93E-04	5.49E-02	1.62E-01	1.00E+00	3.63E-02	1.00E+00	response to nutrient	P
GO:0007585	40	8.94E-01	1.00E+00	9.90E-01	1.00E+00	8.18E-01	1.00E+00	9.89E-01	1.00E+00	8.15E-01	1.00E+00	9.73E-01	1.00E+00	9.60E-01	1.00E+00	8.73E-01	1.00E+00	respiratory gaseous exchange	P
GO:0007586	86	4.12E-01	1.00E+00	9.56E-01	1.00E+00	3.12E-01	1.00E+00	5.14E-01	1.00E+00	5.05E-01	1.00E+00	9.99E-01	1.00E+00	2.01E-01	1.00E+00	2.30E-01	1.00E+00	digestion	P
GO:0007588	49	7.31E-01	1.00E+00	6.27E-01	1.00E+00	2.62E-01	1.00E+00	1.93E-01	1.00E+00	7.96E-01	1.00E+00	7.01E-01	1.00E+00	8.33E-01	1.00E+00	8.36E-01	1.00E+00	excretion	P
GO:0007595	20	9.90E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	9.77E-01	1.00E+00	8.67E-01	1.00E+00	1.59E-01	1.00E+00	9.08E-01	1.00E+00	lactation	P
GO:0007596	148	8.99E-01	1.00E+00	5.87E-01	1.00E+00	7.54E-01	1.00E+00	3.43E-01	1.00E+00	8.16E-01	1.00E+00	5.78E-01	1.00E+00	9.71E-01	1.00E+00	8.19E-01	1.00E+00	blood coagulation	P
GO:0007599	154	8.21E-01	1.00E+00	5.15E-01	1.00E+00	6.34E-01	1.00E+00	2.49E-01	1.00E+00	7.15E-01	1.00E+00	5.38E-01	1.00E+00	9.70E-01	1.00E+00	7.81E-01	1.00E+00	hemostasis	P
GO:0007600	771	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception	P
GO:0007601	218	6.80E-01	1.00E+00	3.60E-01	1.00E+00	3.17E-01	1.00E+00	1.68E-01	1.00E+00	7.73E-01	1.00E+00	3.81E-01	1.00E+00	7.99E-01	1.00E+00	3.90E-01	1.00E+00	visual perception	P
GO:0007602	30	4.19E-01	1.00E+00	2.25E-01	1.00E+00	1.53E-01	1.00E+00	5.35E-01	1.00E+00	3.41E-01	1.00E+00	9.55E-02	1.00E+00	1.00E+00	1.00E+00	5.97E-01	1.00E+00	phototransduction	P
GO:0007605	147	9.70E-01	1.00E+00	9.72E-01	1.00E+00	8.30E-01	1.00E+00	9.54E-01	1.00E+00	9.60E-01	1.00E+00	9.43E-01	1.00E+00	9.18E-01	1.00E+00	9.62E-01	1.00E+00	sensory perception of sound	P
GO:0007606	391	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of chemical stimulus	P
GO:0007608	354	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of smell	P
GO:0007610	444	9.58E-01	1.00E+00	8.33E-01	1.00E+00	9.09E-01	1.00E+00	4.54E-01	1.00E+00	9.28E-01	1.00E+00	8.17E-01	1.00E+00	7.57E-01	1.00E+00	9.27E-01	1.00E+00	behavior	P
GO:0007611	73	7.83E-01	1.00E+00	9.70E-01	1.00E+00	8.52E-01	1.00E+00	6.16E-01	1.00E+00	4.54E-01	1.00E+00	9.87E-01	1.00E+00	9.93E-01	1.00E+00	8.63E-01	1.00E+00	learning and/or memory	P
GO:0007612	40	8.04E-01	1.00E+00	9.93E-01	1.00E+00	5.43E-01	1.00E+00	7.16E-01	1.00E+00	7.43E-01	1.00E+00	9.94E-01	1.00E+00	9.69E-01	1.00E+00	8.68E-01	1.00E+00	learning	P
GO:0007613	20	9.76E-01	1.00E+00	9.88E-01	1.00E+00	8.62E-01	1.00E+00	8.62E-01	1.00E+00	9.64E-01	1.00E+00	8.90E-01	1.00E+00	9.22E-01	1.00E+00	9.85E-01	1.00E+00	memory	P
GO:0007617	14	9.86E-01	1.00E+00	9.44E-01	1.00E+00	9.18E-01	1.00E+00	9.24E-01	1.00E+00	9.89E-01	1.00E+00	9.32E-01	1.00E+00	5.35E-01	1.00E+00	4.11E-01	1.00E+00	mating behavior	P
GO:0007623	33	6.77E-01	1.00E+00	5.88E-01	1.00E+00	7.22E-01	1.00E+00	5.05E-01	1.00E+00	5.59E-01	1.00E+00	4.81E-01	1.00E+00	7.24E-01	1.00E+00	8.61E-01	1.00E+00	circadian rhythm	P
GO:0007626	280	7.21E-01	1.00E+00	3.73E-01	1.00E+00	7.03E-01	1.00E+00	2.67E-01	1.00E+00	6.96E-01	1.00E+00	4.14E-01	1.00E+00	4.25E-01	1.00E+00	4.41E-01	1.00E+00	locomotory behavior	P
GO:0007628	17	3.99E-01	1.00E+00	8.92E-01	1.00E+00	4.05E-01	1.00E+00	3.79E-01	1.00E+00	3.81E-01	1.00E+00	9.89E-01	1.00E+00	6.07E-01	1.00E+00	4.75E-01	1.00E+00	adult walking behavior	P
GO:0007631	48	5.35E-01	1.00E+00	7.06E-01	1.00E+00	7.41E-01	1.00E+00	3.55E-01	1.00E+00	4.75E-01	1.00E+00	7.85E-01	1.00E+00	2.06E-01	1.00E+00	5.98E-01	1.00E+00	feeding behavior	P
GO:0007632	21	6.02E-01	1.00E+00	9.82E-01	1.00E+00	2.24E-01	1.00E+00	7.68E-01	1.00E+00	6.65E-01	1.00E+00	9.81E-01	1.00E+00	7.75E-01	1.00E+00	4.51E-01	1.00E+00	visual behavior	P
GO:0008009	53	8.78E-01	1.00E+00	9.11E-01	1.00E+00	6.97E-01	1.00E+00	5.88E-01	1.00E+00	9.29E-01	1.00E+00	8.11E-01	1.00E+00	6.11E-01	1.00E+00	1.00E+00	1.00E+00	chemokine activity	F
GO:0008013	14	1.25E-03	2.02E-01	4.73E-03	3.60E-01	4.65E-02	1.00E+00	4.26E-02	1.00E+00	5.48E-03	4.18E-01	5.12E-02	1.00E+00	5.09E-02	1.00E+00	3.76E-02	1.00E+00	beta-catenin binding	F
GO:0008015	185	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.76E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.20E-01	1.00E+00	9.95E-01	1.00E+00	circulation	P
GO:0008016	55	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	regulation of heart contraction	P
GO:0008017	56	1.51E-03	2.02E-01	1.83E-03	9.10E-02	4.10E-03	3.27E-01	4.01E-03	2.41E-01	3.42E-03	2.85E-01	4.80E-03	2.70E-01	5.79E-02	1.00E+00	2.76E-01	1.00E+00	microtubule binding	F
GO:0008021	75	2.10E-01	1.00E+00	3.33E-01	1.00E+00	9.10E-02	1.00E+00	2.23E-01	1.00E+00	2.37E-01	1.00E+00	2.96E-01	1.00E+00	6.58E-01	1.00E+00	8.38E-01	1.00E+00	synaptic vesicle	C
GO:0008022	102	4.18E-05	1.00E-02	1.89E-04	1.50E-02	2.94E-03	2.48E-01	4.22E-03	3.46E-01	1.10E-04	1.70E-02	3.21E-05	1.20E-02	7.40E-03	5.44E-01	9.84E-02	1.00E+00	protein C-terminus binding	F
GO:0008023	12	1.02E-01	1.00E+00	3.14E-01	1.00E+00	1.84E-01	1.00E+00	7.33E-01	1.00E+00	1.20E-01	1.00E+00	2.23E-01	1.00E+00	1.36E-01	1.00E+00	4.79E-01	1.00E+00	transcription elongation factor complex	C
GO:0008026	103	1.82E-04	2.50E-02	4.19E-05	9.58E-03	1.40E-03	9.80E-02	3.07E-03	1.47E-01	6.74E-03	5.39E-01	5.71E-05	1.70E-02	9.42E-03	6.30E-01	3.69E-02	1.00E+00	ATP-dependent helicase activity	F
GO:0008028	20	5.08E-01	1.00E+00	6.43E-01	1.00E+00	8.79E-01	1.00E+00	8.43E-01	1.00E+00	3.92E-01	1.00E+00	4.08E-01	1.00E+00	7.77E-01	1.00E+00	8.03E-01	1.00E+00	monocarboxylic acid transporter activity	F
GO:0008033	62	1.52E-03	2.02E-01	3.06E-03	1.97E-01	2.06E-02	1.00E+00	1.46E-02	8.18E-01	2.19E-03	2.85E-01	9.19E-03	7.39E-01	7.04E-02	1.00E+00	8.51E-02	1.00E+00	tRNA processing	P
GO:0008034	29	8.89E-02	1.00E+00	5.78E-02	1.00E+00	4.91E-01	1.00E+00	1.11E-01	1.00E+00	4.06E-02	1.00E+00	7.27E-02	1.00E+00	2.68E-01	1.00E+00	2.32E-01	1.00E+00	lipoprotein binding	F
GO:0008037	29	9.95E-01	1.00E+00	7.74E-01	1.00E+00	9.95E-01	1.00E+00	8.31E-01	1.00E+00	9.72E-01	1.00E+00	6.69E-01	1.00E+00	9.90E-01	1.00E+00	7.34E-01	1.00E+00	cell recognition	P
GO:0008038	17	9.85E-01	1.00E+00	9.88E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.04E-01	1.00E+00	9.71E-01	1.00E+00	9.89E-01	1.00E+00	8.05E-01	1.00E+00	neuron recognition	P
GO:0008045	11	9.41E-01	1.00E+00	9.94E-01	1.00E+00	9.65E-01	1.00E+00	9.94E-01	1.00E+00	8.63E-01	1.00E+00	9.99E-01	1.00E+00	9.13E-01	1.00E+00	2.80E-01	1.00E+00	motor axon guidance	P
GO:0008047	355	5.80E-05	1.10E-02	1.12E-05	9.58E-03	1.69E-03	2.48E-01	1.26E-03	1.15E-01	2.78E-04	1.70E-02	3.11E-04	3.07E-02	5.88E-02	1.00E+00	8.83E-04	9.16E-02	enzyme activator activity	F
GO:0008060	31	9.92E-03	6.67E-01	1.74E-01	1.00E+00	1.41E-02	6.93E-01	3.89E-01	1.00E+00	1.07E-02	5.39E-01	2.05E-01	1.00E+00	3.66E-01	1.00E+00	1.92E-01	1.00E+00	ARF GTPase activator activity	F
GO:0008064	56	8.25E-03	6.34E-01	7.81E-02	1.00E+00	1.93E-02	1.00E+00	2.88E-01	1.00E+00	8.58E-03	5.39E-01	7.76E-02	1.00E+00	5.74E-01	1.00E+00	1.91E-01	1.00E+00	regulation of actin polymerization and/or de	P

GO:0008066	49	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	7.64E-01	1.00E+00	9.90E-01	1.00E+00	glutamate receptor activity	F
GO:0008067	31	9.97E-01	1.00E+00	9.46E-01	1.00E+00	9.99E-01	1.00E+00	9.30E-01	1.00E+00	9.96E-01	1.00E+00	8.62E-01	1.00E+00	5.87E-01	1.00E+00	8.63E-01	1.00E+00	metabotropic glutamate, GABA-B-like recep	F
GO:0008076	166	5.82E-01	1.00E+00	8.17E-01	1.00E+00	2.81E-01	1.00E+00	9.81E-01	1.00E+00	8.03E-01	1.00E+00	6.51E-01	1.00E+00	2.88E-01	1.00E+00	5.83E-01	1.00E+00	voltage-gated potassium channel complex	C
GO:0008080	59	3.26E-04	3.37E-02	2.28E-04	4.19E-02	2.10E-02	1.00E+00	1.90E-01	1.00E+00	7.32E-04	4.00E-02	3.53E-04	3.07E-02	2.07E-02	9.11E-01	1.30E-03	9.16E-02	N-acetyltransferase activity	F
GO:0008081	88	4.87E-01	1.00E+00	6.84E-01	1.00E+00	4.82E-01	1.00E+00	5.79E-01	1.00E+00	6.22E-01	1.00E+00	5.30E-01	1.00E+00	1.29E-01	1.00E+00	9.45E-01	1.00E+00	phosphoric diester hydrolase activity	F
GO:0008083	194	9.57E-01	1.00E+00	9.93E-01	1.00E+00	9.71E-01	1.00E+00	9.78E-01	1.00E+00	8.63E-01	1.00E+00	9.80E-01	1.00E+00	9.08E-01	1.00E+00	9.67E-01	1.00E+00	growth factor activity	F
GO:0008088	13	1.39E-01	1.00E+00	5.62E-02	1.00E+00	3.14E-01	1.00E+00	4.15E-02	1.00E+00	9.68E-02	1.00E+00	5.30E-02	1.00E+00	2.08E-01	1.00E+00	3.24E-01	1.00E+00	axon cargo transport	P
GO:0008092	476	4.80E-05	1.00E-02	2.51E-08	4.97E-03	3.43E-06	2.42E-03	5.83E-05	1.20E-02	3.31E-04	1.98E-02	1.69E-07	9.20E-04	6.60E-01	1.00E+00	2.79E-03	1.85E-01	cytoskeletal protein binding	F
GO:0008094	46	5.71E-03	3.50E-01	2.35E-03	1.77E-01	3.11E-02	1.00E+00	1.17E-01	1.00E+00	8.20E-03	5.39E-01	1.30E-03	6.40E-02	2.24E-01	1.00E+00	4.24E-01	1.00E+00	DNA-dependent ATPase activity	F
GO:0008104	965	1.48E-22	0.00E+00	2.73E-23	0.00E+00	1.08E-12	0.00E+00	4.00E-10	0.00E+00	1.41E-19	0.00E+00	7.25E-22	0.00E+00	4.47E-06	2.00E-03	1.08E-06	1.88E-03	protein localization	P
GO:0008105	12	5.46E-01	1.00E+00	4.78E-01	1.00E+00	4.28E-01	1.00E+00	3.22E-01	1.00E+00	6.88E-01	1.00E+00	7.37E-01	1.00E+00	4.52E-01	1.00E+00	2.76E-01	1.00E+00	asymmetric protein localization	P
GO:0008121	12	2.40E-02	1.00E+00	2.46E-01	1.00E+00	2.93E-02	1.00E+00	2.53E-01	1.00E+00	3.39E-02	1.00E+00	2.13E-01	1.00E+00	3.61E-01	1.00E+00	5.89E-01	1.00E+00	ubiquinol-cytochrome-c reductase activity	F
GO:0008134	453	1.03E-12	0.00E+00	1.58E-12	0.00E+00	3.85E-08	9.68E-04	5.23E-08	9.71E-04	2.80E-12	0.00E+00	2.05E-10	0.00E+00	1.92E-02	9.11E-01	4.16E-04	2.70E-02	transcription factor binding	F
GO:0008135	104	2.85E-07	1.95E-03	3.00E-08	4.97E-03	1.57E-03	2.48E-01	6.70E-04	4.70E-02	7.12E-07	2.45E-03	4.71E-07	2.97E-03	1.41E-03	1.68E-01	4.02E-04	2.70E-02	translation factor activity, nucleic acid bindir	F
GO:0008137	45	3.52E-03	2.73E-01	3.45E-02	1.00E+00	6.59E-02	1.00E+00	1.29E-01	1.00E+00	6.96E-03	5.39E-01	8.39E-02	1.00E+00	4.53E-02	1.00E+00	7.89E-02	1.00E+00	NADH dehydrogenase (ubiquinone) activity	F
GO:0008138	49	1.71E-01	1.00E+00	1.27E-01	1.00E+00	6.27E-01	1.00E+00	3.84E-01	1.00E+00	5.74E-02	1.00E+00	7.96E-02	1.00E+00	8.88E-01	1.00E+00	3.10E-01	1.00E+00	protein tyrosine/serine/threonine phosphata	F
GO:0008144	24	1.59E-01	1.00E+00	4.90E-01	1.00E+00	3.66E-01	1.00E+00	5.94E-01	1.00E+00	4.72E-01	1.00E+00	4.43E-01	1.00E+00	1.40E-02	6.47E-01	3.78E-01	1.00E+00	drug binding	F
GO:0008146	47	5.17E-01	1.00E+00	5.53E-01	1.00E+00	1.45E-01	1.00E+00	7.00E-01	1.00E+00	5.90E-01	1.00E+00	5.72E-01	1.00E+00	7.87E-01	1.00E+00	2.51E-01	1.00E+00	sulfotransferase activity	F
GO:0008150	14949	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.79E-29	0.00E+00	4.40E-39	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.79E-21	0.00E+00	3.85E-28	0.00E+00	biological_process	P
GO:0008152	8837	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.29E-43	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.59E-27	0.00E+00	0.00E+00	0.00E+00	metabolism	P
GO:0008154	74	1.66E-02	6.67E-01	1.05E-01	1.00E+00	2.75E-02	1.00E+00	2.14E-01	1.00E+00	2.92E-02	1.00E+00	1.14E-01	1.00E+00	4.07E-01	1.00E+00	1.85E-01	1.00E+00	actin polymerization and/or depolymerizatio	P
GO:0008156	18	3.86E-06	7.00E-03	6.33E-03	3.60E-01	6.47E-04	3.60E-02	1.09E-01	1.00E+00	7.19E-04	4.00E-02	2.94E-03	2.39E-01	1.49E-02	6.47E-01	4.01E-02	1.00E+00	negative regulation of DNA replication	P
GO:0008168	181	5.14E-09	8.06E-04	1.39E-05	9.58E-03	4.20E-04	3.60E-02	6.87E-03	4.53E-01	9.77E-09	9.64E-04	9.65E-05	1.70E-02	4.29E-03	3.57E-01	8.69E-03	4.81E-01	methyltransferase activity	F
GO:0008170	47	7.32E-04	6.71E-02	1.70E-04	1.50E-02	1.19E-01	1.00E+00	3.21E-03	1.47E-01	1.94E-04	1.70E-02	5.75E-04	5.49E-02	1.74E-01	1.00E+00	3.25E-02	1.00E+00	N-methyltransferase activity	F
GO:0008172	10	2.23E-01	1.00E+00	7.68E-01	1.00E+00	2.43E-02	1.00E+00	9.91E-01	1.00E+00	4.57E-01	1.00E+00	6.07E-01	1.00E+00	2.30E-01	1.00E+00	4.27E-01	1.00E+00	S-methyltransferase activity	F
GO:0008173	24	5.79E-03	3.50E-01	4.43E-01	1.00E+00	1.25E-01	1.00E+00	9.47E-01	1.00E+00	2.67E-03	2.85E-01	3.50E-01	1.00E+00	2.20E-01	1.00E+00	5.01E-01	1.00E+00	RNA methyltransferase activity	F
GO:0008175	11	5.41E-02	1.00E+00	3.41E-01	1.00E+00	2.02E-02	1.00E+00	7.76E-01	1.00E+00	4.19E-02	1.00E+00	3.39E-01	1.00E+00	5.16E-01	1.00E+00	3.52E-01	1.00E+00	tRNA methyltransferase activity	F
GO:0008180	10	2.59E-02	1.00E+00	8.74E-02	1.00E+00	1.06E-01	1.00E+00	4.26E-01	1.00E+00	4.47E-02	1.00E+00	1.36E-01	1.00E+00	2.03E-02	9.11E-01	1.56E-01	1.00E+00	signalosome complex	C
GO:0008186	20	2.32E-04	2.64E-02	2.72E-03	1.77E-01	7.08E-03	4.60E-01	1.44E-02	8.18E-01	1.45E-02	1.00E+00	1.67E-03	1.61E-01	2.46E-02	1.00E+00	3.72E-01	1.00E+00	RNA-dependent ATPase activity	F
GO:0008188	144	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.77E-01	1.00E+00	9.97E-01	1.00E+00	neuropeptide receptor activity	F
GO:0008191	10	7.93E-01	1.00E+00	9.39E-01	1.00E+00	3.80E-01	1.00E+00	7.68E-01	1.00E+00	7.19E-01	1.00E+00	9.70E-01	1.00E+00	8.08E-01	1.00E+00	6.35E-01	1.00E+00	metalloendopeptidase inhibitor activity	F
GO:0008194	107	9.90E-01	1.00E+00	7.16E-01	1.00E+00	8.72E-01	1.00E+00	5.72E-01	1.00E+00	9.71E-01	1.00E+00	4.77E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	UDP-glycosyltransferase activity	F
GO:0008199	15	9.90E-01	1.00E+00	6.18E-01	1.00E+00	8.99E-01	1.00E+00	6.72E-01	1.00E+00	9.94E-01	1.00E+00	5.03E-01	1.00E+00	4.79E-01	1.00E+00	9.91E-01	1.00E+00	ferric iron binding	F
GO:0008200	11	2.30E-01	1.00E+00	4.69E-01	1.00E+00	4.58E-01	1.00E+00	2.59E-01	1.00E+00	1.76E-01	1.00E+00	7.10E-01	1.00E+00	6.98E-01	1.00E+00	2.45E-01	1.00E+00	ion channel inhibitor activity	F
GO:0008201	84	8.76E-01	1.00E+00	9.52E-01	1.00E+00	3.69E-01	1.00E+00	8.99E-01	1.00E+00	9.03E-01	1.00E+00	8.89E-01	1.00E+00	8.74E-01	1.00E+00	8.83E-01	1.00E+00	heparin binding	F
GO:0008202	205	1.77E-01	1.00E+00	6.16E-01	1.00E+00	1.56E-01	1.00E+00	3.07E-01	1.00E+00	1.53E-01	1.00E+00	6.44E-01	1.00E+00	5.56E-01	1.00E+00	4.88E-01	1.00E+00	steroid metabolism	P
GO:0008203	86	3.78E-02	1.00E+00	1.26E-01	1.00E+00	5.05E-02	1.00E+00	1.21E-01	1.00E+00	5.09E-02	1.00E+00	2.27E-01	1.00E+00	2.81E-01	1.00E+00	8.20E-02	1.00E+00	cholesterol metabolism	P
GO:0008206	18	7.58E-02	1.00E+00	5.14E-01	1.00E+00	4.67E-02	1.00E+00	5.38E-01	1.00E+00	7.95E-02	1.00E+00	3.55E-01	1.00E+00	7.26E-01	1.00E+00	9.49E-01	1.00E+00	bile acid metabolism	P
GO:0008207	17	8.74E-01	1.00E+00	9.97E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	9.77E-01	1.00E+00	8.81E-01	1.00E+00	9.98E-01	1.00E+00	C21-steroid hormone metabolism	P
GO:0008209	10	8.93E-01	1.00E+00	9.83E-01	1.00E+00	5.24E-01	1.00E+00	8.42E-01	1.00E+00	9.60E-01	1.00E+00	9.90E-01	1.00E+00	5.20E-01	1.00E+00	9.85E-01	1.00E+00	androgen metabolism	P
GO:0008210	10	1.00E+00	1.00E+00	8.72E-01	1.00E+00	1.00E+00	1.00E+00	7.46E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	7.74E-01	1.00E+00	5.44E-01	1.00E+00	estrogen metabolism	P
GO:0008213	28	4.32E-03	3.28E-01	4.93E-04	6.90E-02	4.55E-01	1.00E+00	1.39E-02	8.18E-01	1.34E-03	7.80E-02	1.11E-03	5.49E-02	1.49E-01	1.00E+00	3.11E-02	1.00E+00	protein amino acid alkylation	P
GO:0008217	70	9.96E-01	1.00E+00	9.90E-01	1.00E+00	6.95E-01	1.00E+00	8.44E-01	1.00E+00	9.99E-01	1.00E+00	9.90E-01	1.00E+00	5.32E-01	1.00E+00	9.79E-01	1.00E+00	blood pressure regulation	P
GO:0008219	929	1.99E-09	8.06E-04	1.06E-14	0.00E+00	1.08E-07	2.42E-03	1.77E-09	0.00E+00	1.99E-07	1.69E-03	2.37E-11	0.00E+00	1.21E-04	2.50E-02	2.68E-07	1.88E-03	cell death	P
GO:0008227	169	1.61E-02	6.67E-01	1.02E-01	1.00E+00	5.32E-03	4.19E-01	1.48E-01	1.00E+00	4.33E-02	1.00E+00	2.32E-01	1.00E+00	2.88E-01	1.00E+00	1.73E-02	1.00E+00	amine receptor activity	F
GO:0008233	706	4.70E-02	1.00E+00	3.84E-04	6.90E-02	8.82E-02	1.00E+00	1.82E-02	1.00E+00	6.63E-02	1.00E+00	1.05E-03	5.49E-02	1.57E-01	1.00E+00	4.34E-03	3.60E-01	peptidase activity	F
GO:0008234	175	1.15E-01	1.00E+00	1.51E-03	9.10E-02	2.00E-01	1.00E+00	2.90E-03	1.47E-01	7.10E-02	1.00E+00	4.31E-03	2.70E-01	4.03E-01	1.00E+00	1.12E-01	1.00E+00	cysteine-type peptidase activity	F
GO:0008235	57	2.74E-01	1.00E+00	1.41E-01	1.00E+00	3.03E-01	1.00E+00	7.81E-02	1.00E+00	4.08E-01	1.00E+00	4.24E-01	1.00E+00	1.99E-01	1.00E+00	1.63E-01	1.00E+00	metalloexopeptidase activity	F
GO:0008236	234	1.21E-01	1.00E+00	9.63E-02	1.00E+00	3.00E-01	1.00E+00	2.34E-01	1.00E+00	1.00E-01	1.00E+00	1.87E-01	1.00E+00	2.33E-01	1.00E+00	9.32E-03	4.81E-01	serine-type peptidase activity	F
GO:0008237	207	7.58E-01	1.00E+00	2.47E-01	1.00E+00	1.59E-01	1.00E+00	3.89E-01	1.00E+00	9.20E-01	1.00E+00	3.07E-01	1.00E+00	7.79E-01	1.00E+00	2.33E-01	1.00E+00	metallopeptidase activity	F
GO:0008238	106	2.42E-01	1.00E+00	2.37E-01	1.00E+00	3.98E-01	1.00E+00	2.13E-01	1.00E+00	3.31E-01	1.00E+00	3.47E-01	1.00E+00	1.13E-01	1.00E+00	2.67E-01	1.00E+00	exopeptidase activity	F
GO:0008239	12	5.22E-01	1.00E+00	2.44E-01	1.00E+00	7.69E-01	1.00E+00	3.63E-01	1.00E+00	6.81E-01	1.00E+00	2.30E-01	1.00E+00	1.44E-01	1.00E+00	2.21E-01	1.00E+00	dipeptidyl-peptidase activity	F
GO:0008270	2351	1.15E-25	0.00E+00	4.00E-36	0.00E+00	2.36E-11	0.00E+00	1.41E-12	0.00E+00	1.14E-24	0.00E+00	3.77E-35	0.00E+00	5.01E-07	1.95E-03	2.82E-11	0.00E+00	zinc ion binding	F
GO:0008271	10	4.00E-01	1.00E+00	9.95E-01	1.00E+00	3.14E-01	1.00E+00	7.88E-01	1.00E+00	4.95E-01	1.00E+00	1.00E+00	1.00E+00	5.44E-01	1.00E+00	7.98E-01	1.00E+00	sulfate porter activity	F
GO:0008272	15	3.51E-01	1.00E+00	8.06E-01	1.00E+00	4.84E-01	1.00E+00	4.73E-01	1.00E+00	3.02E-01	1.00E+00	7.97E-01	1.00E+00	6.07E-01	1.00E+00	8.64E-01	1.00E+00	sulfate transport	P
GO:0008276	42	2.33E-05	8.00E-03	4.83E-06	8.39E-03	6.16E-02	1.00E+00	6.86E-04	4.70E-02	1.81E-05	4.19E-03	2.36E-05	7.63E-03	3.24E-02	1.00E+00	8.57E-03	4.81E-01	protein methyltransferase activity	F
GO:0008277	38	2.25E-01	1.00E+00	3.24E-01	1.00E+00	7.89E-02	1.00E+00	7.38E-01	1.00E+00	3.19E-01	1.00E+00	1.96E-01	1.00E+00	6.18E-01	1.00E+00	6.72E-01	1.00E+00	regulation of G-protein coupled receptor pro	P
GO:0008283	898	7.62E-04	6.71E-02	7.49E-03	3.60E-01	3.03E-02	1.00E+00	2.38E-01	1.00E+00	5.57E-04	4.00E-02	6.09E-03	3.51E-01	1.64E-02	6.63E-01	1.91E-02	1.00E+00	cell proliferation	P
GO:0008284	297	6.13E-01	1.00E+00	6.53E-01	1.00E+00	5.30E-01	1.00E+00	6.87E-01	1.00E+00	4.43E-01	1.00E+00	7.35E-01	1.00E+00	8.69E-01	1.00E+00	2.33E-01	1.00E+00	positive regulation of cell proliferation	P
GO:0008285	284	1.44E-01	1.00E+00	2.87E-01	1.00E+00	2.26E-01	1.00E+00	7.28E-01	1.00E+00	1.45E-01	1.00E+00	2.45E-01	1.00E+00	2.31E-01	1.00E+00	1.68E-01	1.00E+00	negative regulation of cell proliferation	P
GO:0008286	38	7.72E-02	1.00E+00	2.04E-02	1.00E+00	1.24E-01	1.00E+00	2.38E-02	1.00E+00	1.06E-01	1.00E+00	5.63E-02	1.00E+00	3.69E-01	1.00E+00	2.59E-01	1.00E+00	insulin receptor signaling pathway	P
GO:0008287	39	1.08E-01	1.00E+00	2.69E-04	4.19E-02	3.89E-01	1.00E+00	1.83E-03	1.24E-01	1.21E-01	1.00E+00	2.99E-03	2.39E-01	1.94E-01	1.00E+00	6.57E-02	1.00E+00	protein serine/threonine phosphatase comp	C
GO:0008289	340	3.14E-05	1.00E-02	8.61E-08	4.97E-03	3.46E-04	3.60E-02	2.34E-05	8.00E-03	2.79E-04	1.70E-02	1.38E-06	2.97E-03	3.64E-02	1.00E+00	1.76E-03	1.40E-01	lipid binding	F
GO:0008299	16	8.22E-01	1.00E+00	2.90E-01	1.00E+00	6.41E-01	1.00E+00	1.51E-01	1.00E+00	8.52E-01	1.00E+00	2.81E-01	1.00E+00	7.17E-01	1.00E+00	8.89E-01	1.00E+00	isoprenoid biosynthesis	P
GO:0008301	10	3.65E-01	1.00E+00	9.97E-01	1.00E+00	6.55E-01	1.00E+00	8.98E-01	1.00E+00	2.95E-01	1.00E+00	9.52E-01	1.00E+00	3.99E-01	1.00E+00	1.00E+00	1.00E+00	DNA bending activity	F
GO:0008305	30	8.15E-01	1.00E+00	1.01E-01	1.00E+00	5.86E-01	1.00E+00	2.76E-01	1.00E+00	8.07E-01	1.00E+00	1.02E-01	1.00E+00	8.58E-01	1.00E+00	6.45E-01	1.00E+00	integrin complex	C
GO:0008306	11	9.25E-01	1.00E+00	6.91E-01	1.00E+00	9.01E-01	1.00E+00	4.21E-01	1.00E+00	7.28E-01	1.00E+00	7.21E-01	1.00E+00	9.88E-01	1.00E+00	6.61E-01	1.00E+00	associative learning	P
GO:0008307	39	9.24E-01	1.00E+00	8.69E-01	1.00E+00	9.17E-01	1.00E+00	6.97E-01	1.00E+00	9.61E-01	1.00E+00	6.31E-01	1.00E+00	5.44E-01	1.00E+00	1.00E+00	1.00E+00	structural constituent of muscle	F
GO:0008312	11	1.85E-01	1.00E+00	2.54E-01	1.00E+00	1.01E-01	1.00E+00	9.42E-01	1.00E+00	2.44E-01	1.00E+00	2.76E-01	1.00E+00	3.11E-01	1.00E+00	4.49E-02	1.00E+00	7S RNA binding	F
GO:0008324	766	1.47E-01	1.00E+00	7.55E-02	1.00E+00	1.73E-01	1.00E+00	1.81E-01	1.00E+00	1.31E-01	1.00E+00	6.25E-02	1.00E+00	8.14E-01	1.00E+00	2.46E-01	1.00E+00	cation transporter activity	F
GO:0008329	11	3.51E-01	1.00E+00	6.99E-01	1.00E+00	1.00E+00	1.00E+00	6.35E-01	1.00E+00	1.58E-01	1.00E+00	5.96E-01	1.00E+00	7.55E-01	1.00E+00	9.69E-01	1.00E+00	pattern recognition receptor activity	F
GO:0008344	38	2.28E-01	1.00E+00	4.72E-01	1.00E+00	7.14E-01	1.00E+00	2.68E-01	1.00E+00	1.39E-01	1.00E+00	5.78E-01	1.00E+00	2.99E-01	1.00E+00	3.57E-01	1.00E+00	adult locomotory behavior	P
GO:0008354	10	8.79E-01	1.00E+00	3.59E-01	1.00E+00	8.86E-01	1.00E+00	6.76E-01	1.00E+00	7.08E-01	1.00E+00	2.25E-01	1.00E+00	8.52E-01	1.00E+00	7.81E-01	1.00E+00	germ cell migration	P
GO:0008360	46	7.89E-02	1.00E+00	2.86E-03	1.77E-01	3.92E-02	1.00E+00	6.90E-02	1.00E+00	1.70E-01	1.00E+00	6.91E-03	5.30E-01	1.85E-01	1.00E+00	1.27E-02	6.47E-01	regulation of cell shape	P
GO:0008361	219	1.33E-01	1.00E+00	4.17E-02	1.00E+00	1.70E-02	6.93E-01	2.32E-03	1.47E-01	1.76E-01	1.00E+00	1.68E-01	1.00E+00	7.23E-01	1.00E+00	2.15E-01	1.00E+00	regulation of cell size	P

GO:0008366	39	8.87E-02	1.00E+00	2.49E-01	1.00E+00	1.87E-02	1.00E+00	1.91E-01	1.00E+00	3.36E-01	1.00E+00	2.44E-01	1.00E+00	1.46E-01	1.00E+00	6.86E-01	1.00E+00	axon ensheathment	P
GO:0008367	10	7.04E-01	1.00E+00	4.99E-01	1.00E+00	5.27E-01	1.00E+00	6.65E-01	1.00E+00	7.66E-01	1.00E+00	4.53E-01	1.00E+00	7.75E-01	1.00E+00	5.57E-01	1.00E+00	bacterial binding	F
GO:0008373	20	8.30E-01	1.00E+00	2.91E-01	1.00E+00	9.29E-01	1.00E+00	4.31E-01	1.00E+00	7.80E-01	1.00E+00	2.80E-01	1.00E+00	2.92E-01	1.00E+00	1.63E-01	1.00E+00	sialyltransferase activity	F
GO:0008374	37	1.43E-01	1.00E+00	4.41E-01	1.00E+00	4.26E-01	1.00E+00	8.85E-01	1.00E+00	7.90E-02	1.00E+00	2.27E-01	1.00E+00	3.72E-01	1.00E+00	8.01E-01	1.00E+00	O-acyltransferase activity	F
GO:0008375	34	1.17E-01	1.00E+00	2.66E-02	1.00E+00	3.99E-01	1.00E+00	1.40E-01	1.00E+00	5.39E-02	1.00E+00	2.16E-02	1.00E+00	4.65E-01	1.00E+00	5.86E-01	1.00E+00	acetylglucosaminyltransferase activity	F
GO:0008376	29	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.90E-01	1.00E+00	9.58E-01	1.00E+00	9.96E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	acetylgalactosaminyltransferase activity	F
GO:0008378	32	6.38E-01	1.00E+00	2.05E-01	1.00E+00	4.01E-01	1.00E+00	5.38E-01	1.00E+00	7.46E-01	1.00E+00	7.95E-02	1.00E+00	4.51E-01	1.00E+00	9.24E-01	1.00E+00	galactosyltransferase activity	F
GO:0008380	272	2.91E-19	0.00E+00	5.66E-22	0.00E+00	4.71E-09	9.34E-04	3.73E-09	0.00E+00	5.47E-17	0.00E+00	9.40E-19	0.00E+00	4.61E-07	1.95E-03	6.37E-09	7.71E-04	RNA splicing	P
GO:0008395	13	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	5.26E-01	1.00E+00	steroid hydroxylase activity	F
GO:0008406	74	6.99E-01	1.00E+00	7.13E-01	1.00E+00	4.83E-01	1.00E+00	7.94E-01	1.00E+00	6.37E-01	1.00E+00	5.79E-01	1.00E+00	9.22E-01	1.00E+00	6.43E-01	1.00E+00	gonad development	P
GO:0008408	27	3.86E-02	1.00E+00	3.34E-01	1.00E+00	1.97E-02	1.00E+00	3.21E-01	1.00E+00	8.70E-02	1.00E+00	4.17E-01	1.00E+00	3.43E-01	1.00E+00	4.16E-01	1.00E+00	3'-5' exonuclease activity	F
GO:0008415	189	2.66E-06	1.95E-03	9.02E-04	6.90E-02	1.09E-03	9.80E-02	1.89E-01	1.00E+00	1.85E-06	2.60E-03	7.77E-04	5.49E-02	2.66E-02	1.00E+00	3.05E-02	1.00E+00	acyltransferase activity	F
GO:0008417	14	1.24E-01	1.00E+00	1.90E-01	1.00E+00	4.59E-01	1.00E+00	3.31E-01	1.00E+00	9.50E-02	1.00E+00	2.13E-01	1.00E+00	4.12E-01	1.00E+00	7.93E-02	1.00E+00	fucosyltransferase activity	F
GO:0008430	31	2.78E-02	1.00E+00	1.49E-02	1.00E+00	2.39E-01	1.00E+00	8.03E-02	1.00E+00	2.09E-02	1.00E+00	3.99E-02	1.00E+00	7.67E-02	1.00E+00	3.35E-02	1.00E+00	selenium binding	F
GO:0008443	12	9.42E-01	1.00E+00	9.84E-01	1.00E+00	8.96E-01	1.00E+00	9.18E-01	1.00E+00	7.29E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	phosphofructokinase activity	F
GO:0008483	22	1.12E-02	6.67E-01	4.66E-02	1.00E+00	1.46E-02	6.93E-01	7.82E-02	1.00E+00	2.07E-02	1.00E+00	1.10E-01	1.00E+00	3.50E-01	1.00E+00	4.68E-02	1.00E+00	transaminase activity	F
GO:0008484	20	1.85E-01	1.00E+00	4.46E-01	1.00E+00	3.19E-01	1.00E+00	3.04E-01	1.00E+00	1.72E-01	1.00E+00	5.11E-01	1.00E+00	6.24E-01	1.00E+00	7.93E-01	1.00E+00	sulfuric ester hydrolase activity	F
GO:0008493	27	4.42E-01	1.00E+00	2.06E-01	1.00E+00	4.40E-02	1.00E+00	6.96E-01	1.00E+00	6.43E-01	1.00E+00	1.53E-01	1.00E+00	9.27E-01	1.00E+00	2.00E-01	1.00E+00	tetracycline transporter activity	F
GO:0008509	194	7.87E-01	1.00E+00	8.24E-01	1.00E+00	7.52E-01	1.00E+00	6.98E-01	1.00E+00	6.57E-01	1.00E+00	7.61E-01	1.00E+00	8.95E-01	1.00E+00	9.35E-01	1.00E+00	anion transporter activity	F
GO:0008514	10	9.88E-01	1.00E+00	9.81E-01	1.00E+00	9.23E-01	1.00E+00	1.00E+00	1.00E+00	9.00E-01	1.00E+00	8.67E-01	1.00E+00	8.69E-01	1.00E+00	7.20E-01	1.00E+00	organic anion transporter activity	F
GO:0008527	10	9.83E-01	1.00E+00	9.44E-01	1.00E+00	8.53E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	2.56E-01	1.00E+00	3.94E-01	1.00E+00	taste receptor activity	F
GO:0008528	415	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity, G-protein coupled	F
GO:0008533	14	9.50E-01	1.00E+00	9.69E-01	1.00E+00	4.79E-01	1.00E+00	7.40E-01	1.00E+00	9.94E-01	1.00E+00	9.33E-01	1.00E+00	8.71E-01	1.00E+00	9.89E-01	1.00E+00	astacin activity	F
GO:0008536	10	1.27E-01	1.00E+00	1.79E-01	1.00E+00	3.29E-01	1.00E+00	4.25E-01	1.00E+00	9.23E-02	1.00E+00	5.24E-01	1.00E+00	5.09E-01	1.00E+00	1.00E-01	1.00E+00	Ran GTPase binding	F
GO:0008542	18	4.28E-01	1.00E+00	9.82E-01	1.00E+00	1.34E-01	1.00E+00	8.00E-01	1.00E+00	4.95E-01	1.00E+00	9.90E-01	1.00E+00	5.94E-01	1.00E+00	2.41E-01	1.00E+00	visual learning	P
GO:0008543	31	8.09E-01	1.00E+00	9.91E-01	1.00E+00	4.90E-01	1.00E+00	9.81E-01	1.00E+00	7.66E-01	1.00E+00	9.06E-01	1.00E+00	9.23E-01	1.00E+00	9.34E-01	1.00E+00	fibroblast growth factor receptor signaling p	P
GO:0008544	184	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	epidermis development	P
GO:0008553	10	5.29E-02	1.00E+00	8.00E-02	1.00E+00	6.04E-01	1.00E+00	7.64E-02	1.00E+00	4.42E-02	1.00E+00	1.21E-01	1.00E+00	1.61E-01	1.00E+00	3.05E-01	1.00E+00	hydrogen-exporting ATPase activity, phosph	F
GO:0008565	92	1.64E-08	9.77E-04	6.17E-09	4.97E-03	1.52E-04	1.50E-02	1.27E-03	1.15E-01	1.47E-07	1.69E-03	2.78E-08	8.37E-04	3.60E-04	3.40E-02	8.40E-03	4.81E-01	protein transporter activity	F
GO:0008584	31	4.05E-01	1.00E+00	1.88E-01	1.00E+00	5.13E-01	1.00E+00	6.09E-01	1.00E+00	3.16E-01	1.00E+00	1.35E-01	1.00E+00	7.32E-01	1.00E+00	2.33E-01	1.00E+00	male gonad development	P
GO:0008585	43	5.72E-01	1.00E+00	7.67E-01	1.00E+00	2.95E-01	1.00E+00	7.83E-01	1.00E+00	6.16E-01	1.00E+00	7.20E-01	1.00E+00	8.35E-01	1.00E+00	5.00E-01	1.00E+00	female gonad development	P
GO:0008589	14	9.33E-01	1.00E+00	7.97E-01	1.00E+00	6.16E-01	1.00E+00	6.59E-01	1.00E+00	9.75E-01	1.00E+00	9.40E-01	1.00E+00	9.25E-01	1.00E+00	4.71E-01	1.00E+00	regulation of smoothened signaling pathwa	P
GO:0008601	23	1.29E-01	1.00E+00	6.11E-03	3.60E-01	2.23E-01	1.00E+00	3.99E-02	1.00E+00	1.74E-01	1.00E+00	1.06E-02	7.39E-01	1.36E-01	1.00E+00	1.18E-01	1.00E+00	protein phosphatase type 2A regulator activ	F
GO:0008603	27	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.27E-01	1.00E+00	8.24E-01	1.00E+00	9.99E-01	1.00E+00	cAMP-dependent protein kinase regulator a	F
GO:0008610	311	1.91E-02	1.00E+00	3.64E-03	1.97E-01	4.60E-02	1.00E+00	1.25E-02	8.18E-01	5.23E-02	1.00E+00	6.02E-03	3.51E-01	8.79E-02	1.00E+00	2.10E-01	1.00E+00	lipid biosynthesis	P
GO:0008624	45	8.09E-03	6.34E-01	1.28E-02	7.47E-01	7.15E-03	4.60E-01	1.86E-01	1.00E+00	1.84E-02	1.00E+00	2.54E-02	1.00E+00	2.70E-01	1.00E+00	6.59E-03	4.81E-01	induction of apoptosis by extracellular signa	P
GO:0008625	13	1.04E-02	6.67E-01	1.82E-02	1.00E+00	1.79E-01	1.00E+00	4.67E-01	1.00E+00	2.28E-02	1.00E+00	3.32E-02	1.00E+00	3.40E-02	1.00E+00	9.87E-04	9.16E-02	induction of apoptosis via death domain rec	P
GO:0008629	44	1.35E-02	6.67E-01	2.17E-02	1.00E+00	6.50E-02	1.00E+00	1.01E-02	7.13E-01	2.31E-02	1.00E+00	5.75E-02	1.00E+00	1.05E-01	1.00E+00	3.15E-02	1.00E+00	induction of apoptosis by intracellular signal	P
GO:0008630	24	7.83E-02	1.00E+00	7.13E-02	1.00E+00	2.17E-01	1.00E+00	4.10E-02	1.00E+00	9.17E-02	1.00E+00	1.59E-01	1.00E+00	8.47E-02	1.00E+00	4.97E-02	1.00E+00	DNA damage response, signal transduction	P
GO:0008632	106	4.74E-04	3.37E-02	2.68E-06	8.39E-03	2.11E-02	1.00E+00	1.55E-03	1.24E-01	9.89E-04	4.40E-02	1.65E-05	7.63E-03	4.21E-03	3.57E-01	6.87E-04	9.16E-02	apoptotic program	P
GO:0008633	21	4.40E-01	1.00E+00	7.22E-02	1.00E+00	3.16E-01	1.00E+00	1.86E-01	1.00E+00	7.02E-01	1.00E+00	1.07E-01	1.00E+00	1.84E-01	1.00E+00	6.48E-02	1.00E+00	activation of pro-apoptotic gene products	P
GO:0008637	24	2.87E-02	1.00E+00	1.27E-02	7.47E-01	1.35E-01	1.00E+00	1.09E-02	8.18E-01	2.24E-02	1.00E+00	4.12E-02	1.00E+00	6.35E-02	1.00E+00	3.38E-02	1.00E+00	apoptotic mitochondrial changes	P
GO:0008643	73	1.61E-02	6.67E-01	5.59E-03	3.60E-01	6.19E-02	1.00E+00	1.82E-02	1.00E+00	2.27E-02	1.00E+00	2.58E-02	1.00E+00	8.17E-02	1.00E+00	8.15E-02	1.00E+00	carbohydrate transport	P
GO:0008645	43	1.31E-02	6.67E-01	2.39E-02	1.00E+00	3.37E-02	1.00E+00	6.37E-02	1.00E+00	1.90E-02	1.00E+00	5.36E-02	1.00E+00	7.56E-02	1.00E+00	1.25E-01	1.00E+00	hexose transport	P
GO:0008652	90	2.05E-01	1.00E+00	5.27E-02	1.00E+00	2.34E-01	1.00E+00	4.46E-02	1.00E+00	2.33E-01	1.00E+00	8.14E-02	1.00E+00	4.11E-01	1.00E+00	2.53E-01	1.00E+00	amino acid biosynthesis	P
GO:0008654	85	2.24E-02	1.00E+00	6.91E-03	3.60E-01	1.49E-01	1.00E+00	4.30E-02	1.00E+00	3.72E-02	1.00E+00	5.89E-03	3.51E-01	1.11E-01	1.00E+00	1.86E-01	1.00E+00	phospholipid biosynthesis	P
GO:0008656	15	3.11E-03	2.39E-01	6.44E-02	1.00E+00	1.80E-02	1.00E+00	4.59E-01	1.00E+00	2.50E-02	1.00E+00	6.50E-02	1.00E+00	4.76E-02	1.00E+00	8.24E-02	1.00E+00	caspase activator activity	F
GO:0008667	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	2,3-dihydro-2,3-dihydroxybenzoate dehydrc	F
GO:0008757	76	1.17E-07	1.85E-03	1.65E-05	9.58E-03	3.73E-04	3.60E-02	2.56E-02	1.00E+00	2.80E-07	1.69E-03	4.37E-05	1.20E-02	1.04E-02	6.30E-01	5.60E-03	3.60E-01	S-adenosylmethionine-dependent methyltra	F
GO:0009055	357	1.04E-01	1.00E+00	2.21E-01	1.00E+00	2.91E-01	1.00E+00	5.61E-01	1.00E+00	1.99E-01	1.00E+00	1.65E-01	1.00E+00	1.07E-02	6.30E-01	3.47E-01	1.00E+00	electron carrier activity	F
GO:0009056	803	2.67E-14	0.00E+00	4.63E-19	0.00E+00	2.09E-08	9.68E-04	3.40E-11	0.00E+00	3.25E-11	0.00E+00	9.62E-16	0.00E+00	5.01E-06	2.00E-03	6.32E-08	1.88E-03	catabolism	P
GO:0009057	483	4.76E-14	0.00E+00	5.95E-18	0.00E+00	1.75E-08	9.68E-04	5.89E-10	0.00E+00	1.24E-10	0.00E+00	2.20E-15	0.00E+00	3.46E-06	1.95E-03	7.62E-07	1.88E-03	macromolecule catabolism	P
GO:0009058	1572	5.26E-21	0.00E+00	5.09E-19	0.00E+00	5.27E-11	0.00E+00	8.68E-11	0.00E+00	2.21E-18	0.00E+00	1.61E-16	0.00E+00	1.29E-07	8.55E-04	1.57E-06	1.88E-03	biosynthesis	P
GO:0009059	927	3.62E-19	0.00E+00	9.91E-15	0.00E+00	7.04E-09	9.34E-04	3.69E-05	8.00E-03	3.52E-17	0.00E+00	3.89E-14	0.00E+00	2.19E-07	8.55E-04	1.13E-06	1.88E-03	macromolecule biosynthesis	P
GO:0009060	37	4.88E-02	1.00E+00	5.84E-02	1.00E+00	1.01E-02	4.60E-01	4.47E-02	1.00E+00	1.08E-01	1.00E+00	1.08E-01	1.00E+00	2.56E-01	1.00E+00	2.34E-01	1.00E+00	aerobic respiration	P
GO:0009063	61	2.12E-02	1.00E+00	6.18E-03	3.60E-01	9.06E-02	1.00E+00	4.51E-02	1.00E+00	3.24E-02	1.00E+00	4.03E-03	2.70E-01	1.12E-01	1.00E+00	3.90E-01	1.00E+00	amino acid catabolism	P
GO:0009064	50	1.47E-02	6.67E-01	3.80E-02	1.00E+00	3.14E-01	1.00E+00	3.50E-01	1.00E+00	7.69E-03	5.39E-01	1.31E-02	7.39E-01	1.54E-01	1.00E+00	3.58E-01	1.00E+00	glutamine family amino acid metabolism	P
GO:0009065	16	1.27E-01	1.00E+00	7.84E-02	1.00E+00	3.42E-01	1.00E+00	2.35E-01	1.00E+00	1.16E-01	1.00E+00	6.32E-02	1.00E+00	1.86E-01	1.00E+00	3.16E-01	1.00E+00	glutamine family amino acid catabolism	P
GO:0009066	26	4.12E-01	1.00E+00	3.60E-01	1.00E+00	6.84E-01	1.00E+00	2.18E-01	1.00E+00	1.99E-01	1.00E+00	3.60E-01	1.00E+00	8.65E-01	1.00E+00	8.80E-01	1.00E+00	aspartate family amino acid metabolism	P
GO:0009067	14	3.93E-01	1.00E+00	3.37E-01	1.00E+00	5.65E-01	1.00E+00	3.29E-01	1.00E+00	2.20E-01	1.00E+00	3.74E-01	1.00E+00	9.74E-01	1.00E+00	7.04E-01	1.00E+00	aspartate family amino acid biosynthesis	P
GO:0009069	26	5.51E-02	1.00E+00	3.91E-02	1.00E+00	1.04E-01	1.00E+00	7.44E-02	1.00E+00	6.51E-02	1.00E+00	1.96E-02	1.00E+00	2.37E-01	1.00E+00	7.08E-01	1.00E+00	serine family amino acid metabolism	P
GO:0009070	10	2.17E-01	1.00E+00	1.88E-01	1.00E+00	8.53E-02	1.00E+00	4.38E-01	1.00E+00	2.57E-01	1.00E+00	1.11E-01	1.00E+00	9.66E-01	1.00E+00	6.68E-01	1.00E+00	serine family amino acid biosynthesis	P
GO:0009072	71	8.49E-01	1.00E+00	3.95E-01	1.00E+00	5.83E-01	1.00E+00	2.75E-01	1.00E+00	8.85E-01	1.00E+00	5.65E-01	1.00E+00	6.20E-01	1.00E+00	1.75E-01	1.00E+00	aromatic amino acid family metabolism	P
GO:0009073	43	7.62E-01	1.00E+00	5.14E-01	1.00E+00	5.96E-01	1.00E+00	1.98E-01	1.00E+00	7.81E-01	1.00E+00	6.75E-01	1.00E+00	5.70E-01	1.00E+00	3.15E-01	1.00E+00	aromatic amino acid family biosynthesis	P
GO:0009074	14	2.94E-01	1.00E+00	3.47E-01	1.00E+00	2.21E-01	1.00E+00	9.26E-01	1.00E+00	4.68E-01	1.00E+00	2.28E-01	1.00E+00	1.90E-01	1.00E+00	3.98E-01	1.00E+00	aromatic amino acid family catabolism	P
GO:0009075	12	6.77E-01	1.00E+00	9.65E-01	1.00E+00	3.41E-01	1.00E+00	8.26E-01	1.00E+00	6.47E-01	1.00E+00	9.35E-01	1.00E+00	9.54E-01	1.00E+00	9.51E-01	1.00E+00	histidine family amino acid metabolism	P
GO:0009081	13	1.10E-02	6.67E-01	1.13E-02	6.77E-01	5.26E-02	1.00E+00	1.33E-03	1.15E-01	1.04E-02	5.39E-01	6.64E-02	1.00E+00	4.06E-01	1.00E+00	4.67E-01	1.00E+00	branched chain family amino acid metabolis	P
GO:0009084	19	6.36E-02	1.00E+00	8.16E-03	3.60E-01	2.03E-01	1.00E+00	4.46E-02	1.00E+00	7.57E-02	1.00E+00	1.29E-02	7.39E-01	1.07E-01	1.00E+00	5.07E-02	1.00E+00	glutamine family amino acid biosynthesis	P
GO:0009100	153	1.11E-01	1.00E+00	2.68E-03	1.77E-01	5.60E-01	1.00E+00	3.21E-01	1.00E+00	2.65E-02	1.00E+00	7.90E-04	5.49E-02	7.48E-01	1.00E+00	3.07E-02	1.00E+00	glycoprotein metabolism	P
GO:0009101	127	2.68E-01	1.00E+00	7.24E-03	3.60E-01	6.32E-01	1.00E+00	4.14E-01	1.00E+00	1.25E-01	1.00E+00	1.61E-03	1.61E-01	5.83E-01	1.00E+00	5.79E-02	1.00E+00	glycoprotein biosynthesis	P
GO:0009108	88	2.63E-04	3.37E-02	1.52E-02	1.00E+00	3.61E-03	3.27E-01	3.41E-03	2.02E-01	5.81E-04	4.00E-02	9.07E-02	1.00E+00	9.26E-02	1.00E+00	1.08E-01	1.00E+00	coenzyme biosynthesis	P
GO:0009109	27	5.05E-02	1.00E+00	1.26E-01	1.00E+00	7.69E-03	4.60E-01	5.34E-02	1.00E+00	1.01E-01	1.00E+00	2.00E-01	1.00E+00	4.68E-01	1.00E+00	3.36E-01	1.00E+00	coenzyme catabolism	P
GO:0009110	26	1.28E-01	1.00E+00	2.83E-01	1.00E+00	6.40E-02	1.00E+00	2.65E-01	1.00E+00	2.32E-01	1.00E+00	3.25E-01	1.00E+00	4.05E-01	1.00E+00	3.34E-01	1.00E+00	vitamin biosynthesis	P
GO:0009112	19	4.04E-03	3.28E-01	2.79E-02	1.00E+00	3.17E-01	1.00E+00	1.33E-01	1.00E+00	5.43E-03	4.18E-01	2.06E-02	1.00E+00	1.21E-02	6.30E-01	1.09E-01	1.00E+00	nucleobase metabolism	P
GO:0009116	32	5.80E-02	1.00E+00	1.42E-02	7.47E-01	7.62E-01	1.00E+00	1.30E-02	8.18E-01	4.72E-02	1.00E+00	9.55E-02	1.00E+00	4.14E-02	1.00E+00	7.93E-03	4.81E-01	nucleoside metabolism	P

GO:0009117	205	1.42E-03	2.02E-01	2.06E-04	2.80E-02	7.98E-02	1.00E+00	3.62E-04	4.20E-02	1.50E-03	1.76E-01	8.69E-04	5.49E-02	2.72E-02	1.00E+00	5.35E-02	1.00E+00	nucleotide metabolism	P
GO:0009119	13	8.00E-02	1.00E+00	8.05E-02	1.00E+00	7.50E-01	1.00E+00	4.59E-02	1.00E+00	1.15E-01	1.00E+00	1.62E-01	1.00E+00	2.83E-02	1.00E+00	1.81E-01	1.00E+00	ribonucleoside metabolism	P
GO:0009123	24	4.82E-02	1.00E+00	1.55E-02	1.00E+00	5.41E-01	1.00E+00	9.11E-02	1.00E+00	5.71E-02	1.00E+00	9.10E-03	7.39E-01	2.22E-02	1.00E+00	4.78E-01	1.00E+00	nucleoside monophosphate metabolism	P
GO:0009124	24	4.82E-02	1.00E+00	1.55E-02	1.00E+00	5.41E-01	1.00E+00	9.11E-02	1.00E+00	5.71E-02	1.00E+00	9.10E-03	7.39E-01	2.22E-02	1.00E+00	4.78E-01	1.00E+00	nucleoside monophosphate biosynthesis	P
GO:0009126	18	1.16E-01	1.00E+00	6.00E-02	1.00E+00	4.72E-01	1.00E+00	9.88E-02	1.00E+00	1.19E-01	1.00E+00	3.47E-02	1.00E+00	1.14E-01	1.00E+00	9.27E-01	1.00E+00	purine nucleoside monophosphate metabol	P
GO:0009127	18	1.16E-01	1.00E+00	6.00E-02	1.00E+00	4.72E-01	1.00E+00	9.88E-02	1.00E+00	1.19E-01	1.00E+00	3.47E-02	1.00E+00	1.14E-01	1.00E+00	9.27E-01	1.00E+00	purine nucleoside monophosphate biosynth	P
GO:0009132	12	3.74E-01	1.00E+00	3.96E-01	1.00E+00	4.30E-01	1.00E+00	5.37E-01	1.00E+00	4.58E-01	1.00E+00	4.66E-01	1.00E+00	2.29E-01	1.00E+00	1.53E-01	1.00E+00	nucleoside diphosphate metabolism	P
GO:0009141	63	6.90E-03	5.17E-01	4.61E-02	1.00E+00	4.22E-02	1.00E+00	4.84E-02	1.00E+00	4.02E-03	2.85E-01	1.05E-01	1.00E+00	2.66E-01	1.00E+00	5.20E-02	1.00E+00	nucleoside triphosphate metabolism	P
GO:0009142	43	1.06E-03	9.60E-02	1.62E-01	1.00E+00	8.07E-03	4.60E-01	7.19E-02	1.00E+00	1.59E-03	1.76E-01	3.27E-01	1.00E+00	6.37E-02	1.00E+00	1.54E-01	1.00E+00	nucleoside triphosphate biosynthesis	P
GO:0009143	10	6.36E-01	1.00E+00	1.44E-01	1.00E+00	3.15E-01	1.00E+00	3.75E-02	1.00E+00	6.10E-01	1.00E+00	2.22E-01	1.00E+00	9.99E-01	1.00E+00	4.35E-01	1.00E+00	nucleoside triphosphate catabolism	P
GO:0009144	53	2.13E-03	2.02E-01	4.31E-02	1.00E+00	2.04E-02	1.00E+00	1.51E-01	1.00E+00	1.15E-03	7.80E-02	6.24E-02	1.00E+00	2.50E-01	1.00E+00	6.07E-02	1.00E+00	purine nucleoside triphosphate metabolism	P
GO:0009145	39	8.40E-04	8.30E-02	2.38E-01	1.00E+00	2.63E-03	2.48E-01	1.70E-01	1.00E+00	1.69E-03	1.76E-01	3.77E-01	1.00E+00	8.08E-02	1.00E+00	2.30E-01	1.00E+00	purine nucleoside triphosphate biosynthesis	P
GO:0009147	17	6.87E-02	1.00E+00	1.38E-01	1.00E+00	1.63E-01	1.00E+00	5.52E-02	1.00E+00	5.80E-02	1.00E+00	3.02E-01	1.00E+00	1.98E-01	1.00E+00	1.13E-01	1.00E+00	pyrimidine nucleoside triphosphate metabol	P
GO:0009150	72	1.95E-03	2.02E-01	2.50E-02	1.00E+00	4.22E-02	1.00E+00	6.49E-02	1.00E+00	1.27E-03	7.80E-02	2.76E-02	1.00E+00	1.53E-01	1.00E+00	2.35E-01	1.00E+00	purine ribonucleotide metabolism	P
GO:0009152	59	1.32E-03	2.02E-01	1.10E-01	1.00E+00	2.56E-02	1.00E+00	1.10E-01	1.00E+00	2.08E-03	2.85E-01	1.52E-01	1.00E+00	4.66E-02	1.00E+00	3.34E-01	1.00E+00	purine ribonucleotide biosynthesis	P
GO:0009156	23	5.75E-02	1.00E+00	1.69E-02	1.00E+00	4.74E-01	1.00E+00	9.65E-02	1.00E+00	7.91E-02	1.00E+00	1.18E-02	7.39E-01	2.72E-02	1.00E+00	4.20E-01	1.00E+00	ribonucleoside monophosphate biosynthesi	P
GO:0009161	23	5.75E-02	1.00E+00	1.69E-02	1.00E+00	4.74E-01	1.00E+00	9.65E-02	1.00E+00	7.91E-02	1.00E+00	1.18E-02	7.39E-01	2.72E-02	1.00E+00	4.20E-01	1.00E+00	ribonucleoside monophosphate metabolism	P
GO:0009165	133	1.46E-03	2.02E-01	1.05E-02	5.18E-01	1.52E-01	1.00E+00	1.64E-02	8.18E-01	1.18E-03	7.80E-02	1.00E-02	7.39E-01	1.39E-02	6.47E-01	4.51E-01	1.00E+00	nucleotide biosynthesis	P
GO:0009166	24	6.16E-01	1.00E+00	4.06E-02	1.00E+00	4.38E-01	1.00E+00	5.93E-02	1.00E+00	6.22E-01	1.00E+00	3.25E-02	1.00E+00	5.36E-01	1.00E+00	2.49E-01	1.00E+00	nucleotide catabolism	P
GO:0009167	18	1.16E-01	1.00E+00	6.00E-02	1.00E+00	4.72E-01	1.00E+00	9.88E-02	1.00E+00	1.19E-01	1.00E+00	3.47E-02	1.00E+00	1.14E-01	1.00E+00	9.27E-01	1.00E+00	purine ribonucleoside monophosphate meta	P
GO:0009168	18	1.16E-01	1.00E+00	6.00E-02	1.00E+00	4.72E-01	1.00E+00	9.88E-02	1.00E+00	1.19E-01	1.00E+00	3.47E-02	1.00E+00	1.14E-01	1.00E+00	9.27E-01	1.00E+00	purine ribonucleoside monophosphate biosy	P
GO:0009187	45	9.43E-01	1.00E+00	4.21E-01	1.00E+00	8.82E-01	1.00E+00	1.99E-01	1.00E+00	8.50E-01	1.00E+00	4.57E-01	1.00E+00	9.66E-01	1.00E+00	7.46E-01	1.00E+00	cyclic nucleotide metabolism	P
GO:0009190	33	8.52E-01	1.00E+00	5.72E-01	1.00E+00	9.13E-01	1.00E+00	5.48E-01	1.00E+00	7.50E-01	1.00E+00	5.12E-01	1.00E+00	6.29E-01	1.00E+00	7.47E-01	1.00E+00	cyclic nucleotide biosynthesis	P
GO:0009199	52	2.21E-03	2.02E-01	3.70E-02	1.00E+00	2.61E-02	1.00E+00	7.98E-02	1.00E+00	1.13E-03	7.80E-02	6.98E-02	1.00E+00	2.24E-01	1.00E+00	5.95E-02	1.00E+00	ribonucleoside triphosphate metabolism	P
GO:0009201	40	7.39E-04	6.71E-02	1.87E-01	1.00E+00	4.67E-03	3.27E-01	1.13E-01	1.00E+00	1.22E-03	7.80E-02	3.42E-01	1.00E+00	7.61E-02	1.00E+00	1.81E-01	1.00E+00	ribonucleoside triphosphate biosynthesis	P
GO:0009205	51	2.47E-03	2.02E-01	5.05E-02	1.00E+00	1.86E-02	1.00E+00	1.20E-01	1.00E+00	1.53E-03	1.76E-01	8.03E-02	1.00E+00	2.33E-01	1.00E+00	7.93E-02	1.00E+00	purine ribonucleoside triphosphate metabol	P
GO:0009206	39	8.40E-04	8.30E-02	2.38E-01	1.00E+00	2.63E-03	2.48E-01	1.70E-01	1.00E+00	1.69E-03	1.76E-01	3.77E-01	1.00E+00	8.08E-02	1.00E+00	2.30E-01	1.00E+00	purine ribonucleoside triphosphate biosynth	P
GO:0009208	12	2.15E-02	1.00E+00	1.03E-01	1.00E+00	5.38E-02	1.00E+00	8.83E-02	1.00E+00	2.46E-02	1.00E+00	1.88E-01	1.00E+00	1.70E-01	1.00E+00	1.59E-01	1.00E+00	pyrimidine ribonucleoside triphosphate meta	P
GO:0009209	12	2.15E-02	1.00E+00	1.03E-01	1.00E+00	5.38E-02	1.00E+00	8.83E-02	1.00E+00	2.46E-02	1.00E+00	1.88E-01	1.00E+00	1.70E-01	1.00E+00	1.59E-01	1.00E+00	pyrimidine ribonucleoside triphosphate bios	P
GO:0009218	17	1.85E-02	1.00E+00	3.35E-02	1.00E+00	1.78E-01	1.00E+00	1.00E-01	1.00E+00	1.80E-02	1.00E+00	7.12E-02	1.00E+00	9.80E-02	1.00E+00	6.71E-02	1.00E+00	pyrimidine ribonucleotide metabolism	P
GO:0009220	16	2.34E-02	1.00E+00	4.37E-02	1.00E+00	1.51E-01	1.00E+00	6.87E-02	1.00E+00	2.16E-02	1.00E+00	1.00E-01	1.00E+00	1.56E-01	1.00E+00	8.43E-02	1.00E+00	pyrimidine ribonucleotide biosynthesis	P
GO:0009225	15	1.09E-01	1.00E+00	2.19E-02	1.00E+00	3.68E-01	1.00E+00	8.74E-02	1.00E+00	6.84E-02	1.00E+00	4.78E-02	1.00E+00	3.31E-01	1.00E+00	9.15E-02	1.00E+00	nucleotide-sugar metabolism	P
GO:0009237	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	siderophore metabolism	P
GO:0009238	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	enterobactin metabolism	P
GO:0009239	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	enterobactin biosynthesis	P
GO:0009247	14	3.36E-01	1.00E+00	1.20E-01	1.00E+00	7.61E-01	1.00E+00	1.28E-01	1.00E+00	2.94E-01	1.00E+00	1.94E-01	1.00E+00	1.01E-01	1.00E+00	3.09E-01	1.00E+00	glycolipid biosynthesis	P
GO:0009250	30	8.40E-01	1.00E+00	5.21E-01	1.00E+00	9.62E-01	1.00E+00	7.69E-01	1.00E+00	6.35E-01	1.00E+00	4.31E-01	1.00E+00	8.84E-01	1.00E+00	3.48E-01	1.00E+00	glucan biosynthesis	P
GO:0009259	81	4.65E-04	3.37E-02	3.53E-03	1.97E-01	5.25E-02	1.00E+00	3.14E-02	1.00E+00	3.25E-04	1.98E-02	4.93E-03	2.70E-01	5.82E-02	1.00E+00	8.41E-02	1.00E+00	ribonucleotide metabolism	P
GO:0009260	66	4.21E-04	3.37E-02	2.65E-02	1.00E+00	3.71E-02	1.00E+00	4.11E-02	1.00E+00	6.10E-04	4.00E-02	5.18E-02	1.00E+00	2.37E-02	1.00E+00	1.49E-01	1.00E+00	ribonucleotide biosynthesis	P
GO:0009261	10	2.82E-01	1.00E+00	1.02E-01	1.00E+00	2.05E-01	1.00E+00	2.08E-01	1.00E+00	2.87E-01	1.00E+00	9.15E-02	1.00E+00	6.61E-01	1.00E+00	3.58E-01	1.00E+00	ribonucleotide catabolism	P
GO:0009262	15	4.12E-01	1.00E+00	6.83E-02	1.00E+00	6.57E-01	1.00E+00	6.42E-02	1.00E+00	3.28E-01	1.00E+00	9.26E-02	1.00E+00	5.48E-01	1.00E+00	8.80E-02	1.00E+00	deoxyribonucleotide metabolism	P
GO:0009266	250	1.87E-02	1.00E+00	1.80E-01	1.00E+00	2.07E-03	2.48E-01	1.37E-01	1.00E+00	1.21E-01	1.00E+00	1.71E-01	1.00E+00	6.04E-02	1.00E+00	7.56E-01	1.00E+00	response to temperature stimulus	P
GO:0009267	10	3.97E-01	1.00E+00	3.58E-01	1.00E+00	7.10E-01	1.00E+00	7.08E-01	1.00E+00	3.29E-01	1.00E+00	2.88E-01	1.00E+00	2.29E-01	1.00E+00	3.83E-01	1.00E+00	cellular response to starvation	P
GO:0009288	43	4.39E-01	1.00E+00	2.45E-01	1.00E+00	2.86E-01	1.00E+00	2.82E-01	1.00E+00	4.40E-01	1.00E+00	5.17E-01	1.00E+00	6.54E-01	1.00E+00	3.24E-02	1.00E+00	flagellum (sensu Bacteria)	C
GO:0009296	14	8.30E-02	1.00E+00	4.27E-02	1.00E+00	9.54E-02	1.00E+00	1.76E-01	1.00E+00	1.49E-01	1.00E+00	2.40E-02	1.00E+00	1.57E-01	1.00E+00	8.92E-02	1.00E+00	flagellum biogenesis	P
GO:0009303	14	1.84E-03	2.02E-01	1.69E-02	1.00E+00	6.14E-02	1.00E+00	4.20E-02	1.00E+00	3.25E-03	2.85E-01	5.82E-02	1.00E+00	2.09E-01	1.00E+00	7.92E-02	1.00E+00	rRNA transcription	P
GO:0009306	68	2.74E-02	1.00E+00	5.30E-02	1.00E+00	7.73E-02	1.00E+00	1.24E-01	1.00E+00	2.43E-02	1.00E+00	8.68E-02	1.00E+00	5.72E-01	1.00E+00	2.74E-01	1.00E+00	protein secretion	P
GO:0009308	556	9.95E-03	6.67E-01	5.52E-04	6.90E-02	7.75E-03	4.60E-01	1.32E-03	1.15E-01	1.33E-02	1.00E+00	1.93E-03	1.61E-01	4.94E-01	1.00E+00	1.48E-01	1.00E+00	amine metabolism	P
GO:0009309	122	4.51E-01	1.00E+00	8.37E-02	1.00E+00	4.64E-01	1.00E+00	2.94E-02	1.00E+00	4.75E-01	1.00E+00	1.40E-01	1.00E+00	4.08E-01	1.00E+00	1.97E-01	1.00E+00	amine biosynthesis	P
GO:0009310	70	1.39E-02	6.67E-01	1.01E-02	5.18E-01	9.61E-02	1.00E+00	5.33E-02	1.00E+00	2.02E-02	1.00E+00	5.24E-03	2.70E-01	7.59E-02	1.00E+00	6.01E-01	1.00E+00	amine catabolism	P
GO:0009311	20	7.91E-01	1.00E+00	4.33E-01	1.00E+00	9.33E-01	1.00E+00	8.48E-01	1.00E+00	7.32E-01	1.00E+00	2.89E-01	1.00E+00	3.17E-01	1.00E+00	4.15E-01	1.00E+00	oligosaccharide metabolism	P
GO:0009314	137	3.71E-03	3.28E-01	6.19E-03	3.60E-01	1.13E-03	9.80E-02	7.91E-02	1.00E+00	6.58E-03	5.39E-01	1.82E-03	1.61E-01	4.97E-01	1.00E+00	2.47E-01	1.00E+00	response to radiation	P
GO:0009331	13	9.15E-01	1.00E+00	7.19E-02	1.00E+00	7.59E-01	1.00E+00	6.90E-02	1.00E+00	9.64E-01	1.00E+00	4.02E-01	1.00E+00	6.50E-01	1.00E+00	8.45E-02	1.00E+00	glycerol-3-phosphate dehydrogenase comp	C
GO:0009395	15	7.07E-01	1.00E+00	8.79E-01	1.00E+00	9.13E-01	1.00E+00	3.95E-01	1.00E+00	6.25E-01	1.00E+00	9.39E-01	1.00E+00	4.27E-01	1.00E+00	9.34E-01	1.00E+00	phospholipid catabolism	P
GO:0009396	12	1.54E-01	1.00E+00	2.86E-02	1.00E+00	4.32E-01	1.00E+00	4.91E-02	1.00E+00	5.46E-02	1.00E+00	3.94E-02	1.00E+00	9.92E-01	1.00E+00	5.39E-01	1.00E+00	folic acid and derivative biosynthesis	P
GO:0009405	35	6.20E-03	5.17E-01	8.28E-02	1.00E+00	6.04E-02	1.00E+00	7.01E-01	1.00E+00	1.19E-02	5.39E-01	1.32E-01	1.00E+00	2.33E-01	1.00E+00	2.05E-02	1.00E+00	pathogenesis	P
GO:0009408	15	1.69E-02	6.67E-01	5.96E-01	1.00E+00	1.50E-02	6.93E-01	3.27E-01	1.00E+00	6.92E-02	1.00E+00	4.82E-01	1.00E+00	2.92E-02	1.00E+00	9.98E-01	1.00E+00	response to heat	P
GO:0009409	227	9.88E-02	1.00E+00	2.85E-01	1.00E+00	1.07E-02	5.32E-01	1.75E-01	1.00E+00	3.04E-01	1.00E+00	3.08E-01	1.00E+00	2.00E-01	1.00E+00	7.46E-01	1.00E+00	response to cold	P
GO:0009410	34	9.83E-01	1.00E+00	9.52E-01	1.00E+00	8.85E-01	1.00E+00	9.57E-01	1.00E+00	9.77E-01	1.00E+00	9.20E-01	1.00E+00	9.12E-01	1.00E+00	9.72E-01	1.00E+00	response to xenobiotic stimulus	P
GO:0009411	48	6.54E-03	5.17E-01	4.93E-03	3.60E-01	3.29E-02	1.00E+00	2.13E-02	1.00E+00	4.37E-03	3.60E-01	3.94E-03	2.70E-01	2.11E-01	1.00E+00	1.37E-01	1.00E+00	response to UV	P
GO:0009416	108	4.06E-03	3.28E-01	1.52E-02	1.00E+00	5.38E-03	4.19E-01	6.80E-02	1.00E+00	3.46E-03	2.85E-01	8.56E-03	7.39E-01	4.55E-01	1.00E+00	1.80E-01	1.00E+00	response to light stimulus	P
GO:0009434	17	6.63E-01	1.00E+00	3.28E-01	1.00E+00	3.37E-01	1.00E+00	2.64E-01	1.00E+00	6.61E-01	1.00E+00	3.45E-01	1.00E+00	8.66E-01	1.00E+00	4.90E-01	1.00E+00	flagellum (sensu Eukaryota)	C
GO:0009451	36	1.16E-02	6.67E-01	1.74E-01	1.00E+00	1.11E-01	1.00E+00	9.28E-01	1.00E+00	8.81E-03	5.39E-01	1.11E-01	1.00E+00	2.12E-01	1.00E+00	1.09E-01	1.00E+00	RNA modification	P
GO:0009566	78	3.67E-01	1.00E+00	8.19E-01	1.00E+00	4.70E-01	1.00E+00	6.79E-01	1.00E+00	4.08E-01	1.00E+00	8.82E-01	1.00E+00	4.61E-01	1.00E+00	4.32E-01	1.00E+00	fertilization	P
GO:0009581	63	3.46E-01	1.00E+00	4.27E-01	1.00E+00	2.11E-01	1.00E+00	4.11E-01	1.00E+00	2.62E-01	1.00E+00	2.80E-01	1.00E+00	9.84E-01	1.00E+00	8.70E-01	1.00E+00	detection of external stimulus	P
GO:0009582	56	4.24E-01	1.00E+00	2.53E-01	1.00E+00	1.46E-01	1.00E+00	2.47E-01	1.00E+00	3.53E-01	1.00E+00	1.97E-01	1.00E+00	9.99E-01	1.00E+00	7.92E-01	1.00E+00	detection of abiotic stimulus	P
GO:0009583	35	1.99E-01	1.00E+00	1.20E-01	1.00E+00	6.92E-02	1.00E+00	2.49E-01	1.00E+00	1.90E-01	1.00E+00	7.64E-02	1.00E+00	9.95E-01	1.00E+00	4.85E-01	1.00E+00	detection of light stimulus	P
GO:0009593	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	detection of chemical stimulus	P
GO:0009595	15	7.22E-01	1.00E+00	8.08E-01	1.00E+00	9.08E-01	1.00E+00	5.64E-01	1.00E+00	6.12E-01	1.00E+00	7.66E-01	1.00E+00	4.98E-01	1.00E+00	8.29E-01	1.00E+00	detection of biotic stimulus	P
GO:0009605	852	8.51E-01	1.00E+00	1.53E-01	1.00E+00	4.89E-01	1.00E+00	2.76E-01	1.00E+00	8.07E-01	1.00E+00	1.03E-01	1.00E+00	9.51E-01	1.00E+00	4.36E-01	1.00E+00	response to external stimulus	P
GO:0009607	333	1.33E-01	1.00E+00	2.16E-01	1.00E+00	4.55E-01	1.00E+00	7.57E-01	1.00E+00	7.20E-02	1.00E+00	8.35E-02	1.00E+00	4.24E-01	1.00E+00	3.91E-01	1.00E+00	response to biotic stimulus	P
GO:0009611	567	9.85E-01	1.00E+00	5.32E-01	1.00E+00	7.14E-01	1.00E+00	3.62E-01	1.00E+00	9.89E-01	1.00E+00	5.23E-01	1.00E+00	9.37E-01	1.00E+00	6.54E-01	1.00E+00	response to wounding	P
GO:0009612	31	1.65E-01	1.00E+00	1.40E-01	1.00E+00	1.77E-01	1.00E+00	2.74E-01	1.00E+00	1.64E-01	1.00E+00	1.31E-01	1.00E+00	7.90E-01	1.00E+00	4.44E-01	1.00E+00	response to mechanical stimulus	P
GO:0009615	117	5.17E-02	1.00E+00	4.31E-01	1.00E+00	7.65E-02	1.00E+00	7.62E-01	1.00E+00	8.47E-02	1.00E+00	4.46E-01	1.00E+00	1.32E-01	1.00E+00	1.79E-01	1.00E+00	response to virus	P
GO:0009617	126	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.85E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	response to bacterium	P

GO:0009620	24	1.00E+00	1.00E+00	9.74E-01	1.00E+00	9.48E-01	1.00E+00	8.78E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.16E-01	1.00E+00	response to fungus	P
GO:0009628	445	1.15E-04	2.50E-02	2.25E-03	1.77E-01	7.22E-06	2.66E-03	1.80E-02	1.00E+00	1.77E-03	1.76E-01	1.19E-03	6.40E-02	1.10E-01	1.00E+00	3.36E-01	1.00E+00	response to abiotic stimulus	P
GO:0009636	27	1.92E-01	1.00E+00	9.28E-02	1.00E+00	2.39E-01	1.00E+00	7.85E-02	1.00E+00	1.58E-01	1.00E+00	7.34E-02	1.00E+00	6.87E-01	1.00E+00	5.13E-01	1.00E+00	response to toxin	P
GO:0009650	10	1.82E-01	1.00E+00	6.87E-02	1.00E+00	1.65E-01	1.00E+00	2.85E-01	1.00E+00	2.46E-01	1.00E+00	3.69E-02	1.00E+00	1.68E-01	1.00E+00	2.75E-01	1.00E+00	UV protection	P
GO:0009653	1381	9.25E-01	1.00E+00	4.64E-01	1.00E+00	5.79E-01	1.00E+00	2.38E-01	1.00E+00	9.41E-01	1.00E+00	5.59E-01	1.00E+00	6.95E-01	1.00E+00	3.00E-01	1.00E+00	morphogenesis	P
GO:0009698	43	7.62E-01	1.00E+00	5.14E-01	1.00E+00	5.96E-01	1.00E+00	1.98E-01	1.00E+00	7.81E-01	1.00E+00	6.75E-01	1.00E+00	5.70E-01	1.00E+00	3.15E-01	1.00E+00	phenylpropanoid metabolism	P
GO:0009712	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	catechol metabolism	P
GO:0009719	499	5.28E-09	8.06E-04	2.69E-07	8.39E-03	8.36E-05	1.20E-02	4.67E-06	8.00E-03	4.06E-08	9.64E-04	1.15E-06	2.97E-03	2.86E-03	1.95E-01	9.89E-02	1.00E+00	response to endogenous stimulus	P
GO:0009725	124	3.65E-01	1.00E+00	4.51E-01	1.00E+00	7.61E-01	1.00E+00	2.63E-01	1.00E+00	4.25E-01	1.00E+00	6.08E-01	1.00E+00	7.79E-02	1.00E+00	3.08E-01	1.00E+00	response to hormone stimulus	P
GO:0009743	27	7.96E-02	1.00E+00	2.46E-01	1.00E+00	1.27E-01	1.00E+00	3.92E-01	1.00E+00	5.36E-02	1.00E+00	1.90E-01	1.00E+00	4.34E-01	1.00E+00	7.36E-01	1.00E+00	response to carbohydrate stimulus	P
GO:0009746	20	3.22E-02	1.00E+00	1.68E-01	1.00E+00	7.21E-02	1.00E+00	3.77E-01	1.00E+00	2.18E-02	1.00E+00	1.28E-01	1.00E+00	2.00E-01	1.00E+00	6.94E-01	1.00E+00	response to hexose stimulus	P
GO:0009749	20	3.22E-02	1.00E+00	1.68E-01	1.00E+00	7.21E-02	1.00E+00	3.77E-01	1.00E+00	2.18E-02	1.00E+00	1.28E-01	1.00E+00	2.00E-01	1.00E+00	6.94E-01	1.00E+00	response to glucose stimulus	P
GO:0009755	37	1.46E-02	6.67E-01	1.60E-02	1.00E+00	6.01E-02	1.00E+00	4.68E-03	3.46E-01	3.45E-02	1.00E+00	4.36E-02	1.00E+00	4.45E-02	1.00E+00	2.02E-01	1.00E+00	hormone-mediated signaling	P
GO:0009790	454	6.56E-01	1.00E+00	9.88E-01	1.00E+00	7.11E-01	1.00E+00	9.94E-01	1.00E+00	5.43E-01	1.00E+00	9.63E-01	1.00E+00	7.20E-01	1.00E+00	8.53E-01	1.00E+00	embryonic development	P
GO:0009791	74	3.88E-01	1.00E+00	5.69E-01	1.00E+00	1.56E-01	1.00E+00	4.21E-01	1.00E+00	4.01E-01	1.00E+00	5.38E-01	1.00E+00	8.20E-01	1.00E+00	6.53E-01	1.00E+00	post-embryonic development	P
GO:0009792	247	1.02E-01	1.00E+00	6.55E-01	1.00E+00	3.68E-01	1.00E+00	7.98E-01	1.00E+00	9.68E-02	1.00E+00	6.10E-01	1.00E+00	1.03E-01	1.00E+00	3.97E-01	1.00E+00	embryonic development (sensu Metazoa)	P
GO:0009798	21	7.86E-01	1.00E+00	8.38E-01	1.00E+00	7.01E-01	1.00E+00	9.56E-01	1.00E+00	6.92E-01	1.00E+00	6.77E-01	1.00E+00	8.88E-01	1.00E+00	7.28E-01	1.00E+00	axis specification	P
GO:0009799	34	8.25E-01	1.00E+00	2.33E-01	1.00E+00	9.92E-01	1.00E+00	4.06E-01	1.00E+00	7.26E-01	1.00E+00	2.34E-01	1.00E+00	4.85E-01	1.00E+00	1.95E-01	1.00E+00	determination of symmetry	P
GO:0009855	34	8.25E-01	1.00E+00	2.33E-01	1.00E+00	9.92E-01	1.00E+00	4.06E-01	1.00E+00	7.26E-01	1.00E+00	2.34E-01	1.00E+00	4.85E-01	1.00E+00	1.95E-01	1.00E+00	determination of bilateral symmetry	P
GO:0009880	46	9.86E-01	1.00E+00	1.00E+00	1.00E+00	8.77E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	embryonic pattern specification	P
GO:0009881	15	5.09E-01	1.00E+00	4.69E-01	1.00E+00	3.36E-02	1.00E+00	3.53E-01	1.00E+00	5.67E-01	1.00E+00	2.88E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	photoreceptor activity	F
GO:0009887	715	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	8.26E-01	1.00E+00	5.11E-01	1.00E+00	organ morphogenesis	P
GO:0009888	450	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.36E-01	1.00E+00	tissue development	P
GO:0009889	237	5.53E-05	1.10E-02	4.86E-06	8.39E-03	1.28E-06	2.42E-03	4.95E-05	8.00E-03	3.79E-03	2.85E-01	3.47E-05	1.20E-02	9.03E-03	6.30E-01	1.23E-02	6.47E-01	regulation of biosynthesis	P
GO:0009890	54	7.26E-02	1.00E+00	9.96E-02	1.00E+00	1.17E-02	5.32E-01	3.66E-01	1.00E+00	2.90E-01	1.00E+00	1.06E-01	1.00E+00	8.34E-02	1.00E+00	7.04E-02	1.00E+00	negative regulation of biosynthesis	P
GO:0009891	93	7.83E-02	1.00E+00	3.74E-02	1.00E+00	9.01E-03	4.60E-01	1.21E-02	8.18E-01	3.25E-01	1.00E+00	9.07E-02	1.00E+00	6.06E-02	1.00E+00	1.15E-01	1.00E+00	positive regulation of biosynthesis	P
GO:0009892	513	4.20E-09	8.06E-04	2.35E-07	8.39E-03	1.91E-06	2.42E-03	3.38E-04	4.20E-02	3.73E-08	9.64E-04	1.19E-06	2.97E-03	3.45E-02	1.00E+00	2.14E-03	1.40E-01	negative regulation of metabolism	P
GO:0009893	567	2.08E-02	1.00E+00	1.26E-03	9.10E-02	6.79E-03	4.60E-01	5.96E-03	3.46E-01	6.84E-02	1.00E+00	2.11E-03	1.61E-01	1.33E-01	1.00E+00	1.32E-01	1.00E+00	positive regulation of metabolism	P
GO:0009894	40	7.95E-02	1.00E+00	2.86E-01	1.00E+00	6.24E-02	1.00E+00	4.88E-01	1.00E+00	1.98E-01	1.00E+00	1.65E-01	1.00E+00	1.39E-01	1.00E+00	7.13E-01	1.00E+00	regulation of catabolism	P
GO:0009895	12	8.88E-01	1.00E+00	9.97E-01	1.00E+00	5.57E-01	1.00E+00	8.17E-01	1.00E+00	9.69E-01	1.00E+00	9.86E-01	1.00E+00	8.33E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of catabolism	P
GO:0009896	10	6.24E-01	1.00E+00	5.32E-01	1.00E+00	3.24E-01	1.00E+00	7.48E-01	1.00E+00	9.56E-01	1.00E+00	3.89E-01	1.00E+00	1.63E-01	1.00E+00	8.07E-01	1.00E+00	positive regulation of catabolism	P
GO:0009897	97	6.95E-01	1.00E+00	6.41E-01	1.00E+00	8.41E-01	1.00E+00	8.92E-01	1.00E+00	4.90E-01	1.00E+00	4.59E-01	1.00E+00	7.74E-01	1.00E+00	7.86E-01	1.00E+00	external side of plasma membrane	C
GO:0009898	11	7.97E-01	1.00E+00	5.15E-01	1.00E+00	7.58E-01	1.00E+00	6.88E-01	1.00E+00	9.70E-01	1.00E+00	5.74E-01	1.00E+00	1.03E-01	1.00E+00	2.64E-01	1.00E+00	internal side of plasma membrane	C
GO:0009913	73	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	epidermal cell differentiation	P
GO:0009925	25	5.08E-01	1.00E+00	5.08E-01	1.00E+00	6.51E-01	1.00E+00	9.79E-01	1.00E+00	6.80E-01	1.00E+00	4.60E-01	1.00E+00	4.53E-02	1.00E+00	1.33E-01	1.00E+00	basal plasma membrane	C
GO:0009948	12	9.84E-01	1.00E+00	9.03E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	8.11E-01	1.00E+00	8.25E-01	1.00E+00	1.00E+00	1.00E+00	6.40E-01	1.00E+00	anterior/posterior axis specification	P
GO:0009952	116	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	anterior/posterior pattern formation	P
GO:0009953	45	7.34E-01	1.00E+00	9.88E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	6.69E-01	1.00E+00	8.63E-01	1.00E+00	7.43E-01	1.00E+00	9.97E-01	1.00E+00	dorsal/ventral pattern formation	P
GO:0009954	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	proximal/distal pattern formation	P
GO:0009966	543	6.29E-03	5.17E-01	4.54E-04	6.90E-02	3.23E-04	3.60E-02	2.66E-03	1.47E-01	1.80E-02	1.00E+00	6.01E-04	5.49E-02	6.73E-01	1.00E+00	4.68E-01	1.00E+00	regulation of signal transduction	P
GO:0009967	190	4.47E-02	1.00E+00	1.85E-02	1.00E+00	4.98E-02	1.00E+00	7.21E-02	1.00E+00	8.51E-02	1.00E+00	4.27E-02	1.00E+00	9.72E-02	1.00E+00	6.08E-02	1.00E+00	positive regulation of signal transduction	P
GO:0009968	132	8.68E-02	1.00E+00	1.55E-01	1.00E+00	7.42E-02	1.00E+00	8.45E-02	1.00E+00	1.09E-01	1.00E+00	2.23E-01	1.00E+00	5.51E-01	1.00E+00	6.17E-01	1.00E+00	negative regulation of signal transduction	P
GO:0009975	23	9.35E-01	1.00E+00	2.35E-01	1.00E+00	6.08E-01	1.00E+00	1.75E-01	1.00E+00	9.25E-01	1.00E+00	2.12E-01	1.00E+00	9.05E-01	1.00E+00	7.73E-01	1.00E+00	cyclase activity	F
GO:0009982	37	6.43E-01	1.00E+00	4.61E-01	1.00E+00	7.80E-01	1.00E+00	2.64E-01	1.00E+00	5.27E-01	1.00E+00	5.67E-01	1.00E+00	6.68E-01	1.00E+00	3.50E-01	1.00E+00	pseudouridine synthase activity	F
GO:0009986	233	6.17E-01	1.00E+00	3.84E-01	1.00E+00	6.14E-01	1.00E+00	1.04E-01	1.00E+00	4.71E-01	1.00E+00	4.93E-01	1.00E+00	7.98E-01	1.00E+00	7.44E-01	1.00E+00	cell surface	C
GO:0009987	13550	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.41E-34	0.00E+00	5.76E-42	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.05E-19	0.00E+00	1.16E-26	0.00E+00	cellular process	P
GO:0009991	87	6.82E-02	1.00E+00	1.85E-02	1.00E+00	2.55E-01	1.00E+00	4.74E-01	1.00E+00	6.16E-02	1.00E+00	9.91E-03	7.39E-01	1.81E-01	1.00E+00	5.04E-02	1.00E+00	response to extracellular stimulus	P
GO:0009994	14	2.00E-01	1.00E+00	8.62E-01	1.00E+00	3.93E-01	1.00E+00	2.96E-01	1.00E+00	1.60E-01	1.00E+00	8.16E-01	1.00E+00	9.50E-02	1.00E+00	8.70E-01	1.00E+00	oocyte differentiation	P
GO:0010001	41	2.71E-01	1.00E+00	9.44E-01	1.00E+00	8.50E-02	1.00E+00	8.35E-01	1.00E+00	4.11E-01	1.00E+00	9.22E-01	1.00E+00	2.64E-01	1.00E+00	9.53E-01	1.00E+00	glial cell differentiation	P
GO:0010008	110	8.40E-05	1.24E-02	1.60E-04	1.50E-02	7.82E-02	1.00E+00	6.61E-03	4.53E-01	1.27E-04	1.70E-02	1.14E-03	5.49E-02	2.42E-03	1.95E-01	9.90E-03	4.81E-01	endosome membrane	C
GO:0010033	83	9.79E-02	1.00E+00	1.57E-01	1.00E+00	1.07E-01	1.00E+00	2.54E-01	1.00E+00	9.59E-02	1.00E+00	1.11E-01	1.00E+00	4.14E-01	1.00E+00	6.93E-01	1.00E+00	response to organic substance	P
GO:0010035	57	8.10E-01	1.00E+00	2.86E-01	1.00E+00	5.51E-01	1.00E+00	6.40E-01	1.00E+00	7.58E-01	1.00E+00	1.34E-01	1.00E+00	9.87E-01	1.00E+00	6.45E-01	1.00E+00	response to inorganic substance	P
GO:0010038	50	8.46E-01	1.00E+00	3.72E-01	1.00E+00	5.81E-01	1.00E+00	6.15E-01	1.00E+00	7.88E-01	1.00E+00	2.54E-01	1.00E+00	9.89E-01	1.00E+00	5.20E-01	1.00E+00	response to metal ion	P
GO:0010092	13	7.62E-01	1.00E+00	9.91E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	5.49E-01	1.00E+00	9.50E-01	1.00E+00	9.16E-01	1.00E+00	9.67E-01	1.00E+00	specification of organ identity	P
GO:0010165	12	1.89E-01	1.00E+00	2.02E-01	1.00E+00	3.74E-01	1.00E+00	6.76E-01	1.00E+00	1.22E-01	1.00E+00	7.19E-02	1.00E+00	6.91E-01	1.00E+00	8.69E-01	1.00E+00	response to X-ray	P
GO:0010181	12	2.64E-01	1.00E+00	2.06E-01	1.00E+00	3.43E-01	1.00E+00	1.30E-01	1.00E+00	1.85E-01	1.00E+00	2.22E-01	1.00E+00	4.48E-01	1.00E+00	7.93E-01	1.00E+00	FMN binding	F
GO:0010212	12	3.97E-01	1.00E+00	1.09E-01	1.00E+00	2.37E-01	1.00E+00	2.53E-01	1.00E+00	4.27E-01	1.00E+00	5.10E-02	1.00E+00	4.90E-01	1.00E+00	5.47E-01	1.00E+00	response to ionizing radiation	P
GO:0012501	882	6.30E-10	8.06E-04	6.48E-14	0.00E+00	5.23E-08	1.00E-03	3.11E-08	9.71E-04	7.09E-08	1.69E-03	4.74E-11	0.00E+00	1.13E-04	2.50E-02	3.92E-07	1.88E-03	programmed cell death	P
GO:0012502	245	3.97E-05	1.00E-02	3.37E-06	8.39E-03	1.68E-04	1.50E-02	2.72E-05	8.00E-03	2.21E-04	1.70E-02	1.02E-04	1.70E-02	4.09E-02	1.00E+00	6.24E-03	3.60E-01	induction of programmed cell death	P
GO:0012505	1112	4.55E-10	8.06E-04	1.08E-13	0.00E+00	7.03E-05	1.20E-02	2.44E-05	8.00E-03	3.44E-09	9.64E-04	2.31E-13	0.00E+00	3.30E-05	5.44E-03	6.65E-05	9.00E-03	endomembrane system	C
GO:0012506	127	3.48E-05	1.00E-02	7.58E-05	1.00E-02	7.92E-04	4.50E-02	5.58E-03	3.46E-01	3.87E-05	5.00E-03	1.11E-04	1.70E-02	3.17E-02	1.00E+00	1.50E-01	1.00E+00	vesicle membrane	C
GO:0012510	14	9.70E-02	1.00E+00	6.15E-02	1.00E+00	2.66E-01	1.00E+00	3.84E-01	1.00E+00	1.07E-01	1.00E+00	4.47E-02	1.00E+00	7.26E-02	1.00E+00	6.84E-01	1.00E+00	trans-Golgi network transport vesicle membr	C
GO:0014003	10	2.19E-01	1.00E+00	8.25E-01	1.00E+00	2.04E-01	1.00E+00	4.75E-01	1.00E+00	2.22E-01	1.00E+00	8.37E-01	1.00E+00	3.80E-01	1.00E+00	1.00E+00	1.00E+00	oligodendrocyte development	P
GO:0014013	11	9.51E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	8.49E-01	1.00E+00	8.92E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	7.17E-01	1.00E+00	regulation of gliogenesis	P
GO:0014020	29	3.77E-01	1.00E+00	2.54E-01	1.00E+00	8.00E-02	1.00E+00	4.82E-01	1.00E+00	5.65E-01	1.00E+00	1.92E-01	1.00E+00	6.77E-01	1.00E+00	2.85E-01	1.00E+00	primary neural tube formation	P
GO:0014031	40	9.97E-01	1.00E+00	9.84E-01	1.00E+00	9.70E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.57E-01	1.00E+00	8.88E-01	1.00E+00	8.84E-01	1.00E+00	mesenchymal cell development	P
GO:0014032	27	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.56E-01	1.00E+00	9.96E-01	1.00E+00	neural crest cell development	P
GO:0014033	27	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.56E-01	1.00E+00	9.96E-01	1.00E+00	neural crest cell differentiation	P
GO:0014065	10	1.92E-01	1.00E+00	3.26E-01	1.00E+00	3.71E-01	1.00E+00	5.71E-01	1.00E+00	2.24E-01	1.00E+00	3.05E-01	1.00E+00	1.24E-02	6.30E-01	2.43E-01	1.00E+00	phosphoinositide 3-kinase cascade	P
GO:0014069	22	9.54E-01	1.00E+00	9.71E-01	1.00E+00	6.01E-01	1.00E+00	9.93E-01	1.00E+00	9.83E-01	1.00E+00	8.65E-01	1.00E+00	6.50E-01	1.00E+00	8.58E-01	1.00E+00	postsynaptic density	C
GO:0015002	28	2.16E-01	1.00E+00	6.64E-02	1.00E+00	1.17E-01	1.00E+00	1.83E-01	1.00E+00	2.84E-01	1.00E+00	7.30E-02	1.00E+00	8.97E-01	1.00E+00	1.47E-01	1.00E+00	heme-copper terminal oxidase activity	F
GO:0015012	10	9.56E-01	1.00E+00	9.63E-01	1.00E+00	8.88E-01	1.00E+00	8.20E-01	1.00E+00	6.99E-01	1.00E+00	8.89E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	heparan sulfate proteoglycan biosynthesis	P
GO:0015020	22	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	glucuronosyltransferase activity	F
GO:0015026	16	3.04E-01	1.00E+00	6.40E-01	1.00E+00	3.30E-01	1.00E+00	6.27E-01	1.00E+00	2.53E-01	1.00E+00	6.70E-01	1.00E+00	4.68E-01	1.00E+00	6.34E-01	1.00E+00	coreceptor activity	F
GO:0015031	827	1.98E-24	0.00E+00	1.45E-25	0.00E+00	2.93E-13	0.00E+00	3.90E-11	0.00E+00	1.25E-21	0.00E+00	2.89E-24	0.00E+00	1.25E-06	1.95E-03	5.09E-07	1.88E-03	protein transport	P

GO:0015035	14	8.79E-01	1.00E+00	9.65E-01	1.00E+00	9.05E-01	1.00E+00	9.96E-01	1.00E+00	8.08E-01	1.00E+00	8.74E-01	1.00E+00	5.85E-01	1.00E+00	7.16E-01	1.00E+00	protein disulfide oxidoreductase activity	F
GO:0015036	18	6.73E-01	1.00E+00	9.20E-01	1.00E+00	7.85E-01	1.00E+00	8.74E-01	1.00E+00	6.12E-01	1.00E+00	9.32E-01	1.00E+00	6.60E-01	1.00E+00	6.74E-01	1.00E+00	disulfide oxidoreductase activity	F
GO:0015057	40	6.84E-01	1.00E+00	4.89E-01	1.00E+00	4.59E-01	1.00E+00	7.32E-01	1.00E+00	5.76E-01	1.00E+00	4.44E-01	1.00E+00	9.72E-01	1.00E+00	4.47E-01	1.00E+00	thrombin receptor activity	F
GO:0015074	16	1.23E-01	1.00E+00	6.96E-01	1.00E+00	4.70E-01	1.00E+00	8.62E-01	1.00E+00	1.55E-01	1.00E+00	4.74E-01	1.00E+00	6.32E-02	1.00E+00	8.26E-01	1.00E+00	DNA integration	P
GO:0015075	931	7.86E-02	1.00E+00	1.33E-01	1.00E+00	1.79E-01	1.00E+00	2.33E-01	1.00E+00	4.53E-02	1.00E+00	9.57E-02	1.00E+00	8.40E-01	1.00E+00	4.16E-01	1.00E+00	ion transporter activity	F
GO:0015077	131	3.73E-03	3.28E-01	1.95E-01	1.00E+00	4.00E-02	1.00E+00	6.32E-02	1.00E+00	2.68E-03	2.85E-01	2.48E-01	1.00E+00	2.54E-01	1.00E+00	6.65E-01	1.00E+00	monovalent inorganic cation transporter act	F
GO:0015078	120	2.34E-03	2.02E-01	9.30E-02	1.00E+00	4.29E-02	1.00E+00	3.45E-02	1.00E+00	1.53E-03	1.76E-01	1.23E-01	1.00E+00	1.85E-01	1.00E+00	5.70E-01	1.00E+00	hydrogen ion transporter activity	F
GO:0015082	48	1.57E-01	1.00E+00	6.07E-03	3.60E-01	9.67E-01	1.00E+00	1.52E-01	1.00E+00	6.77E-02	1.00E+00	7.85E-04	5.49E-02	4.88E-01	1.00E+00	5.91E-01	1.00E+00	di-, tri-valent inorganic cation transporter ac	F
GO:0015085	13	9.58E-01	1.00E+00	1.50E-01	1.00E+00	9.61E-01	1.00E+00	3.29E-01	1.00E+00	9.21E-01	1.00E+00	7.31E-02	1.00E+00	9.66E-01	1.00E+00	8.29E-01	1.00E+00	calcium ion transporter activity	F
GO:0015103	48	3.56E-01	1.00E+00	3.99E-01	1.00E+00	4.66E-01	1.00E+00	3.01E-01	1.00E+00	1.98E-01	1.00E+00	5.25E-01	1.00E+00	8.33E-01	1.00E+00	3.47E-01	1.00E+00	inorganic anion transporter activity	F
GO:0015106	24	5.21E-01	1.00E+00	4.99E-01	1.00E+00	3.34E-01	1.00E+00	4.96E-01	1.00E+00	5.22E-01	1.00E+00	5.15E-01	1.00E+00	6.32E-01	1.00E+00	6.90E-01	1.00E+00	bicarbonate transporter activity	F
GO:0015108	25	3.50E-01	1.00E+00	5.03E-01	1.00E+00	1.80E-01	1.00E+00	4.11E-01	1.00E+00	4.76E-01	1.00E+00	5.69E-01	1.00E+00	3.88E-01	1.00E+00	6.63E-01	1.00E+00	chloride transporter activity	F
GO:0015114	13	3.97E-01	1.00E+00	3.19E-01	1.00E+00	8.86E-01	1.00E+00	3.56E-01	1.00E+00	1.24E-01	1.00E+00	4.48E-01	1.00E+00	9.73E-01	1.00E+00	9.15E-02	1.00E+00	phosphate transporter activity	F
GO:0015116	12	3.90E-01	1.00E+00	9.88E-01	1.00E+00	4.90E-01	1.00E+00	6.48E-01	1.00E+00	4.06E-01	1.00E+00	9.98E-01	1.00E+00	4.80E-01	1.00E+00	8.01E-01	1.00E+00	sulfate transporter activity	F
GO:0015125	11	8.23E-01	1.00E+00	8.65E-01	1.00E+00	7.76E-01	1.00E+00	4.54E-01	1.00E+00	9.26E-01	1.00E+00	9.75E-01	1.00E+00	4.26E-01	1.00E+00	7.00E-01	1.00E+00	bile acid transporter activity	F
GO:0015144	46	8.51E-02	1.00E+00	2.33E-02	1.00E+00	2.00E-01	1.00E+00	2.38E-02	1.00E+00	1.06E-01	1.00E+00	7.00E-02	1.00E+00	1.69E-01	1.00E+00	2.92E-01	1.00E+00	carbohydrate transporter activity	F
GO:0015145	17	3.95E-02	1.00E+00	1.89E-02	1.00E+00	4.37E-02	1.00E+00	4.23E-02	1.00E+00	7.06E-02	1.00E+00	5.00E-02	1.00E+00	7.06E-02	1.00E+00	3.00E-01	1.00E+00	monosaccharide transporter activity	F
GO:0015149	16	8.21E-02	1.00E+00	4.29E-02	1.00E+00	7.12E-02	1.00E+00	9.65E-02	1.00E+00	1.29E-01	1.00E+00	8.84E-02	1.00E+00	1.44E-01	1.00E+00	3.36E-01	1.00E+00	hexose transporter activity	F
GO:0015171	55	8.65E-01	1.00E+00	1.06E-01	1.00E+00	6.55E-01	1.00E+00	2.93E-01	1.00E+00	8.61E-01	1.00E+00	6.95E-02	1.00E+00	8.62E-01	1.00E+00	4.76E-01	1.00E+00	amino acid transporter activity	F
GO:0015172	11	9.58E-01	1.00E+00	2.17E-01	1.00E+00	7.98E-01	1.00E+00	2.02E-01	1.00E+00	9.42E-01	1.00E+00	2.07E-01	1.00E+00	8.71E-01	1.00E+00	7.38E-01	1.00E+00	acidic amino acid transporter activity	F
GO:0015175	18	6.27E-01	1.00E+00	2.95E-01	1.00E+00	7.76E-01	1.00E+00	3.72E-01	1.00E+00	7.70E-01	1.00E+00	1.66E-01	1.00E+00	3.01E-01	1.00E+00	8.42E-01	1.00E+00	neutral amino acid transporter activity	F
GO:0015179	36	9.53E-01	1.00E+00	2.18E-01	1.00E+00	7.40E-01	1.00E+00	2.56E-01	1.00E+00	9.48E-01	1.00E+00	1.53E-01	1.00E+00	8.01E-01	1.00E+00	9.21E-01	1.00E+00	L-amino acid transporter activity	F
GO:0015197	20	9.45E-01	1.00E+00	8.76E-02	1.00E+00	7.30E-01	1.00E+00	1.14E-01	1.00E+00	9.62E-01	1.00E+00	9.58E-02	1.00E+00	9.05E-01	1.00E+00	4.19E-01	1.00E+00	peptide transporter activity	F
GO:0015203	21	1.00E+00	1.00E+00	8.23E-01	1.00E+00	9.58E-01	1.00E+00	7.65E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	9.72E-01	1.00E+00	4.07E-01	1.00E+00	polyamine transporter activity	F
GO:0015232	12	5.99E-01	1.00E+00	6.56E-01	1.00E+00	6.86E-01	1.00E+00	2.70E-01	1.00E+00	5.58E-01	1.00E+00	9.71E-01	1.00E+00	5.91E-01	1.00E+00	5.77E-01	1.00E+00	heme transporter activity	F
GO:0015238	35	6.20E-01	1.00E+00	2.81E-01	1.00E+00	1.67E-01	1.00E+00	7.72E-01	1.00E+00	6.72E-01	1.00E+00	2.00E-01	1.00E+00	9.93E-01	1.00E+00	3.64E-01	1.00E+00	drug transporter activity	F
GO:0015247	15	7.00E-01	1.00E+00	4.71E-01	1.00E+00	5.16E-01	1.00E+00	4.16E-01	1.00E+00	4.38E-01	1.00E+00	6.16E-01	1.00E+00	1.00E+00	1.00E+00	1.46E-01	1.00E+00	aminophospholipid transporter activity	F
GO:0015248	13	2.95E-01	1.00E+00	8.35E-01	1.00E+00	1.99E-01	1.00E+00	6.01E-01	1.00E+00	2.40E-01	1.00E+00	7.42E-01	1.00E+00	8.98E-01	1.00E+00	9.86E-01	1.00E+00	sterol transporter activity	F
GO:0015267	520	3.15E-01	1.00E+00	4.14E-01	1.00E+00	2.78E-01	1.00E+00	5.23E-01	1.00E+00	3.19E-01	1.00E+00	3.14E-01	1.00E+00	5.19E-01	1.00E+00	4.90E-01	1.00E+00	channel or pore class transporter activity	F
GO:0015268	517	3.04E-01	1.00E+00	3.77E-01	1.00E+00	2.88E-01	1.00E+00	4.94E-01	1.00E+00	3.04E-01	1.00E+00	2.80E-01	1.00E+00	5.06E-01	1.00E+00	4.75E-01	1.00E+00	alpha-type channel activity	F
GO:0015269	15	6.13E-01	1.00E+00	8.16E-01	1.00E+00	7.10E-01	1.00E+00	9.90E-01	1.00E+00	4.85E-01	1.00E+00	5.25E-01	1.00E+00	8.57E-01	1.00E+00	8.97E-01	1.00E+00	calcium-activated potassium channel activit	F
GO:0015276	106	8.56E-01	1.00E+00	9.33E-01	1.00E+00	5.14E-01	1.00E+00	7.24E-01	1.00E+00	8.24E-01	1.00E+00	8.84E-01	1.00E+00	9.89E-01	1.00E+00	9.36E-01	1.00E+00	ligand-gated ion channel activity	F
GO:0015290	297	8.69E-01	1.00E+00	3.41E-01	1.00E+00	9.50E-01	1.00E+00	7.10E-01	1.00E+00	7.09E-01	1.00E+00	1.65E-01	1.00E+00	9.32E-01	1.00E+00	7.88E-01	1.00E+00	electrochemical potential-driven transporter	F
GO:0015291	297	8.69E-01	1.00E+00	3.41E-01	1.00E+00	9.50E-01	1.00E+00	7.10E-01	1.00E+00	7.09E-01	1.00E+00	1.65E-01	1.00E+00	9.32E-01	1.00E+00	7.88E-01	1.00E+00	porter activity	F
GO:0015293	173	9.73E-01	1.00E+00	7.82E-01	1.00E+00	9.89E-01	1.00E+00	8.59E-01	1.00E+00	9.15E-01	1.00E+00	6.44E-01	1.00E+00	9.43E-01	1.00E+00	8.28E-01	1.00E+00	symporter activity	F
GO:0015294	110	9.82E-01	1.00E+00	9.15E-01	1.00E+00	9.77E-01	1.00E+00	8.30E-01	1.00E+00	9.82E-01	1.00E+00	8.70E-01	1.00E+00	8.81E-01	1.00E+00	9.47E-01	1.00E+00	solute:cation symporter activity	F
GO:0015296	75	8.07E-01	1.00E+00	5.56E-01	1.00E+00	9.04E-01	1.00E+00	6.33E-01	1.00E+00	7.92E-01	1.00E+00	4.71E-01	1.00E+00	3.78E-01	1.00E+00	6.89E-01	1.00E+00	anion:cation symporter activity	F
GO:0015297	90	7.06E-01	1.00E+00	3.65E-01	1.00E+00	4.82E-01	1.00E+00	8.79E-01	1.00E+00	5.57E-01	1.00E+00	1.97E-01	1.00E+00	9.93E-01	1.00E+00	7.77E-01	1.00E+00	antiporter activity	F
GO:0015298	42	8.10E-01	1.00E+00	4.78E-01	1.00E+00	3.87E-01	1.00E+00	7.39E-01	1.00E+00	7.53E-01	1.00E+00	3.90E-01	1.00E+00	9.99E-01	1.00E+00	5.59E-01	1.00E+00	solute:cation antiporter activity	F
GO:0015299	42	8.10E-01	1.00E+00	4.78E-01	1.00E+00	3.87E-01	1.00E+00	7.39E-01	1.00E+00	7.53E-01	1.00E+00	3.90E-01	1.00E+00	9.99E-01	1.00E+00	5.59E-01	1.00E+00	solute:hydrogen antiporter activity	F
GO:0015300	47	6.39E-01	1.00E+00	3.80E-01	1.00E+00	4.03E-01	1.00E+00	8.25E-01	1.00E+00	5.35E-01	1.00E+00	2.30E-01	1.00E+00	9.96E-01	1.00E+00	6.11E-01	1.00E+00	solute:solute antiporter activity	F
GO:0015301	25	5.81E-01	1.00E+00	5.26E-01	1.00E+00	3.95E-01	1.00E+00	4.72E-01	1.00E+00	5.90E-01	1.00E+00	5.43E-01	1.00E+00	5.81E-01	1.00E+00	7.31E-01	1.00E+00	anion:anion antiporter activity	F
GO:0015307	26	4.23E-01	1.00E+00	1.64E-01	1.00E+00	5.87E-02	1.00E+00	6.33E-01	1.00E+00	6.15E-01	1.00E+00	1.26E-01	1.00E+00	8.98E-01	1.00E+00	1.67E-01	1.00E+00	drug:hydrogen antiporter activity	F
GO:0015370	106	9.72E-01	1.00E+00	9.01E-01	1.00E+00	9.64E-01	1.00E+00	7.76E-01	1.00E+00	9.75E-01	1.00E+00	8.73E-01	1.00E+00	8.50E-01	1.00E+00	9.41E-01	1.00E+00	solute:sodium symporter activity	F
GO:0015380	23	4.27E-01	1.00E+00	4.04E-01	1.00E+00	2.76E-01	1.00E+00	4.20E-01	1.00E+00	4.37E-01	1.00E+00	4.33E-01	1.00E+00	5.56E-01	1.00E+00	6.46E-01	1.00E+00	anion exchanger activity	F
GO:0015385	14	9.60E-01	1.00E+00	8.71E-01	1.00E+00	9.99E-01	1.00E+00	4.67E-01	1.00E+00	7.01E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	sodium:hydrogen antiporter activity	F
GO:0015399	110	5.86E-02	1.00E+00	9.34E-02	1.00E+00	5.27E-01	1.00E+00	2.38E-01	1.00E+00	2.13E-02	1.00E+00	1.16E-01	1.00E+00	3.99E-01	1.00E+00	1.47E-01	1.00E+00	primary active transporter activity	F
GO:0015405	110	5.86E-02	1.00E+00	9.34E-02	1.00E+00	5.27E-01	1.00E+00	2.38E-01	1.00E+00	2.13E-02	1.00E+00	1.16E-01	1.00E+00	3.99E-01	1.00E+00	1.47E-01	1.00E+00	P-P-bond-hydrolysis-driven transporter acti	F
GO:0015450	21	1.30E-01	1.00E+00	1.42E-01	1.00E+00	6.56E-01	1.00E+00	3.09E-01	1.00E+00	1.24E-01	1.00E+00	1.05E-01	1.00E+00	1.71E-01	1.00E+00	3.61E-01	1.00E+00	protein translocase activity	F
GO:0015457	46	7.20E-01	1.00E+00	9.41E-01	1.00E+00	9.96E-01	1.00E+00	8.57E-01	1.00E+00	4.60E-01	1.00E+00	9.12E-01	1.00E+00	5.42E-01	1.00E+00	9.33E-01	1.00E+00	auxiliary transport protein activity	F
GO:0015459	20	8.09E-01	1.00E+00	9.97E-01	1.00E+00	9.96E-01	1.00E+00	9.27E-01	1.00E+00	5.58E-01	1.00E+00	9.94E-01	1.00E+00	8.17E-01	1.00E+00	9.37E-01	1.00E+00	potassium channel regulator activity	F
GO:0015464	34	7.14E-01	1.00E+00	9.57E-01	1.00E+00	8.14E-01	1.00E+00	7.14E-01	1.00E+00	5.68E-01	1.00E+00	9.92E-01	1.00E+00	5.93E-01	1.00E+00	5.79E-01	1.00E+00	acetylcholine receptor activity	F
GO:0015485	17	2.50E-01	1.00E+00	4.84E-01	1.00E+00	8.57E-02	1.00E+00	7.40E-01	1.00E+00	2.22E-01	1.00E+00	3.24E-01	1.00E+00	9.95E-01	1.00E+00	5.64E-01	1.00E+00	cholesterol binding	F
GO:0015491	21	9.72E-01	1.00E+00	7.35E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	7.69E-01	1.00E+00	6.01E-01	1.00E+00	9.97E-01	1.00E+00	9.73E-01	1.00E+00	cation:cation antiporter activity	F
GO:0015520	26	4.23E-01	1.00E+00	1.64E-01	1.00E+00	5.87E-02	1.00E+00	6.33E-01	1.00E+00	6.15E-01	1.00E+00	1.26E-01	1.00E+00	8.98E-01	1.00E+00	1.67E-01	1.00E+00	tetracycline:hydrogen antiporter activity	F
GO:0015629	320	5.89E-03	3.50E-01	1.98E-05	9.58E-03	9.72E-04	9.80E-02	3.86E-04	4.20E-02	1.17E-02	5.39E-01	6.66E-05	1.70E-02	5.45E-01	1.00E+00	3.78E-02	1.00E+00	actin cytoskeleton	C
GO:0015630	425	1.96E-10	0.00E+00	7.34E-08	4.97E-03	3.03E-07	2.42E-03	2.57E-04	2.70E-02	4.53E-09	9.64E-04	1.54E-07	9.20E-04	5.30E-03	3.57E-01	1.59E-02	8.49E-01	microtubule cytoskeleton	C
GO:0015631	74	1.66E-04	2.50E-02	1.12E-04	1.50E-02	3.03E-03	2.48E-01	2.62E-03	1.47E-01	5.07E-04	2.20E-02	9.21E-04	5.49E-02	5.18E-02	1.00E+00	2.16E-02	1.00E+00	tubulin binding	F
GO:0015645	11	6.17E-01	1.00E+00	6.76E-01	1.00E+00	8.85E-01	1.00E+00	7.94E-01	1.00E+00	6.02E-01	1.00E+00	5.21E-01	1.00E+00	1.89E-01	1.00E+00	6.74E-01	1.00E+00	fatty-acid ligase activity	F
GO:0015662	58	2.90E-01	1.00E+00	8.31E-02	1.00E+00	6.92E-01	1.00E+00	4.08E-01	1.00E+00	1.03E-01	1.00E+00	1.04E-01	1.00E+00	8.85E-01	1.00E+00	4.01E-02	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0015669	18	2.65E-01	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	1.84E-01	1.00E+00	9.99E-01	1.00E+00	1.05E-01	1.00E+00	1.37E-01	1.00E+00	gas transport	P
GO:0015671	16	2.49E-01	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	1.46E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-02	1.00E+00	1.80E-01	1.00E+00	oxygen transport	P
GO:0015672	463	3.21E-01	1.00E+00	5.53E-01	1.00E+00	3.86E-01	1.00E+00	3.30E-01	1.00E+00	2.37E-01	1.00E+00	6.05E-01	1.00E+00	8.64E-01	1.00E+00	6.28E-01	1.00E+00	monovalent inorganic cation transport	P
GO:0015674	240	2.68E-01	1.00E+00	2.41E-02	1.00E+00	6.21E-01	1.00E+00	1.81E-01	1.00E+00	2.74E-01	1.00E+00	3.44E-03	2.70E-01	2.44E-01	1.00E+00	8.88E-01	1.00E+00	di-, tri-valent inorganic cation transport	P
GO:0015695	10	1.00E+00	1.00E+00	8.61E-01	1.00E+00	6.18E-01	1.00E+00	6.34E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.56E-01	1.00E+00	7.10E-01	1.00E+00	organic cation transport	P
GO:0015698	192	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	inorganic anion transport	P
GO:0015711	14	5.92E-01	1.00E+00	7.83E-01	1.00E+00	9.32E-01	1.00E+00	8.97E-01	1.00E+00	4.28E-01	1.00E+00	5.29E-01	1.00E+00	6.46E-01	1.00E+00	7.81E-01	1.00E+00	organic anion transport	P
GO:0015718	16	3.16E-01	1.00E+00	2.87E-01	1.00E+00	4.56E-01	1.00E+00	8.44E-01	1.00E+00	1.57E-01	1.00E+00	9.59E-02	1.00E+00	1.00E+00	1.00E+00	8.33E-01	1.00E+00	monocarboxylic acid transport	P
GO:0015749	43	1.31E-02	6.67E-01	2.39E-02	1.00E+00	3.37E-02	1.00E+00	6.37E-02	1.00E+00	1.90E-02	1.00E+00	5.36E-02	1.00E+00	7.56E-02	1.00E+00	1.25E-01	1.00E+00	monosaccharide transport	P
GO:0015758	42	1.36E-02	6.67E-01	2.26E-02	1.00E+00	4.31E-02	1.00E+00	1.03E-01	1.00E+00	1.93E-02	1.00E+00	3.72E-02	1.00E+00	6.60E-02	1.00E+00	1.08E-01	1.00E+00	glucose transport	P
GO:0015800	18	2.58E-02	1.00E+00	3.17E-03	1.97E-01	1.13E-01	1.00E+00	5.72E-02	1.00E+00	9.66E-03	5.39E-01	4.94E-03	2.70E-01	7.34E-01	1.00E+00	7.66E-02	1.00E+00	acidic amino acid transport	P
GO:0015804	16	5.86E-01	1.00E+00	2.97E-01	1.00E+00	8.03E-01	1.00E+00	3.42E-01	1.00E+00	6.80E-01	1.00E+00	1.55E-01	1.00E+00	3.76E-01	1.00E+00	9.24E-01	1.00E+00	neutral amino acid transport	P
GO:0015807	14	1.96E-01	1.00E+00	4.88E-02	1.00E+00	8.30E-01	1.00E+00	6.60E-01	1.00E+00	1.14E-01	1.00E+00	6.05E-03	3.51E-01	4.12E-01	1.00E+00	9.30E-01	1.00E+00	L-amino acid transport	P
GO:0015813	18	2.58E-02	1.00E+00	3.17E-03	1.97E-01	1.13E-01	1.00E+00	5.72E-02	1.00E+00	9.66E-03	5.39E-01	4.94E-03	2.70E-01	7.34E-01	1.00E+00	7.66E-02	1.00E+00	glutamate transport	P
GO:0015833	64	9.11E-01	1.00E+00	2.98E-01	1.00E+00	6.26E-01	1.00E+00	4.81E-01	1.00E+00	8.75E-01	1.00E+00	2.15E-01	1.00E+00	9.90E-01	1.00E+00	5.43E-01	1.00E+00	peptide transport	P

GO:0015837	93	4.98E-01	1.00E+00	6.53E-02	1.00E+00	4.12E-01	1.00E+00	3.73E-01	1.00E+00	3.52E-01	1.00E+00	1.77E-02	8.81E-01	9.83E-01	1.00E+00	6.57E-01	1.00E+00	amine transport	P
GO:0015849	149	3.03E-01	1.00E+00	3.10E-01	1.00E+00	7.43E-01	1.00E+00	8.61E-01	1.00E+00	1.57E-01	1.00E+00	9.01E-02	1.00E+00	6.50E-01	1.00E+00	8.61E-01	1.00E+00	organic acid transport	P
GO:0015886	11	6.14E-01	1.00E+00	5.67E-01	1.00E+00	6.87E-01	1.00E+00	2.10E-01	1.00E+00	5.44E-01	1.00E+00	9.48E-01	1.00E+00	6.46E-01	1.00E+00	5.03E-01	1.00E+00	heme transport	P
GO:0015893	31	4.02E-01	1.00E+00	1.14E-01	1.00E+00	7.61E-02	1.00E+00	7.60E-01	1.00E+00	5.83E-01	1.00E+00	6.66E-02	1.00E+00	9.23E-01	1.00E+00	1.26E-01	1.00E+00	drug transport	P
GO:0015904	26	4.23E-01	1.00E+00	1.64E-01	1.00E+00	5.87E-02	1.00E+00	6.33E-01	1.00E+00	6.15E-01	1.00E+00	1.26E-01	1.00E+00	8.98E-01	1.00E+00	1.67E-01	1.00E+00	tetracycline transport	P
GO:0015908	12	3.08E-02	1.00E+00	2.78E-02	1.00E+00	5.34E-02	1.00E+00	3.18E-02	1.00E+00	8.39E-02	1.00E+00	3.65E-02	1.00E+00	1.33E-01	1.00E+00	1.24E-01	1.00E+00	fatty acid transport	P
GO:0015914	18	4.14E-01	1.00E+00	3.30E-01	1.00E+00	2.52E-01	1.00E+00	2.40E-01	1.00E+00	2.22E-01	1.00E+00	4.15E-01	1.00E+00	1.00E+00	1.00E+00	3.27E-01	1.00E+00	phospholipid transport	P
GO:0015918	16	8.34E-02	1.00E+00	2.49E-01	1.00E+00	3.76E-02	1.00E+00	1.30E-01	1.00E+00	9.21E-02	1.00E+00	3.57E-01	1.00E+00	5.50E-01	1.00E+00	4.69E-01	1.00E+00	sterol transport	P
GO:0015923	16	5.45E-01	1.00E+00	1.42E-01	1.00E+00	3.53E-01	1.00E+00	2.94E-01	1.00E+00	5.97E-01	1.00E+00	9.69E-02	1.00E+00	7.37E-01	1.00E+00	4.39E-01	1.00E+00	mannosidase activity	F
GO:0015924	10	6.03E-01	1.00E+00	1.65E-01	1.00E+00	3.61E-01	1.00E+00	3.93E-01	1.00E+00	7.20E-01	1.00E+00	1.13E-01	1.00E+00	8.49E-01	1.00E+00	4.11E-01	1.00E+00	mannosyl-oligosaccharide mannosidase ac	F
GO:0015926	11	4.46E-01	1.00E+00	2.47E-01	1.00E+00	5.53E-01	1.00E+00	3.66E-01	1.00E+00	4.61E-01	1.00E+00	6.04E-02	1.00E+00	1.73E-01	1.00E+00	9.97E-01	1.00E+00	glucosidase activity	F
GO:0015929	12	2.37E-02	1.00E+00	2.47E-01	1.00E+00	6.05E-01	1.00E+00	4.17E-01	1.00E+00	9.72E-03	5.39E-01	7.93E-01	1.00E+00	1.01E-01	1.00E+00	1.52E-02	8.49E-01	hexosaminidase activity	F
GO:0015931	103	2.35E-07	1.95E-03	3.22E-11	0.00E+00	4.68E-05	1.20E-02	4.32E-06	8.00E-03	9.38E-07	2.45E-03	1.18E-10	0.00E+00	2.59E-02	1.00E+00	5.65E-04	9.16E-02	nucleobase, nucleoside, nucleotide and nuc	P
GO:0015932	24	7.99E-03	6.34E-01	1.09E-03	9.10E-02	4.41E-03	3.27E-01	2.11E-01	1.00E+00	1.41E-02	1.00E+00	1.79E-04	2.60E-02	1.88E-01	1.00E+00	3.63E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	F
GO:0015934	32	3.96E-02	1.00E+00	1.90E-01	1.00E+00	2.28E-01	1.00E+00	6.02E-01	1.00E+00	9.50E-02	1.00E+00	1.19E-01	1.00E+00	7.00E-03	5.44E-01	4.69E-01	1.00E+00	large ribosomal subunit	C
GO:0015935	40	3.00E-02	1.00E+00	2.12E-02	1.00E+00	1.27E-01	1.00E+00	1.45E-01	1.00E+00	4.23E-02	1.00E+00	4.75E-02	1.00E+00	1.24E-01	1.00E+00	1.16E-01	1.00E+00	small ribosomal subunit	C
GO:0015936	13	1.99E-01	1.00E+00	6.46E-01	1.00E+00	8.17E-02	1.00E+00	8.47E-01	1.00E+00	4.15E-01	1.00E+00	5.60E-01	1.00E+00	1.80E-01	1.00E+00	7.10E-01	1.00E+00	coenzyme A metabolism	P
GO:0015980	211	2.50E-04	3.37E-02	4.00E-04	6.90E-02	2.33E-04	2.40E-02	1.03E-02	7.13E-01	6.97E-04	4.00E-02	6.69E-04	5.49E-02	2.05E-01	1.00E+00	9.92E-02	1.00E+00	energy derivation by oxidation of organic cc	P
GO:0015985	20	2.95E-03	2.39E-01	4.46E-01	1.00E+00	3.27E-02	1.00E+00	1.56E-01	1.00E+00	2.87E-03	2.85E-01	6.01E-01	1.00E+00	6.96E-02	1.00E+00	4.72E-01	1.00E+00	energy coupled proton transport, down elec	P
GO:0015986	20	2.95E-03	2.39E-01	4.46E-01	1.00E+00	3.27E-02	1.00E+00	1.56E-01	1.00E+00	2.87E-03	2.85E-01	6.01E-01	1.00E+00	6.96E-02	1.00E+00	4.72E-01	1.00E+00	ATP synthesis coupled proton transport	P
GO:0015992	71	3.97E-03	3.28E-01	7.49E-02	1.00E+00	1.71E-01	1.00E+00	6.65E-02	1.00E+00	2.73E-03	2.85E-01	7.59E-02	1.00E+00	1.23E-01	1.00E+00	7.11E-01	1.00E+00	proton transport	P
GO:0016010	18	1.00E+00	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	6.58E-01	1.00E+00	8.67E-01	1.00E+00	9.52E-01	1.00E+00	dystrophin-associated glycoprotein complex	C
GO:0016020	7368	3.99E-03	3.28E-01	1.68E-06	8.39E-03	3.88E-02	1.00E+00	7.18E-02	1.00E+00	1.13E-03	7.80E-02	1.93E-08	8.37E-04	4.21E-01	1.00E+00	3.97E-02	1.00E+00	membrane	C
GO:0016021	5470	9.81E-01	1.00E+00	5.84E-01	1.00E+00	9.72E-01	1.00E+00	9.54E-01	1.00E+00	9.07E-01	1.00E+00	2.47E-01	1.00E+00	9.82E-01	1.00E+00	7.42E-01	1.00E+00	integral to membrane	C
GO:0016023	411	1.03E-06	1.95E-03	2.73E-06	8.39E-03	1.33E-03	9.80E-02	4.27E-04	4.20E-02	1.05E-06	2.60E-03	2.59E-06	2.97E-03	4.75E-03	3.57E-01	1.08E-01	1.00E+00	cytoplasmic membrane-bound vesicle	C
GO:0016032	73	1.27E-02	6.67E-01	1.55E-01	1.00E+00	2.34E-01	1.00E+00	3.96E-01	1.00E+00	7.86E-03	5.39E-01	1.03E-01	1.00E+00	8.60E-02	1.00E+00	3.76E-01	1.00E+00	viral life cycle	P
GO:0016042	145	5.64E-02	1.00E+00	1.39E-01	1.00E+00	1.35E-01	1.00E+00	3.26E-01	1.00E+00	9.34E-02	1.00E+00	2.60E-01	1.00E+00	1.37E-01	1.00E+00	3.49E-02	1.00E+00	lipid catabolism	P
GO:0016043	2348	2.41E-29	0.00E+00	4.41E-31	0.00E+00	3.38E-17	0.00E+00	2.49E-11	0.00E+00	5.11E-27	0.00E+00	6.72E-29	0.00E+00	5.88E-06	2.00E-03	5.43E-13	0.00E+00	cell organization and biogenesis	P
GO:0016044	123	2.17E-03	2.02E-01	4.62E-03	3.60E-01	2.93E-02	1.00E+00	1.23E-01	1.00E+00	6.50E-03	5.39E-01	2.97E-03	2.39E-01	3.78E-02	1.00E+00	8.35E-02	1.00E+00	membrane organization and biogenesis	P
GO:0016049	208	1.08E-01	1.00E+00	2.41E-02	1.00E+00	2.74E-02	1.00E+00	1.39E-03	1.15E-01	1.23E-01	1.00E+00	1.27E-01	1.00E+00	6.84E-01	1.00E+00	1.32E-01	1.00E+00	cell growth	P
GO:0016051	138	2.72E-01	1.00E+00	1.65E-01	1.00E+00	4.28E-01	1.00E+00	1.31E-01	1.00E+00	2.25E-01	1.00E+00	3.22E-01	1.00E+00	6.00E-01	1.00E+00	1.84E-01	1.00E+00	carbohydrate biosynthesis	P
GO:0016052	120	6.08E-04	3.37E-02	3.63E-03	1.97E-01	6.20E-04	3.60E-02	3.53E-02	1.00E+00	3.17E-03	2.85E-01	5.91E-03	3.51E-01	1.24E-01	1.00E+00	5.29E-02	1.00E+00	carbohydrate catabolism	P
GO:0016053	90	1.83E-01	1.00E+00	1.23E-02	6.77E-01	2.20E-01	1.00E+00	9.63E-02	1.00E+00	3.64E-01	1.00E+00	1.45E-02	7.39E-01	1.28E-01	1.00E+00	2.91E-01	1.00E+00	organic acid biosynthesis	P
GO:0016054	10	1.41E-01	1.00E+00	1.09E-01	1.00E+00	2.12E-01	1.00E+00	2.92E-01	1.00E+00	1.86E-01	1.00E+00	1.64E-01	1.00E+00	3.01E-01	1.00E+00	8.40E-02	1.00E+00	organic acid catabolism	P
GO:0016055	130	1.42E-02	6.67E-01	1.35E-02	7.47E-01	2.19E-01	1.00E+00	4.54E-02	1.00E+00	6.90E-03	5.39E-01	8.84E-03	7.39E-01	1.37E-01	1.00E+00	3.50E-01	1.00E+00	Wnt receptor signaling pathway	P
GO:0016064	118	7.91E-01	1.00E+00	5.28E-01	1.00E+00	7.31E-01	1.00E+00	4.96E-01	1.00E+00	7.05E-01	1.00E+00	4.25E-01	1.00E+00	8.51E-01	1.00E+00	9.09E-01	1.00E+00	immunoglobulin mediated immune respons	P
GO:0016068	52	7.20E-01	1.00E+00	5.14E-01	1.00E+00	3.79E-01	1.00E+00	6.43E-01	1.00E+00	8.17E-01	1.00E+00	3.67E-01	1.00E+00	6.00E-01	1.00E+00	8.04E-01	1.00E+00	type I hypersensitivity	P
GO:0016070	642	9.72E-32	0.00E+00	1.25E-29	0.00E+00	1.10E-13	0.00E+00	5.07E-12	0.00E+00	9.27E-28	0.00E+00	2.37E-25	0.00E+00	1.59E-10	0.00E+00	1.25E-11	0.00E+00	RNA metabolism	P
GO:0016071	343	6.50E-22	0.00E+00	2.24E-23	0.00E+00	6.17E-11	9.34E-04	1.85E-09	0.00E+00	1.79E-18	0.00E+00	4.33E-21	0.00E+00	3.69E-08	8.55E-04	8.18E-10	7.71E-04	mRNA metabolism	P
GO:0016072	77	5.11E-03	3.28E-01	3.29E-02	1.00E+00	1.51E-01	1.00E+00	1.67E-01	1.00E+00	3.27E-03	2.85E-01	1.01E-01	1.00E+00	1.24E-01	1.00E+00	5.88E-02	1.00E+00	rRNA metabolism	P
GO:0016073	12	9.31E-03	6.67E-01	6.61E-02	1.00E+00	1.74E-01	1.00E+00	1.00E-01	1.00E+00	3.70E-03	2.85E-01	6.17E-02	1.00E+00	5.55E-02	1.00E+00	5.44E-01	1.00E+00	snRNA metabolism	P
GO:0016079	13	3.57E-01	1.00E+00	1.79E-01	1.00E+00	5.82E-01	1.00E+00	4.02E-01	1.00E+00	3.56E-01	1.00E+00	1.54E-01	1.00E+00	3.18E-01	1.00E+00	2.07E-01	1.00E+00	synaptic vesicle exocytosis	P
GO:0016089	43	7.62E-01	1.00E+00	5.14E-01	1.00E+00	5.96E-01	1.00E+00	1.98E-01	1.00E+00	7.81E-01	1.00E+00	6.75E-01	1.00E+00	5.70E-01	1.00E+00	3.15E-01	1.00E+00	aromatic amino acid family biosynthesis, sh	P
GO:0016125	94	5.40E-02	1.00E+00	2.05E-01	1.00E+00	6.32E-02	1.00E+00	2.09E-01	1.00E+00	6.50E-02	1.00E+00	2.70E-01	1.00E+00	3.52E-01	1.00E+00	1.67E-01	1.00E+00	sterol metabolism	P
GO:0016126	35	3.18E-01	1.00E+00	4.20E-01	1.00E+00	3.45E-01	1.00E+00	2.34E-01	1.00E+00	2.99E-01	1.00E+00	5.00E-01	1.00E+00	4.68E-01	1.00E+00	5.30E-01	1.00E+00	sterol biosynthesis	P
GO:0016127	10	1.89E-01	1.00E+00	5.22E-01	1.00E+00	1.96E-02	1.00E+00	1.09E-01	1.00E+00	5.67E-01	1.00E+00	9.44E-01	1.00E+00	4.47E-01	1.00E+00	2.10E-01	1.00E+00	sterol catabolism	P
GO:0016180	12	9.31E-03	6.67E-01	6.61E-02	1.00E+00	1.74E-01	1.00E+00	1.00E-01	1.00E+00	3.70E-03	2.85E-01	6.17E-02	1.00E+00	5.55E-02	1.00E+00	5.44E-01	1.00E+00	snRNA processing	P
GO:0016192	550	8.80E-14	0.00E+00	3.95E-15	0.00E+00	1.65E-09	9.34E-04	4.25E-08	9.71E-04	3.16E-12	0.00E+00	1.27E-13	0.00E+00	5.19E-03	3.57E-01	4.41E-04	2.70E-02	vesicle-mediated transport	P
GO:0016197	47	4.85E-02	1.00E+00	4.89E-02	1.00E+00	4.61E-02	1.00E+00	2.76E-01	1.00E+00	3.16E-02	1.00E+00	5.86E-02	1.00E+00	8.94E-01	1.00E+00	1.67E-01	1.00E+00	endosome transport	P
GO:0016202	16	1.88E-01	1.00E+00	1.74E-01	1.00E+00	4.43E-01	1.00E+00	4.90E-01	1.00E+00	2.03E-01	1.00E+00	1.71E-01	1.00E+00	9.16E-02	1.00E+00	1.55E-01	1.00E+00	regulation of striated muscle development	P
GO:0016208	25	7.19E-01	1.00E+00	8.99E-01	1.00E+00	6.81E-01	1.00E+00	4.84E-01	1.00E+00	7.19E-01	1.00E+00	8.93E-01	1.00E+00	5.28E-01	1.00E+00	9.92E-01	1.00E+00	AMP binding	F
GO:0016209	60	5.55E-01	1.00E+00	5.33E-01	1.00E+00	4.10E-01	1.00E+00	3.37E-01	1.00E+00	5.41E-01	1.00E+00	8.18E-01	1.00E+00	7.12E-01	1.00E+00	2.81E-01	1.00E+00	antioxidant activity	F
GO:0016229	37	9.48E-01	1.00E+00	9.36E-01	1.00E+00	8.81E-01	1.00E+00	9.32E-01	1.00E+00	9.61E-01	1.00E+00	9.22E-01	1.00E+00	4.61E-01	1.00E+00	5.00E-01	1.00E+00	steroid dehydrogenase activity	F
GO:0016236	14	2.66E-02	1.00E+00	5.54E-03	3.60E-01	2.79E-02	1.00E+00	2.24E-01	1.00E+00	1.29E-02	1.00E+00	2.15E-03	1.61E-01	6.29E-01	1.00E+00	3.45E-01	1.00E+00	macroautophagy	P
GO:0016247	43	7.03E-01	1.00E+00	9.29E-01	1.00E+00	9.92E-01	1.00E+00	8.06E-01	1.00E+00	4.84E-01	1.00E+00	9.11E-01	1.00E+00	4.79E-01	1.00E+00	9.22E-01	1.00E+00	channel regulator activity	F
GO:0016248	11	2.30E-01	1.00E+00	4.69E-01	1.00E+00	4.58E-01	1.00E+00	2.59E-01	1.00E+00	1.76E-01	1.00E+00	7.10E-01	1.00E+00	6.98E-01	1.00E+00	2.45E-01	1.00E+00	channel inhibitor activity	F
GO:0016251	37	5.69E-06	7.00E-03	4.04E-04	6.90E-02	2.76E-03	2.48E-01	2.80E-03	1.47E-01	3.67E-05	5.00E-03	4.31E-03	2.70E-01	3.63E-03	3.57E-01	5.76E-02	1.00E+00	general RNA polymerase II transcription fac	F
GO:0016254	17	3.06E-01	1.00E+00	9.69E-01	1.00E+00	9.82E-01	1.00E+00	7.43E-01	1.00E+00	1.76E-01	1.00E+00	9.94E-01	1.00E+00	2.06E-01	1.00E+00	4.09E-01	1.00E+00	preassembly of GPI anchor in ER membran	F
GO:0016265	932	2.17E-09	8.06E-04	8.79E-15	0.00E+00	8.19E-08	2.42E-03	1.49E-09	0.00E+00	2.45E-07	1.69E-03	2.12E-11	0.00E+00	1.35E-04	2.50E-02	2.12E-07	1.88E-03	death	P
GO:0016272	10	3.36E-01	1.00E+00	2.44E-01	1.00E+00	1.37E-01	1.00E+00	3.94E-02	1.00E+00	2.65E-01	1.00E+00	4.61E-01	1.00E+00	9.99E-01	1.00E+00	8.93E-01	1.00E+00	prefoldin complex	C
GO:0016278	27	8.49E-05	1.24E-02	1.88E-06	8.39E-03	5.84E-03	4.60E-01	1.54E-03	1.24E-01	1.13E-04	1.70E-02	2.75E-05	1.20E-02	5.42E-02	1.00E+00	1.44E-02	8.49E-01	lysine N-methyltransferase activity	F
GO:0016279	27	8.49E-05	1.24E-02	1.88E-06	8.39E-03	5.84E-03	4.60E-01	1.54E-03	1.24E-01	1.13E-04	1.70E-02	2.75E-05	1.20E-02	5.42E-02	1.00E+00	1.44E-02	8.49E-01	protein-lysine N-methyltransferase activity	F
GO:0016282	16	8.68E-05	1.24E-02	2.27E-04	4.19E-02	1.61E-03	2.48E-01	1.63E-01	1.00E+00	3.11E-04	1.98E-02	6.33E-04	5.49E-02	2.83E-02	1.00E+00	1.32E-01	1.00E+00	eukaryotic 43S preinitiation complex	C
GO:0016284	11	6.28E-01	1.00E+00	2.00E-01	1.00E+00	9.45E-01	1.00E+00	2.76E-01	1.00E+00	5.55E-01	1.00E+00	3.54E-01	1.00E+00	2.65E-01	1.00E+00	8.43E-02	1.00E+00	alanine aminopeptidase activity	F
GO:0016289	15	1.07E-03	9.60E-02	4.53E-02	1.00E+00	3.76E-02	1.00E+00	5.43E-03	3.46E-01	3.91E-04	2.20E-02	1.58E-01	1.00E+00	1.79E-01	1.00E+00	1.36E-01	1.00E+00	CoA hydrolase activity	F
GO:0016298	108	8.94E-01	1.00E+00	9.13E-01	1.00E+00	4.88E-01	1.00E+00	9.98E-01	1.00E+00	9.67E-01	1.00E+00	8.11E-01	1.00E+00	3.46E-01	1.00E+00	2.69E-01	1.00E+00	lipase activity	F
GO:0016301	904	1.97E-08	9.77E-04	4.54E-15	0.00E+00	4.92E-05	1.20E-02	2.32E-09	0.00E+00	6.74E-08	1.69E-03	7.32E-12	0.00E+00	1.27E-02	6.30E-01	5.74E-07	1.88E-03	kinase activity	F
GO:0016303	11	2.65E-02	1.00E+00	1.55E-01	1.00E+00	1.70E-02	6.93E-01	4.41E-02	1.00E+00	1.06E-01	1.00E+00	3.26E-01	1.00E+00	8.36E-02	1.00E+00	1.40E-01	1.00E+00	phosphatidylinositol 3-kinase activity	F
GO:0016307	12	2.13E-01	1.00E+00	5.42E-02	1.00E+00	4.07E-01	1.00E+00	4.63E-02	1.00E+00	3.69E-01	1.00E+00	9.50E-02	1.00E+00	7.06E-02	1.00E+00	2.58E-01	1.00E+00	phosphatidylinositol phosphate kinase activ	F
GO:0016310	858	3.58E-08	9.77E-04	3.15E-14	0.00E+00	6.94E-05	1.20E-02	5.66E-11	0.00E+00	8.42E-08	1.69E-03	1.24E-10	0.00E+00	1.07E-02	6.30E-01	7.19E-06	1.88E-03	phosphorylation	P
GO:0016311	166	7.21E-02	1.00E+00	1.14E-04	1.50E-02	1.64E-01	1.00E+00	3.74E-03	2.02E-01	8.90E-02	1.00E+00	3.24E-04	3.07E-02	2.41E-01	1.00E+00	9.40E-03	4.81E-01	dephosphorylation	P
GO:0016323	133	4.62E-01	1.00E+00	6.09E-02	1.00E+00	6.96E-02	1.00E+00	9.81E-02	1.00E+00	5.07E-01	1.00E+00	4.61E-02	1.00E+00	9.81E-01	1.00E+00	7.18E-01	1.00E+00	basolateral plasma membrane	C
GO:0016324	97	6.80E-01	1.00E+00	1.10E-01	1.00E+00	2.16E-01	1.00E+00	2.97E-01	1.00E+00	7.32E-01	1.00E+00	1.37E-01	1.00E+00	8.64E-01	1.00E+00	3.65E-01	1.00E+00	apical plasma membrane	C
GO:0016327	105	1.17E-02	6.67E-01	6.20E-03	3.60E-01	3.95E-02	1.00E+00	2.75E-03	1.47E-01	3.40E-03	2.85E-01	1.76E-02	8.81E-01	4.30E-01	1.00E+00	1.97E-01	1.00E+00	apicolateral plasma membrane	C
GO:0016328	12	4.58E-01	1.00E+00	2.19E-01	1.00E+00	3.31E-01	1.00E+00	8.85E-01	1.00E+00	6.14E-01	1.00E+00	1.75E-01	1.00E+00	1.02E-01	1.00E+00	2.27E-01	1.00E+00	lateral plasma membrane	C

GO:0016331	54	5.57E-01	1.00E+00	5.28E-01	1.00E+00	5.62E-01	1.00E+00	7.09E-01	1.00E+00	4.11E-01	1.00E+00	5.48E-01	1.00E+00	8.12E-01	1.00E+00	1.38E-01	1.00E+00	morphogenesis of embryonic epithelium	P
GO:0016337	255	1.00E+00	1.00E+00	9.81E-01	1.00E+00	9.41E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	9.83E-01	1.00E+00	9.56E-01	1.00E+00	cell-cell adhesion	P
GO:0016338	21	2.14E-01	1.00E+00	7.65E-02	1.00E+00	3.65E-02	1.00E+00	3.03E-01	1.00E+00	2.57E-01	1.00E+00	4.03E-02	1.00E+00	7.25E-01	1.00E+00	3.46E-01	1.00E+00	calcium-independent cell-cell adhesion	P
GO:0016339	23	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.51E-01	1.00E+00	9.96E-01	1.00E+00	calcium-dependent cell-cell adhesion	P
GO:0016358	38	3.84E-01	1.00E+00	5.85E-01	1.00E+00	3.04E-01	1.00E+00	3.95E-01	1.00E+00	3.28E-01	1.00E+00	6.95E-01	1.00E+00	7.25E-01	1.00E+00	4.72E-01	1.00E+00	dendrite development	P
GO:0016363	46	1.63E-03	2.02E-01	3.36E-04	4.19E-02	1.29E-02	5.32E-01	4.56E-03	3.46E-01	2.12E-02	1.00E+00	5.63E-04	5.49E-02	1.02E-02	6.30E-01	4.07E-02	1.00E+00	nuclear matrix	C
GO:0016407	71	1.57E-04	2.50E-02	2.85E-04	4.19E-02	1.87E-02	1.00E+00	1.46E-01	1.00E+00	3.33E-04	1.98E-02	7.58E-04	5.49E-02	1.99E-02	9.11E-01	8.34E-04	9.16E-02	acetyltransferase activity	F
GO:0016408	12	1.78E-01	1.00E+00	9.08E-02	1.00E+00	5.86E-02	1.00E+00	3.15E-01	1.00E+00	2.53E-01	1.00E+00	1.74E-01	1.00E+00	8.96E-01	1.00E+00	1.39E-01	1.00E+00	C-acyltransferase activity	F
GO:0016409	14	2.67E-01	1.00E+00	4.91E-01	1.00E+00	6.74E-01	1.00E+00	5.12E-01	1.00E+00	1.76E-01	1.00E+00	5.13E-01	1.00E+00	3.98E-01	1.00E+00	3.11E-01	1.00E+00	palmitoyltransferase activity	F
GO:0016410	72	5.95E-04	3.37E-02	4.03E-04	6.90E-02	2.38E-02	1.00E+00	1.73E-01	1.00E+00	1.11E-03	7.80E-02	4.82E-04	4.10E-02	1.44E-02	6.47E-01	1.30E-03	9.16E-02	N-acyltransferase activity	F
GO:0016411	15	8.42E-02	1.00E+00	6.18E-01	1.00E+00	2.62E-01	1.00E+00	8.48E-01	1.00E+00	3.25E-02	1.00E+00	4.25E-01	1.00E+00	7.83E-01	1.00E+00	5.08E-01	1.00E+00	acylglycerol O-acyltransferase activity	F
GO:0016439	31	8.07E-01	1.00E+00	4.01E-01	1.00E+00	9.21E-01	1.00E+00	3.55E-01	1.00E+00	7.37E-01	1.00E+00	3.59E-01	1.00E+00	5.40E-01	1.00E+00	6.77E-01	1.00E+00	tRNA-pseudouridine synthase activity	F
GO:0016444	26	3.15E-01	1.00E+00	6.83E-02	1.00E+00	6.39E-01	1.00E+00	2.09E-01	1.00E+00	1.77E-01	1.00E+00	6.13E-02	1.00E+00	8.54E-01	1.00E+00	3.84E-01	1.00E+00	somatic cell DNA recombination	P
GO:0016445	29	3.06E-01	1.00E+00	9.50E-02	1.00E+00	5.29E-01	1.00E+00	2.63E-01	1.00E+00	1.72E-01	1.00E+00	7.11E-02	1.00E+00	9.36E-01	1.00E+00	5.50E-01	1.00E+00	somatic diversification of immunoglobulins	P
GO:0016447	26	3.15E-01	1.00E+00	6.83E-02	1.00E+00	6.39E-01	1.00E+00	2.09E-01	1.00E+00	1.77E-01	1.00E+00	6.13E-02	1.00E+00	8.54E-01	1.00E+00	3.84E-01	1.00E+00	somatic recombination of immunoglobulin g	P
GO:0016455	16	1.38E-02	6.67E-01	3.42E-02	1.00E+00	9.64E-03	4.60E-01	5.22E-02	1.00E+00	4.87E-02	1.00E+00	2.89E-02	1.00E+00	1.29E-01	1.00E+00	5.78E-01	1.00E+00	RNA polymerase II transcription mediator a	F
GO:0016458	31	1.50E-03	2.02E-01	8.86E-04	6.90E-02	2.94E-02	1.00E+00	1.26E-02	8.18E-01	2.73E-03	2.85E-01	8.29E-03	7.39E-01	1.88E-02	9.11E-01	1.21E-03	9.16E-02	gene silencing	P
GO:0016459	59	5.03E-01	1.00E+00	6.08E-03	3.60E-01	3.49E-01	1.00E+00	3.16E-02	1.00E+00	5.98E-01	1.00E+00	3.71E-03	2.70E-01	5.25E-01	1.00E+00	2.97E-01	1.00E+00	myosin complex	C
GO:0016462	767	2.92E-14	0.00E+00	1.39E-12	0.00E+00	1.06E-07	2.42E-03	6.62E-04	4.70E-02	2.65E-12	0.00E+00	1.16E-13	0.00E+00	3.21E-06	1.95E-03	1.00E-04	2.00E-02	pyrophosphatase activity	F
GO:0016469	51	1.49E-03	2.02E-01	2.35E-01	1.00E+00	3.84E-02	1.00E+00	3.43E-02	1.00E+00	2.13E-03	2.85E-01	4.34E-01	1.00E+00	4.20E-02	1.00E+00	5.55E-01	1.00E+00	proton-transporting two-sector ATPase com	C
GO:0016477	357	9.42E-01	1.00E+00	8.31E-01	1.00E+00	6.19E-01	1.00E+00	5.59E-01	1.00E+00	9.67E-01	1.00E+00	9.28E-01	1.00E+00	6.96E-01	1.00E+00	4.28E-01	1.00E+00	cell migration	P
GO:0016478	12	8.87E-02	1.00E+00	6.80E-03	3.60E-01	1.23E-01	1.00E+00	1.30E-01	1.00E+00	9.34E-02	1.00E+00	6.00E-03	3.51E-01	1.72E-01	1.00E+00	4.13E-02	1.00E+00	negative regulation of translation	P
GO:0016481	351	8.08E-07	1.95E-03	1.13E-06	8.39E-03	2.81E-03	2.48E-01	2.46E-04	2.70E-02	3.29E-07	1.69E-03	5.55E-06	4.00E-03	7.17E-02	1.00E+00	7.49E-03	4.81E-01	negative regulation of transcription	P
GO:0016485	107	1.06E-02	6.67E-01	2.46E-02	1.00E+00	7.45E-02	1.00E+00	1.50E-02	8.18E-01	1.29E-02	1.00E+00	2.12E-02	1.00E+00	3.91E-02	1.00E+00	7.81E-01	1.00E+00	protein processing	P
GO:0016491	896	1.59E-03	2.02E-01	8.61E-04	6.90E-02	6.88E-03	4.60E-01	3.71E-03	2.02E-01	1.34E-02	1.00E+00	2.99E-03	2.39E-01	4.96E-03	3.57E-01	9.13E-02	1.00E+00	oxidoreductase activity	F
GO:0016493	41	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	C-C chemokine receptor activity	F
GO:0016494	36	9.48E-01	1.00E+00	9.85E-01	1.00E+00	6.87E-01	1.00E+00	5.00E-01	1.00E+00	9.17E-01	1.00E+00	9.87E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	C-X-C chemokine receptor activity	F
GO:0016500	28	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	9.77E-01	1.00E+00	9.39E-01	1.00E+00	protein-hormone receptor activity	F
GO:0016502	136	9.97E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	9.88E-01	1.00E+00	9.49E-01	1.00E+00	9.96E-01	1.00E+00	nucleotide receptor activity	F
GO:0016503	12	3.61E-01	1.00E+00	4.19E-01	1.00E+00	3.29E-01	1.00E+00	9.95E-01	1.00E+00	4.11E-01	1.00E+00	2.80E-01	1.00E+00	2.19E-01	1.00E+00	1.43E-01	1.00E+00	pheromone receptor activity	F
GO:0016504	21	3.39E-02	1.00E+00	2.14E-01	1.00E+00	5.03E-02	1.00E+00	4.97E-01	1.00E+00	1.24E-01	1.00E+00	2.52E-01	1.00E+00	7.31E-02	1.00E+00	1.28E-01	1.00E+00	protease activator activity	F
GO:0016505	17	1.01E-02	6.67E-01	1.44E-01	1.00E+00	2.07E-02	1.00E+00	5.09E-01	1.00E+00	6.03E-02	1.00E+00	1.64E-01	1.00E+00	5.64E-02	1.00E+00	1.01E-01	1.00E+00	apoptotic protease activator activity	F
GO:0016525	20	4.35E-01	1.00E+00	4.28E-01	1.00E+00	3.09E-01	1.00E+00	4.63E-01	1.00E+00	4.23E-01	1.00E+00	4.36E-01	1.00E+00	7.20E-01	1.00E+00	2.06E-01	1.00E+00	negative regulation of angiogenesis	P
GO:0016527	10	7.36E-01	1.00E+00	9.95E-01	1.00E+00	5.64E-01	1.00E+00	9.98E-01	1.00E+00	8.83E-01	1.00E+00	9.56E-01	1.00E+00	3.16E-01	1.00E+00	9.26E-01	1.00E+00	brain-specific angiogenesis inhibitor activity	F
GO:0016528	17	6.04E-01	1.00E+00	7.04E-01	1.00E+00	8.15E-01	1.00E+00	4.49E-01	1.00E+00	3.93E-01	1.00E+00	8.02E-01	1.00E+00	9.09E-01	1.00E+00	6.06E-01	1.00E+00	sarcoplasm	C
GO:0016529	14	4.91E-01	1.00E+00	4.51E-01	1.00E+00	7.32E-01	1.00E+00	3.17E-01	1.00E+00	3.30E-01	1.00E+00	4.86E-01	1.00E+00	8.22E-01	1.00E+00	5.95E-01	1.00E+00	sarcoplasmic reticulum	C
GO:0016540	63	1.39E-02	6.67E-01	1.40E-02	7.47E-01	1.58E-01	1.00E+00	1.41E-02	8.18E-01	1.85E-02	1.00E+00	1.17E-02	7.39E-01	7.17E-03	5.44E-01	6.14E-01	1.00E+00	protein autoprocessing	P
GO:0016558	10	1.35E-01	1.00E+00	1.05E-01	1.00E+00	2.46E-01	1.00E+00	2.40E-01	1.00E+00	1.57E-01	1.00E+00	6.20E-02	1.00E+00	1.71E-01	1.00E+00	2.12E-01	1.00E+00	protein import into peroxisome matrix	P
GO:0016563	329	6.67E-07	1.95E-03	4.40E-07	8.39E-03	2.36E-06	2.42E-03	2.44E-04	2.70E-02	4.83E-06	2.60E-03	5.34E-06	4.00E-03	7.11E-02	1.00E+00	4.96E-03	3.60E-01	transcriptional activator activity	F
GO:0016564	243	5.87E-04	3.37E-02	1.41E-03	9.10E-02	7.77E-03	4.60E-01	7.95E-03	4.55E-01	2.63E-04	1.70E-02	6.14E-03	3.51E-01	5.27E-01	1.00E+00	2.18E-02	1.00E+00	transcriptional repressor activity	F
GO:0016566	21	6.11E-01	1.00E+00	9.62E-01	1.00E+00	8.19E-01	1.00E+00	9.99E-01	1.00E+00	5.54E-01	1.00E+00	8.27E-01	1.00E+00	3.79E-01	1.00E+00	8.09E-01	1.00E+00	specific transcriptional repressor activity	F
GO:0016567	104	3.38E-03	2.73E-01	1.97E-03	1.29E-01	5.46E-03	4.19E-01	3.96E-02	1.00E+00	1.85E-02	1.00E+00	7.84E-04	5.49E-02	3.53E-01	1.00E+00	2.65E-01	1.00E+00	protein ubiquitination	P
GO:0016568	211	1.15E-11	0.00E+00	4.29E-17	0.00E+00	1.41E-06	2.42E-03	1.12E-07	1.96E-03	1.44E-11	0.00E+00	1.53E-15	0.00E+00	1.18E-02	6.30E-01	1.01E-06	1.88E-03	chromatin modification	P
GO:0016569	56	3.22E-04	3.37E-02	2.34E-05	9.58E-03	6.00E-03	4.60E-01	1.93E-03	1.24E-01	4.39E-04	2.20E-02	3.56E-05	1.20E-02	1.08E-01	1.00E+00	2.55E-03	1.85E-01	covalent chromatin modification	P
GO:0016570	53	1.23E-03	2.02E-01	1.55E-04	1.50E-02	1.11E-02	5.32E-01	6.35E-03	3.64E-01	1.70E-03	1.76E-01	1.20E-04	1.70E-02	1.92E-01	1.00E+00	1.26E-02	6.47E-01	histone modification	P
GO:0016571	15	1.22E-02	6.67E-01	3.26E-03	1.97E-01	2.83E-01	1.00E+00	3.70E-03	2.02E-01	9.37E-03	5.39E-01	1.21E-02	7.39E-01	1.58E-01	1.00E+00	6.65E-02	1.00E+00	histone methylation	P
GO:0016573	14	5.13E-03	3.28E-01	3.91E-04	6.90E-02	2.01E-02	1.00E+00	4.32E-02	1.00E+00	6.11E-03	5.39E-01	5.81E-04	5.49E-02	2.93E-01	1.00E+00	1.17E-02	6.47E-01	histone acetylation	P
GO:0016575	14	2.28E-01	1.00E+00	2.43E-01	1.00E+00	4.78E-02	1.00E+00	4.54E-01	1.00E+00	4.60E-01	1.00E+00	9.38E-02	1.00E+00	3.83E-01	1.00E+00	7.75E-01	1.00E+00	histone deacetylation	P
GO:0016585	31	2.69E-02	1.00E+00	4.91E-03	3.60E-01	2.10E-01	1.00E+00	1.28E-03	1.15E-01	7.43E-03	5.39E-01	1.88E-02	1.00E+00	1.76E-01	1.00E+00	1.76E-02	1.00E+00	chromatin remodeling complex	C
GO:0016591	95	2.25E-07	1.95E-03	6.18E-07	8.39E-03	1.03E-04	1.20E-02	6.83E-05	1.20E-02	8.48E-06	2.88E-03	2.02E-06	2.97E-03	5.17E-04	6.50E-02	1.62E-01	1.00E+00	DNA-directed RNA polymerase II, holoenzy	C
GO:0016597	20	8.73E-01	1.00E+00	9.25E-01	1.00E+00	5.55E-01	1.00E+00	9.15E-01	1.00E+00	9.73E-01	1.00E+00	9.48E-01	1.00E+00	2.95E-01	1.00E+00	4.34E-01	1.00E+00	amino acid binding	F
GO:0016599	16	4.57E-02	1.00E+00	4.19E-01	1.00E+00	4.25E-02	1.00E+00	9.31E-01	1.00E+00	9.48E-02	1.00E+00	4.51E-01	1.00E+00	5.25E-02	1.00E+00	1.51E-01	1.00E+00	caveolar membrane	C
GO:0016601	14	2.73E-01	1.00E+00	8.01E-01	1.00E+00	3.17E-01	1.00E+00	7.70E-01	1.00E+00	1.95E-01	1.00E+00	8.45E-01	1.00E+00	8.66E-01	1.00E+00	3.44E-01	1.00E+00	Rac protein signal transduction	P
GO:0016604	120	1.37E-09	8.06E-04	2.72E-08	4.97E-03	1.11E-05	3.00E-03	2.66E-04	2.70E-02	1.09E-08	9.64E-04	8.31E-08	8.37E-04	3.79E-02	1.00E+00	1.93E-03	1.40E-01	nuclear body	C
GO:0016605	21	2.11E-02	1.00E+00	1.33E-03	9.10E-02	3.83E-02	1.00E+00	1.38E-02	8.18E-01	1.01E-02	5.39E-01	1.07E-03	5.49E-02	8.40E-01	1.00E+00	2.59E-01	1.00E+00	PML body	C
GO:0016607	83	3.30E-07	1.95E-03	2.16E-05	9.58E-03	6.97E-04	4.50E-02	1.01E-03	8.30E-02	2.36E-06	2.60E-03	1.93E-04	2.60E-02	1.43E-02	6.47E-01	1.47E-03	9.16E-02	nuclear speck	C
GO:0016614	151	2.59E-01	1.00E+00	2.55E-01	1.00E+00	1.30E-01	1.00E+00	9.40E-02	1.00E+00	6.48E-01	1.00E+00	4.96E-01	1.00E+00	4.27E-02	1.00E+00	7.72E-02	1.00E+00	oxidoreductase activity, acting on CH-OH g	F
GO:0016616	134	2.32E-01	1.00E+00	3.65E-01	1.00E+00	9.87E-02	1.00E+00	1.77E-01	1.00E+00	6.26E-01	1.00E+00	5.34E-01	1.00E+00	4.81E-02	1.00E+00	1.27E-01	1.00E+00	oxidoreductase activity, acting on the CH-O	F
GO:0016620	23	4.37E-03	3.28E-01	4.43E-01	1.00E+00	1.12E-02	5.32E-01	4.35E-01	1.00E+00	1.07E-02	5.39E-01	3.20E-01	1.00E+00	4.13E-01	1.00E+00	8.02E-01	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016627	91	2.78E-01	1.00E+00	4.38E-01	1.00E+00	2.37E-01	1.00E+00	2.40E-01	1.00E+00	3.27E-01	1.00E+00	5.15E-01	1.00E+00	4.29E-01	1.00E+00	4.20E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016628	57	3.75E-01	1.00E+00	4.50E-01	1.00E+00	3.21E-01	1.00E+00	2.09E-01	1.00E+00	4.31E-01	1.00E+00	6.06E-01	1.00E+00	4.18E-01	1.00E+00	2.40E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016634	10	4.40E-01	1.00E+00	5.96E-01	1.00E+00	5.98E-01	1.00E+00	5.20E-01	1.00E+00	3.36E-01	1.00E+00	5.66E-01	1.00E+00	4.72E-01	1.00E+00	6.32E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016638	17	2.70E-01	1.00E+00	1.50E-01	1.00E+00	8.99E-01	1.00E+00	3.03E-01	1.00E+00	1.81E-01	1.00E+00	9.70E-02	1.00E+00	2.25E-01	1.00E+00	5.09E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016641	14	4.02E-01	1.00E+00	2.76E-01	1.00E+00	8.89E-01	1.00E+00	4.53E-01	1.00E+00	3.00E-01	1.00E+00	1.98E-01	1.00E+00	2.80E-01	1.00E+00	5.54E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016645	29	1.47E-01	1.00E+00	2.93E-02	1.00E+00	1.68E-01	1.00E+00	4.56E-03	3.46E-01	1.55E-01	1.00E+00	7.35E-02	1.00E+00	5.01E-01	1.00E+00	7.00E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016646	19	1.56E-01	1.00E+00	4.22E-02	1.00E+00	1.84E-01	1.00E+00	1.93E-02	1.00E+00	1.55E-01	1.00E+00	5.26E-02	1.00E+00	5.69E-01	1.00E+00	7.21E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016651	75	1.90E-03	2.02E-01	1.88E-02	1.00E+00	5.15E-02	1.00E+00	1.15E-01	1.00E+00	2.64E-03	2.85E-01	4.98E-02	1.00E+00	1.80E-02	9.11E-01	3.00E-02	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016652	10	2.21E-02	1.00E+00	3.15E-02	1.00E+00	5.15E-02	1.00E+00	9.23E-02	1.00E+00	2.26E-02	1.00E+00	1.33E-02	7.39E-01	7.20E-02	1.00E+00	1.77E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016655	50	3.95E-03	3.28E-01	4.12E-02	1.00E+00	7.27E-02	1.00E+00	1.20E-01	1.00E+00	6.50E-03	5.39E-01	1.09E-01	1.00E+00	4.79E-02	1.00E+00	6.04E-02	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016667	20	2.06E-02	1.00E+00	1.16E-01	1.00E+00	9.67E-02	1.00E+00	3.09E-01	1.00E+00	7.74E-02	1.00E+00	2.00E-01	1.00E+00	1.33E-02	6.30E-01	7.99E-02	1.00E+00	oxidoreductase activity, acting on sulfur gro	F
GO:0016675	28	2.16E-01	1.00E+00	6.64E-02	1.00E+00	1.17E-01	1.00E+00	1.83E-01	1.00E+00	2.84E-01	1.00E+00	7.30E-02	1.00E+00	8.97E-01	1.00E+00	1.47E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016676	28	2.16E-01	1.00E+00	6.64E-02	1.00E+00	1.17E-01	1.00E+00	1.83E-01	1.00E+00	2.84E-01	1.00E+00	7.30E-02	1.00E+00	8.97E-01	1.00E+00	1.47E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016679	12	2.40E-02	1.00E+00	2.46E-01	1.00E+00	2.93E-02	1.00E+00	2.53E-01	1.00E+00	3.39E-02	1.00E+00	2.13E-01	1.00E+00	3.61E-01	1.00E+00	5.89E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F
GO:0016681	12	2.40E-02	1.00E+00	2.46E-01	1.00E+00	2.93E-02	1.00E+00	2.53E-01	1.00E+00	3.39E-02	1.00E+00	2.13E-01	1.00E+00	3.61E-01	1.00E+00	5.89E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F
GO:0016684	47	7.16E-01	1.00E+00	7.96E-01	1.00E+00	6.76E-01	1.00E+00	6.84E-01	1.00E+00	5.11E-01	1.00E+00	8.59E-01	1.00E+00	9.88E-01	1.00E+00	6.52E-01	1.00E+00	oxidoreductase activity, acting on peroxide a	F

GO:0016701	62	3.36E-02	1.00E+00	8.87E-04	6.90E-02	1.40E-02	6.93E-01	2.64E-01	1.00E+00	1.44E-01	1.00E+00	3.60E-04	3.07E-02	1.11E-01	1.00E+00	3.70E-02	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016702	61	3.65E-02	1.00E+00	7.81E-04	6.90E-02	1.02E-02	4.60E-01	2.31E-01	1.00E+00	1.66E-01	1.00E+00	2.53E-04	2.60E-02	1.24E-01	1.00E+00	5.50E-02	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016705	135	9.16E-01	1.00E+00	8.06E-01	1.00E+00	6.82E-01	1.00E+00	9.92E-01	1.00E+00	9.11E-01	1.00E+00	4.58E-01	1.00E+00	7.47E-01	1.00E+00	9.46E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016706	26	7.21E-02	1.00E+00	1.04E-03	9.10E-02	3.97E-02	1.00E+00	9.23E-02	1.00E+00	1.16E-01	1.00E+00	2.47E-04	2.60E-02	3.42E-01	1.00E+00	1.68E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016709	35	8.93E-01	1.00E+00	8.74E-01	1.00E+00	9.53E-01	1.00E+00	8.94E-01	1.00E+00	8.18E-01	1.00E+00	6.72E-01	1.00E+00	6.32E-01	1.00E+00	9.95E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016712	40	9.34E-01	1.00E+00	9.94E-01	1.00E+00	8.71E-01	1.00E+00	1.00E+00	1.00E+00	9.16E-01	1.00E+00	8.51E-01	1.00E+00	7.35E-01	1.00E+00	9.82E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016740	1848	5.13E-19	0.00E+00	3.48E-25	0.00E+00	6.16E-09	9.34E-04	6.96E-14	0.00E+00	1.58E-18	0.00E+00	2.12E-20	0.00E+00	1.97E-04	3.40E-02	6.61E-10	7.71E-04	transferase activity	F
GO:0016741	189	1.47E-08	9.77E-04	1.82E-05	9.58E-03	5.29E-04	3.60E-02	1.36E-02	8.18E-01	3.57E-08	9.64E-04	1.07E-04	1.70E-02	3.99E-03	3.57E-01	5.32E-03	3.60E-01	transferase activity, transferring one-carbon	F
GO:0016746	205	2.48E-06	1.95E-03	4.16E-04	6.90E-02	8.50E-04	7.56E-02	1.36E-01	1.00E+00	2.80E-06	2.60E-03	4.27E-04	4.10E-02	1.79E-02	9.11E-01	2.02E-02	1.00E+00	transferase activity, transferring acyl groups	F
GO:0016747	191	1.85E-06	1.95E-03	4.71E-04	6.90E-02	1.08E-03	9.80E-02	1.38E-01	1.00E+00	1.47E-06	2.60E-03	4.54E-04	4.10E-02	2.08E-02	9.11E-01	2.58E-02	1.00E+00	transferase activity, transferring groups othe	F
GO:0016755	24	3.84E-01	1.00E+00	5.57E-01	1.00E+00	4.05E-01	1.00E+00	9.63E-01	1.00E+00	3.61E-01	1.00E+00	3.60E-01	1.00E+00	5.74E-01	1.00E+00	4.13E-01	1.00E+00	transferase activity, transferring amino-acyl	F
GO:0016757	256	7.91E-01	1.00E+00	1.46E-01	1.00E+00	9.19E-01	1.00E+00	2.38E-01	1.00E+00	5.62E-01	1.00E+00	7.39E-02	1.00E+00	8.34E-01	1.00E+00	7.19E-01	1.00E+00	transferase activity, transferring glycosyl gro	F
GO:0016758	172	8.42E-01	1.00E+00	2.69E-01	1.00E+00	9.23E-01	1.00E+00	5.73E-01	1.00E+00	5.25E-01	1.00E+00	1.07E-01	1.00E+00	9.86E-01	1.00E+00	8.33E-01	1.00E+00	transferase activity, transferring hexosyl gro	F
GO:0016763	49	5.69E-02	1.00E+00	3.37E-02	1.00E+00	1.96E-01	1.00E+00	2.51E-03	1.47E-01	1.21E-01	1.00E+00	1.02E-01	1.00E+00	9.31E-02	1.00E+00	5.20E-01	1.00E+00	transferase activity, transferring pentosyl gr	F
GO:0016765	49	5.03E-01	1.00E+00	1.29E-01	1.00E+00	2.44E-01	1.00E+00	1.83E-01	1.00E+00	6.57E-01	1.00E+00	2.37E-01	1.00E+00	5.96E-01	1.00E+00	7.91E-02	1.00E+00	transferase activity, transferring alkyl or aryl	F
GO:0016769	30	4.51E-03	3.28E-01	6.69E-02	1.00E+00	6.46E-03	4.60E-01	2.45E-01	1.00E+00	1.14E-02	5.39E-01	1.19E-01	1.00E+00	3.19E-01	1.00E+00	2.14E-02	1.00E+00	transferase activity, transferring nitrogenous	F
GO:0016772	1054	2.59E-12	0.00E+00	5.86E-20	0.00E+00	2.64E-06	2.42E-03	5.96E-13	0.00E+00	1.66E-11	0.00E+00	1.26E-15	0.00E+00	1.84E-03	1.95E-01	4.93E-08	1.88E-03	transferase activity, transferring phosphorus	F
GO:0016773	809	2.52E-06	1.95E-03	2.54E-13	0.00E+00	1.34E-03	9.80E-02	2.51E-09	0.00E+00	1.76E-06	2.60E-03	2.57E-10	0.00E+00	7.89E-02	1.00E+00	8.21E-06	1.88E-03	phosphotransferase activity, alcohol group a	F
GO:0016775	18	1.20E-01	1.00E+00	4.45E-01	1.00E+00	4.63E-02	1.00E+00	8.60E-01	1.00E+00	1.86E-01	1.00E+00	4.38E-01	1.00E+00	5.19E-01	1.00E+00	5.77E-02	1.00E+00	phosphotransferase activity, nitrogenous gr	F
GO:0016776	38	3.93E-02	1.00E+00	1.80E-02	1.00E+00	1.12E-01	1.00E+00	2.40E-03	1.47E-01	5.71E-02	1.00E+00	1.86E-01	1.00E+00	1.31E-01	1.00E+00	5.02E-02	1.00E+00	phosphotransferase activity, phosphate gro	F
GO:0016779	127	1.14E-05	7.00E-03	2.08E-05	9.58E-03	8.34E-03	4.60E-01	1.48E-04	1.70E-02	1.61E-05	4.19E-03	1.13E-04	1.70E-02	6.17E-02	1.00E+00	7.82E-02	1.00E+00	nucleotidyltransferase activity	F
GO:0016780	17	3.06E-01	1.00E+00	3.28E-01	1.00E+00	6.66E-01	1.00E+00	1.38E-01	1.00E+00	1.71E-01	1.00E+00	6.12E-01	1.00E+00	5.61E-01	1.00E+00	3.00E-01	1.00E+00	phosphotransferase activity, for other substi	F
GO:0016782	54	6.97E-01	1.00E+00	4.62E-01	1.00E+00	2.74E-01	1.00E+00	5.85E-01	1.00E+00	6.80E-01	1.00E+00	4.40E-01	1.00E+00	8.76E-01	1.00E+00	3.79E-01	1.00E+00	transferase activity, transferring sulfur-conta	F
GO:0016787	2486	3.40E-21	0.00E+00	1.81E-23	0.00E+00	3.42E-12	0.00E+00	1.20E-09	0.00E+00	8.93E-19	0.00E+00	5.32E-22	0.00E+00	2.60E-06	1.95E-03	7.25E-09	7.71E-04	hydrolase activity	F
GO:0016788	726	3.26E-07	1.95E-03	2.90E-08	4.97E-03	1.53E-05	3.72E-03	6.34E-05	1.20E-02	3.92E-06	2.60E-03	2.53E-07	9.41E-04	2.80E-02	1.00E+00	1.28E-03	9.16E-02	hydrolase activity, acting on ester bonds	F
GO:0016789	148	1.90E-01	1.00E+00	3.31E-01	1.00E+00	2.84E-02	1.00E+00	5.95E-01	1.00E+00	3.84E-01	1.00E+00	4.09E-01	1.00E+00	2.93E-01	1.00E+00	7.14E-02	1.00E+00	carboxylic ester hydrolase activity	F
GO:0016790	100	4.22E-02	1.00E+00	2.79E-03	1.77E-01	1.74E-01	1.00E+00	3.65E-03	2.02E-01	2.30E-02	1.00E+00	1.02E-02	7.39E-01	3.55E-01	1.00E+00	1.07E-01	1.00E+00	thiolester hydrolase activity	F
GO:0016791	272	8.75E-05	1.24E-02	4.75E-08	4.97E-03	1.30E-02	5.32E-01	1.10E-04	1.20E-02	2.79E-04	1.70E-02	6.07E-07	2.97E-03	6.14E-03	3.57E-01	1.60E-04	2.00E-02	phosphoric monoester hydrolase activity	F
GO:0016796	22	1.10E-01	1.00E+00	5.64E-01	1.00E+00	7.78E-02	1.00E+00	5.07E-01	1.00E+00	1.55E-01	1.00E+00	7.39E-01	1.00E+00	3.89E-01	1.00E+00	2.59E-01	1.00E+00	exonuclease activity, active with either ribo-	F
GO:0016798	155	1.09E-01	1.00E+00	7.60E-02	1.00E+00	4.21E-01	1.00E+00	1.64E-01	1.00E+00	7.24E-02	1.00E+00	8.96E-02	1.00E+00	2.04E-01	1.00E+00	2.47E-01	1.00E+00	hydrolase activity, acting on glycosyl bonds	F
GO:0016799	20	3.55E-01	1.00E+00	5.88E-01	1.00E+00	3.03E-01	1.00E+00	1.69E-01	1.00E+00	3.21E-01	1.00E+00	6.52E-01	1.00E+00	7.74E-01	1.00E+00	8.37E-01	1.00E+00	hydrolase activity, hydrolyzing N-glycosyl co	F
GO:0016805	13	4.20E-02	1.00E+00	2.79E-02	1.00E+00	9.76E-02	1.00E+00	5.59E-02	1.00E+00	5.39E-02	1.00E+00	1.88E-01	1.00E+00	1.07E-01	1.00E+00	1.59E-01	1.00E+00	dipeptidase activity	F
GO:0016806	12	5.22E-01	1.00E+00	2.44E-01	1.00E+00	7.69E-01	1.00E+00	3.63E-01	1.00E+00	6.81E-01	1.00E+00	2.30E-01	1.00E+00	1.44E-01	1.00E+00	2.21E-01	1.00E+00	dipeptidyl-peptidase and tripeptidyl-peptidas	F
GO:0016810	120	2.69E-02	1.00E+00	9.26E-02	1.00E+00	2.20E-01	1.00E+00	6.54E-01	1.00E+00	9.32E-03	5.39E-01	2.99E-02	1.00E+00	4.12E-01	1.00E+00	2.76E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016811	57	3.49E-02	1.00E+00	1.56E-01	1.00E+00	3.35E-01	1.00E+00	9.14E-01	1.00E+00	1.02E-02	5.39E-01	1.05E-01	1.00E+00	4.22E-01	1.00E+00	2.13E-02	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016812	11	9.79E-01	1.00E+00	8.72E-01	1.00E+00	7.20E-01	1.00E+00	5.76E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	6.59E-01	1.00E+00	8.99E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016813	13	2.07E-01	1.00E+00	1.70E-01	1.00E+00	1.59E-01	1.00E+00	1.53E-01	1.00E+00	2.90E-01	1.00E+00	1.57E-01	1.00E+00	3.75E-01	1.00E+00	5.43E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016814	32	3.41E-02	1.00E+00	8.05E-02	1.00E+00	2.99E-01	1.00E+00	4.30E-01	1.00E+00	2.14E-02	1.00E+00	2.27E-02	1.00E+00	2.06E-01	1.00E+00	8.98E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016817	773	2.00E-14	0.00E+00	5.58E-13	0.00E+00	8.67E-08	2.42E-03	4.19E-04	4.20E-02	1.60E-12	0.00E+00	5.78E-14	0.00E+00	3.63E-06	2.00E-03	6.84E-05	9.00E-03	hydrolase activity, acting on acid anhydrides	F
GO:0016818	771	3.47E-14	0.00E+00	1.31E-12	0.00E+00	1.26E-07	2.42E-03	5.07E-04	4.70E-02	2.61E-12	0.00E+00	1.32E-13	0.00E+00	4.08E-06	2.00E-03	1.11E-04	2.00E-02	hydrolase activity, acting on acid anhydrides	F
GO:0016820	130	7.99E-02	1.00E+00	1.62E-01	1.00E+00	5.02E-01	1.00E+00	1.88E-01	1.00E+00	2.07E-02	1.00E+00	2.53E-01	1.00E+00	6.94E-01	1.00E+00	2.27E-01	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016829	165	6.51E-02	1.00E+00	1.50E-02	1.00E+00	4.11E-03	3.27E-01	1.78E-02	1.00E+00	1.56E-01	1.00E+00	2.09E-02	1.00E+00	6.28E-01	1.00E+00	5.30E-01	1.00E+00	lyase activity	F
GO:0016830	45	2.14E-01	1.00E+00	1.43E-01	1.00E+00	3.87E-02	1.00E+00	1.68E-01	1.00E+00	3.17E-01	1.00E+00	1.50E-01	1.00E+00	7.94E-01	1.00E+00	4.69E-01	1.00E+00	carbon-carbon lyase activity	F
GO:0016831	33	3.30E-01	1.00E+00	1.76E-01	1.00E+00	1.18E-01	1.00E+00	1.16E-01	1.00E+00	4.04E-01	1.00E+00	3.35E-01	1.00E+00	8.10E-01	1.00E+00	1.73E-01	1.00E+00	carboxy-lyase activity	F
GO:0016835	57	2.76E-02	1.00E+00	9.71E-02	1.00E+00	2.78E-02	1.00E+00	4.27E-02	1.00E+00	6.28E-02	1.00E+00	1.06E-01	1.00E+00	2.05E-01	1.00E+00	6.87E-01	1.00E+00	carbon-oxygen lyase activity	F
GO:0016836	48	1.88E-02	1.00E+00	4.13E-02	1.00E+00	1.16E-02	5.32E-01	3.30E-02	1.00E+00	7.00E-02	1.00E+00	5.54E-02	1.00E+00	1.10E-01	1.00E+00	4.26E-01	1.00E+00	hydro-lyase activity	F
GO:0016846	16	1.21E-01	1.00E+00	5.88E-01	1.00E+00	1.54E-02	6.93E-01	8.70E-01	1.00E+00	1.92E-01	1.00E+00	5.01E-01	1.00E+00	4.99E-01	1.00E+00	4.54E-01	1.00E+00	carbon-sulfur lyase activity	F
GO:0016849	21	9.90E-01	1.00E+00	2.55E-01	1.00E+00	9.85E-01	1.00E+00	3.43E-01	1.00E+00	9.54E-01	1.00E+00	2.03E-01	1.00E+00	8.59E-01	1.00E+00	4.81E-01	1.00E+00	phosphorus-oxygen lyase activity	F
GO:0016853	192	5.04E-02	1.00E+00	1.32E-01	1.00E+00	1.56E-01	1.00E+00	1.36E-01	1.00E+00	9.86E-02	1.00E+00	2.50E-01	1.00E+00	4.97E-02	1.00E+00	1.20E-01	1.00E+00	isomerase activity	F
GO:0016854	17	5.71E-01	1.00E+00	8.46E-01	1.00E+00	4.98E-01	1.00E+00	8.51E-01	1.00E+00	7.05E-01	1.00E+00	9.35E-01	1.00E+00	2.55E-01	1.00E+00	3.10E-01	1.00E+00	racemase and epimerase activity	F
GO:0016857	10	4.92E-01	1.00E+00	6.41E-01	1.00E+00	6.39E-01	1.00E+00	8.24E-01	1.00E+00	4.57E-01	1.00E+00	7.78E-01	1.00E+00	6.81E-01	1.00E+00	1.97E-01	1.00E+00	racemase and epimerase activity, acting on	F
GO:0016859	45	1.39E-02	6.67E-01	7.98E-02	1.00E+00	3.06E-02	1.00E+00	3.12E-01	1.00E+00	5.89E-02	1.00E+00	6.28E-02	1.00E+00	7.21E-03	5.44E-01	3.78E-01	1.00E+00	cis-trans isomerase activity	F
GO:0016860	40	5.23E-01	1.00E+00	2.04E-01	1.00E+00	8.18E-01	1.00E+00	2.89E-01	1.00E+00	5.37E-01	1.00E+00	2.12E-01	1.00E+00	2.64E-01	1.00E+00	2.94E-01	1.00E+00	intramolecular oxidoreductase activity	F
GO:0016861	11	6.25E-01	1.00E+00	5.45E-01	1.00E+00	2.38E-01	1.00E+00	5.00E-01	1.00E+00	7.94E-01	1.00E+00	6.68E-01	1.00E+00	5.93E-01	1.00E+00	3.74E-01	1.00E+00	intramolecular oxidoreductase activity, inter	F
GO:0016862	10	2.35E-01	1.00E+00	1.40E-01	1.00E+00	3.15E-01	1.00E+00	8.64E-02	1.00E+00	3.93E-01	1.00E+00	2.21E-01	1.00E+00	3.14E-01	1.00E+00	7.99E-01	1.00E+00	intramolecular oxidoreductase activity, inter	F
GO:0016863	12	6.61E-01	1.00E+00	7.83E-01	1.00E+00	1.00E+00	1.00E+00	7.58E-01	1.00E+00	3.29E-01	1.00E+00	7.57E-01	1.00E+00	2.41E-01	1.00E+00	3.54E-01	1.00E+00	intramolecular oxidoreductase activity, trans	F
GO:0016866	55	6.79E-01	1.00E+00	7.65E-01	1.00E+00	6.94E-01	1.00E+00	4.26E-01	1.00E+00	4.65E-01	1.00E+00	8.54E-01	1.00E+00	9.89E-01	1.00E+00	4.20E-01	1.00E+00	intramolecular transferase activity	F
GO:0016868	16	4.64E-01	1.00E+00	8.92E-01	1.00E+00	4.98E-01	1.00E+00	5.84E-01	1.00E+00	2.44E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	4.42E-01	1.00E+00	intramolecular transferase activity, phospho	F
GO:0016874	423	2.04E-09	8.06E-04	3.83E-11	0.00E+00	3.73E-06	2.66E-03	1.15E-05	8.00E-03	2.31E-09	9.64E-04	1.33E-10	0.00E+00	2.20E-01	1.00E+00	3.62E-04	2.70E-02	ligase activity	F
GO:0016875	73	1.46E-03	2.02E-01	4.95E-03	3.60E-01	9.69E-03	4.60E-01	7.68E-02	1.00E+00	2.90E-03	2.85E-01	7.36E-03	5.30E-01	1.06E-01	1.00E+00	9.87E-02	1.00E+00	ligase activity, forming carbon-oxygen bond	F
GO:0016876	73	1.46E-03	2.02E-01	4.95E-03	3.60E-01	9.69E-03	4.60E-01	7.68E-02	1.00E+00	2.90E-03	2.85E-01	7.36E-03	5.30E-01	1.06E-01	1.00E+00	9.87E-02	1.00E+00	ligase activity, forming aminoacyl-tRNA and	F
GO:0016877	27	9.83E-01	1.00E+00	6.70E-01	1.00E+00	9.76E-01	1.00E+00	9.33E-01	1.00E+00	9.54E-01	1.00E+00	3.46E-01	1.00E+00	8.71E-01	1.00E+00	8.07E-01	1.00E+00	ligase activity, forming carbon-sulfur bonds	F
GO:0016878	18	9.97E-01	1.00E+00	5.18E-01	1.00E+00	9.68E-01	1.00E+00	9.62E-01	1.00E+00	9.91E-01	1.00E+00	2.28E-01	1.00E+00	8.99E-01	1.00E+00	5.03E-01	1.00E+00	acid-thiol ligase activity	F
GO:0016879	237	1.22E-06	1.95E-03	1.86E-08	4.97E-03	2.57E-03	2.48E-01	7.24E-05	1.20E-02	1.22E-07	1.69E-03	1.38E-07	9.20E-04	4.59E-01	1.00E+00	4.39E-03	3.60E-01	ligase activity, forming carbon-nitrogen bon	F
GO:0016881	198	1.14E-07	1.85E-03	1.70E-08	4.97E-03	2.39E-04	2.40E-02	7.25E-05	1.20E-02	1.51E-07	1.69E-03	1.67E-07	9.20E-04	9.50E-02	1.00E+00	1.90E-03	1.40E-01	acid-amino acid ligase activity	F
GO:0016884	10	5.08E-01	1.00E+00	7.51E-01	1.00E+00	6.14E-01	1.00E+00	9.93E-01	1.00E+00	2.99E-01	1.00E+00	5.47E-01	1.00E+00	9.98E-01	1.00E+00	4.45E-01	1.00E+00	carbon-nitrogen ligase activity, with glutamir	F
GO:0016887	359	6.92E-07	1.95E-03	1.23E-06	8.39E-03	6.63E-05	1.20E-02	1.67E-03	1.24E-01	3.76E-06	2.60E-03	1.96E-06	2.97E-03	8.60E-02	1.00E+00	1.83E-02	1.00E+00	ATPase activity	F
GO:0016891	23	1.05E-01	1.00E+00	1.53E-02	1.00E+00	1.75E-01	1.00E+00	7.00E-02	1.00E+00	1.01E-01	1.00E+00	2.50E-02	1.00E+00	8.28E-01	1.00E+00	2.13E-01	1.00E+00	endoribonuclease activity, producing 5'-pho	F
GO:0016892	19	9.85E-01	1.00E+00	4.98E-01	1.00E+00	9.85E-01	1.00E+00	9.86E-01	1.00E+00	7.87E-01	1.00E+00	9.94E-02	1.00E+00	9.25E-01	1.00E+00	8.05E-01	1.00E+00	endoribonuclease activity, producing 3'-pho	F
GO:0016893	29	4.92E-02	1.00E+00	1.94E-02	1.00E+00	5.32E-02	1.00E+00	9.25E-02	1.00E+00	7.16E-02	1.00E+00	5.27E-02	1.00E+00	6.98E-01	1.00E+00	5.72E-02	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016894	21	8.57E-01	1.00E+00	5.30E-01	1.00E+00	9.47E-01	1.00E+00	9.50E-01	1.00E+00	4.92E-01	1.00E+00	1.53E-01	1.00E+00	9.70E-01	1.00E+00	8.91E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016895	10	9.65E-01	1.00E+00	9.06E-01	1.00E+00	3.21E-01	1.00E+00	6.09E-01	1.00E+00	1.00E+00	1.00E+00	8.95E-01	1.00E+00	8.74E-01	1.00E+00	8.86E-01	1.00E+00	exodeoxyribonuclease activity, producing 5'	F
GO:0016896	13	7.43E-03	6.34E-01	2.04E-01	1.00E+00	6.29E-02	1.00E+00	2.27E-01	1.00E+00	8.49E-03	5.39E-01	4.99E-01	1.00E+00	1.08E-01	1.00E+00	1.17E-01	1.00E+00	exoribonuclease activity, producing 5'-phos	F
GO:0016903	32	1.38E-02	6.67E-01	3.34E-01	1.00E+00	1.58E-02	6.93E-01	3.17E-01	1.00E+00	2.91E-02	1.00E+00	2.81E-01	1.00E+00	3.47E-01	1.00E+00	7.94E-01	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016917	56	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.96E-01	1.00E+00	5.53E-01	1.00E+00	9.98E-01	1.00E+00	GABA receptor activity	F

GO:0016918	12	5.47E-01	1.00E+00	6.04E-01	1.00E+00	7.29E-01	1.00E+00	9.50E-01	1.00E+00	6.09E-01	1.00E+00	4.18E-01	1.00E+00	1.50E-01	1.00E+00	5.69E-01	1.00E+00	retinal binding	F
GO:0016986	27	3.83E-03	3.28E-01	7.81E-03	3.60E-01	6.37E-02	1.00E+00	2.17E-01	1.00E+00	4.74E-03	4.18E-01	1.22E-02	7.39E-01	2.20E-01	1.00E+00	2.62E-03	1.85E-01	transcription initiation factor activity	F
GO:0016998	17	8.04E-01	1.00E+00	5.65E-01	1.00E+00	7.61E-01	1.00E+00	3.66E-01	1.00E+00	9.06E-01	1.00E+00	7.27E-01	1.00E+00	2.27E-01	1.00E+00	4.74E-01	1.00E+00	cell wall catabolism	P
GO:0017004	10	7.33E-01	1.00E+00	5.61E-01	1.00E+00	4.54E-01	1.00E+00	3.07E-01	1.00E+00	8.00E-01	1.00E+00	9.28E-01	1.00E+00	7.10E-01	1.00E+00	4.26E-01	1.00E+00	cytochrome complex assembly	P
GO:0017015	26	3.54E-01	1.00E+00	1.11E-01	1.00E+00	2.31E-01	1.00E+00	8.94E-03	7.13E-01	3.53E-01	1.00E+00	2.53E-01	1.00E+00	7.26E-01	1.00E+00	4.89E-01	1.00E+00	regulation of transforming growth factor beta	P
GO:0017016	66	3.32E-01	1.00E+00	5.24E-02	1.00E+00	7.58E-01	1.00E+00	3.88E-01	1.00E+00	2.49E-01	1.00E+00	1.24E-01	1.00E+00	3.80E-01	1.00E+00	3.79E-03	1.85E-01	Ras GTPase binding	F
GO:0017017	13	8.23E-01	1.00E+00	9.06E-01	1.00E+00	5.12E-01	1.00E+00	6.72E-01	1.00E+00	6.20E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	2.59E-01	1.00E+00	MAP kinase phosphatase activity	F
GO:0017022	20	2.92E-01	1.00E+00	6.02E-03	3.60E-01	4.21E-01	1.00E+00	2.62E-02	1.00E+00	2.41E-01	1.00E+00	1.82E-03	1.61E-01	4.63E-01	1.00E+00	2.64E-01	1.00E+00	myosin binding	F
GO:0017038	122	4.14E-06	7.00E-03	3.25E-08	4.97E-03	1.68E-02	6.93E-01	2.16E-03	1.24E-01	5.69E-06	2.88E-03	4.66E-08	8.37E-04	3.20E-03	1.95E-01	9.68E-03	4.81E-01	protein import	P
GO:0017040	10	9.02E-02	1.00E+00	2.06E-01	1.00E+00	4.51E-01	1.00E+00	8.59E-01	1.00E+00	7.53E-02	1.00E+00	2.39E-01	1.00E+00	1.28E-01	1.00E+00	3.27E-02	1.00E+00	ceramidase activity	F
GO:0017046	12	7.72E-01	1.00E+00	9.85E-01	1.00E+00	4.70E-01	1.00E+00	7.92E-01	1.00E+00	8.87E-01	1.00E+00	9.99E-01	1.00E+00	2.45E-01	1.00E+00	6.28E-01	1.00E+00	peptide hormone binding	F
GO:0017048	28	4.67E-01	1.00E+00	5.76E-02	1.00E+00	8.73E-01	1.00E+00	1.62E-01	1.00E+00	3.78E-01	1.00E+00	6.15E-02	1.00E+00	4.14E-01	1.00E+00	6.82E-02	1.00E+00	Rho GTPase binding	F
GO:0017053	12	4.19E-01	1.00E+00	6.26E-01	1.00E+00	4.34E-01	1.00E+00	7.56E-02	1.00E+00	4.85E-01	1.00E+00	7.19E-01	1.00E+00	2.98E-01	1.00E+00	8.00E-01	1.00E+00	transcriptional repressor complex	C
GO:0017076	2028	1.18E-26	0.00E+00	1.14E-36	0.00E+00	7.39E-15	0.00E+00	2.75E-16	0.00E+00	3.07E-23	0.00E+00	2.02E-34	0.00E+00	8.64E-09	0.00E+00	4.16E-09	7.71E-04	purine nucleotide binding	F
GO:0017111	739	1.41E-14	0.00E+00	1.69E-12	0.00E+00	4.26E-08	9.68E-04	6.52E-04	4.70E-02	1.24E-12	0.00E+00	1.71E-13	0.00E+00	6.17E-06	2.00E-03	1.12E-04	2.00E-02	nucleoside-triphosphatase activity	F
GO:0017124	30	8.05E-01	1.00E+00	2.42E-02	1.00E+00	3.70E-01	1.00E+00	1.49E-01	1.00E+00	9.56E-01	1.00E+00	1.24E-02	7.39E-01	1.95E-01	1.00E+00	3.18E-01	1.00E+00	SH3 domain binding	F
GO:0017127	11	2.90E-01	1.00E+00	7.64E-01	1.00E+00	3.07E-01	1.00E+00	5.68E-01	1.00E+00	2.13E-01	1.00E+00	6.85E-01	1.00E+00	7.79E-01	1.00E+00	9.39E-01	1.00E+00	cholesterol transporter activity	F
GO:0017137	21	4.43E-01	1.00E+00	4.93E-01	1.00E+00	5.70E-01	1.00E+00	9.85E-01	1.00E+00	4.65E-01	1.00E+00	4.88E-01	1.00E+00	3.48E-01	1.00E+00	8.14E-02	1.00E+00	Rab GTPase binding	F
GO:0017148	41	1.32E-01	1.00E+00	1.35E-01	1.00E+00	6.66E-02	1.00E+00	5.70E-01	1.00E+00	3.06E-01	1.00E+00	9.66E-02	1.00E+00	1.76E-01	1.00E+00	1.09E-01	1.00E+00	negative regulation of protein biosynthesis	P
GO:0017153	59	7.75E-01	1.00E+00	8.68E-01	1.00E+00	9.65E-01	1.00E+00	8.15E-01	1.00E+00	7.49E-01	1.00E+00	8.24E-01	1.00E+00	3.51E-01	1.00E+00	9.35E-01	1.00E+00	sodium:dicarboxylate symporter activity	F
GO:0017156	23	3.71E-01	1.00E+00	4.63E-01	1.00E+00	3.58E-01	1.00E+00	3.91E-01	1.00E+00	4.90E-01	1.00E+00	7.23E-01	1.00E+00	2.84E-01	1.00E+00	1.23E-01	1.00E+00	calcium ion-dependent exocytosis	P
GO:0017157	18	1.09E-02	6.67E-01	4.93E-02	1.00E+00	4.24E-02	1.00E+00	1.11E-01	1.00E+00	9.71E-03	5.39E-01	1.42E-01	1.00E+00	2.95E-01	1.00E+00	4.36E-03	3.60E-01	regulation of exocytosis	P
GO:0018024	27	8.49E-05	1.24E-02	1.88E-06	8.39E-03	5.84E-03	4.60E-01	1.54E-03	1.24E-01	1.13E-04	1.70E-02	2.75E-05	1.20E-02	5.42E-02	1.00E+00	1.44E-02	8.49E-01	histone-lysine N-methyltransferase activity	F
GO:0018105	16	5.31E-02	1.00E+00	7.31E-02	1.00E+00	3.94E-01	1.00E+00	6.33E-02	1.00E+00	1.68E-02	1.00E+00	8.61E-02	1.00E+00	6.03E-01	1.00E+00	4.18E-01	1.00E+00	peptidyl-serine phosphorylation	P
GO:0018108	69	1.65E-01	1.00E+00	2.89E-01	1.00E+00	3.95E-02	1.00E+00	5.61E-02	1.00E+00	2.21E-01	1.00E+00	4.32E-01	1.00E+00	6.22E-01	1.00E+00	8.89E-01	1.00E+00	peptidyl-tyrosine phosphorylation	P
GO:0018149	18	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	9.61E-01	1.00E+00	9.94E-01	1.00E+00	peptide cross-linking	P
GO:0018193	146	4.83E-04	3.37E-02	1.08E-04	1.50E-02	2.42E-03	2.48E-01	3.61E-05	8.00E-03	6.38E-04	4.00E-02	9.53E-04	5.49E-02	1.77E-01	1.00E+00	7.02E-02	1.00E+00	peptidyl-amino acid modification	P
GO:0018205	10	1.56E-02	6.67E-01	3.70E-02	1.00E+00	7.45E-02	1.00E+00	1.98E-02	1.00E+00	1.15E-02	5.39E-01	6.66E-02	1.00E+00	5.44E-02	1.00E+00	1.37E-01	1.00E+00	peptidyl-lysine modification	P
GO:0018209	19	1.16E-01	1.00E+00	1.62E-01	1.00E+00	5.62E-01	1.00E+00	1.51E-01	1.00E+00	5.77E-02	1.00E+00	1.44E-01	1.00E+00	4.56E-01	1.00E+00	5.63E-01	1.00E+00	peptidyl-serine modification	P
GO:0018212	71	1.23E-01	1.00E+00	1.60E-01	1.00E+00	2.17E-02	1.00E+00	4.72E-02	1.00E+00	1.93E-01	1.00E+00	2.49E-01	1.00E+00	5.66E-01	1.00E+00	7.33E-01	1.00E+00	peptidyl-tyrosine modification	P
GO:0018298	16	7.45E-01	1.00E+00	6.01E-01	1.00E+00	1.89E-01	1.00E+00	3.77E-01	1.00E+00	7.65E-01	1.00E+00	3.67E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	protein-chromophore linkage	P
GO:0018958	75	8.66E-01	1.00E+00	5.67E-01	1.00E+00	4.94E-01	1.00E+00	8.43E-02	1.00E+00	9.09E-01	1.00E+00	7.69E-01	1.00E+00	7.76E-01	1.00E+00	3.30E-01	1.00E+00	phenol metabolism	P
GO:0019001	413	2.10E-07	1.95E-03	1.42E-06	8.39E-03	1.38E-03	9.80E-02	1.82E-02	1.00E+00	6.28E-07	2.45E-03	3.27E-07	2.97E-03	1.71E-05	5.44E-03	1.57E-02	8.49E-01	guanyl nucleotide binding	F
GO:0019012	18	4.81E-01	1.00E+00	5.70E-01	1.00E+00	9.45E-01	1.00E+00	5.97E-01	1.00E+00	2.59E-01	1.00E+00	7.17E-01	1.00E+00	8.41E-01	1.00E+00	1.73E-01	1.00E+00	virion	C
GO:0019028	18	4.81E-01	1.00E+00	5.70E-01	1.00E+00	9.45E-01	1.00E+00	5.97E-01	1.00E+00	2.59E-01	1.00E+00	7.17E-01	1.00E+00	8.41E-01	1.00E+00	1.73E-01	1.00E+00	viral capsid	C
GO:0019048	15	6.31E-03	5.17E-01	7.40E-02	1.00E+00	3.21E-02	1.00E+00	1.67E-01	1.00E+00	1.14E-02	5.39E-01	8.19E-02	1.00E+00	6.86E-02	1.00E+00	4.52E-01	1.00E+00	virus-host interaction	P
GO:0019058	55	4.61E-02	1.00E+00	2.79E-01	1.00E+00	4.33E-01	1.00E+00	4.74E-01	1.00E+00	3.18E-02	1.00E+00	2.08E-01	1.00E+00	8.34E-02	1.00E+00	4.10E-01	1.00E+00	viral infectious cycle	P
GO:0019059	23	2.45E-01	1.00E+00	4.04E-01	1.00E+00	6.03E-01	1.00E+00	8.24E-01	1.00E+00	2.40E-01	1.00E+00	2.29E-01	1.00E+00	1.45E-01	1.00E+00	7.83E-01	1.00E+00	initiation of viral infection	P
GO:0019079	29	1.02E-01	1.00E+00	5.14E-01	1.00E+00	2.76E-01	1.00E+00	5.52E-01	1.00E+00	1.20E-01	1.00E+00	5.70E-01	1.00E+00	1.97E-01	1.00E+00	2.13E-01	1.00E+00	viral genome replication	P
GO:0019098	17	9.98E-01	1.00E+00	9.55E-01	1.00E+00	9.32E-01	1.00E+00	9.55E-01	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	6.24E-01	1.00E+00	1.76E-01	1.00E+00	reproductive behavior	P
GO:0019104	11	5.05E-01	1.00E+00	2.55E-01	1.00E+00	4.79E-01	1.00E+00	1.07E-01	1.00E+00	4.35E-01	1.00E+00	3.71E-01	1.00E+00	7.24E-01	1.00E+00	6.77E-01	1.00E+00	DNA N-glycosylase activity	F
GO:0019198	18	8.40E-01	1.00E+00	6.68E-01	1.00E+00	5.96E-01	1.00E+00	6.22E-01	1.00E+00	9.22E-01	1.00E+00	6.65E-01	1.00E+00	6.06E-01	1.00E+00	6.01E-01	1.00E+00	transmembrane receptor protein phosphata	F
GO:0019199	135	1.00E+00	1.00E+00	9.46E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.94E-01	1.00E+00	9.16E-01	1.00E+00	8.72E-01	1.00E+00	4.70E-01	1.00E+00	transmembrane receptor protein kinase acti	F
GO:0019200	31	1.91E-01	1.00E+00	1.39E-01	1.00E+00	7.63E-01	1.00E+00	7.42E-01	1.00E+00	7.30E-02	1.00E+00	7.13E-02	1.00E+00	7.72E-01	1.00E+00	3.34E-01	1.00E+00	carbohydrate kinase activity	F
GO:0019201	22	2.55E-01	1.00E+00	6.08E-02	1.00E+00	4.64E-01	1.00E+00	1.81E-02	1.00E+00	2.97E-01	1.00E+00	2.06E-01	1.00E+00	2.37E-01	1.00E+00	3.65E-01	1.00E+00	nucleotide kinase activity	F
GO:0019205	50	2.01E-03	2.02E-01	2.05E-03	1.29E-01	3.83E-02	1.00E+00	1.97E-03	1.24E-01	4.92E-03	4.18E-01	1.64E-02	8.60E-01	1.92E-02	9.11E-01	2.54E-02	1.00E+00	nucleobase, nucleoside, nucleotide kinase a	F
GO:0019206	14	2.49E-02	1.00E+00	1.46E-03	9.10E-02	3.97E-01	1.00E+00	2.10E-02	1.00E+00	2.60E-02	1.00E+00	6.73E-03	5.30E-01	7.03E-02	1.00E+00	5.05E-02	1.00E+00	nucleoside kinase activity	F
GO:0019207	103	4.34E-01	1.00E+00	6.44E-01	1.00E+00	4.01E-01	1.00E+00	8.63E-01	1.00E+00	3.38E-01	1.00E+00	4.31E-01	1.00E+00	7.18E-01	1.00E+00	8.80E-01	1.00E+00	kinase regulator activity	F
GO:0019208	55	3.36E-01	1.00E+00	1.48E-02	1.00E+00	5.11E-01	1.00E+00	3.08E-02	1.00E+00	3.09E-01	1.00E+00	3.66E-02	1.00E+00	4.61E-01	1.00E+00	3.30E-02	1.00E+00	phosphatase regulator activity	F
GO:0019209	20	1.72E-01	1.00E+00	6.71E-01	1.00E+00	1.55E-01	1.00E+00	9.95E-01	1.00E+00	1.32E-01	1.00E+00	3.85E-01	1.00E+00	9.94E-01	1.00E+00	8.98E-01	1.00E+00	kinase activator activity	F
GO:0019210	33	1.59E-01	1.00E+00	5.50E-02	1.00E+00	4.80E-01	1.00E+00	4.75E-02	1.00E+00	5.98E-02	1.00E+00	1.75E-01	1.00E+00	6.54E-01	1.00E+00	2.05E-01	1.00E+00	kinase inhibitor activity	F
GO:0019212	27	4.39E-01	1.00E+00	1.09E-01	1.00E+00	7.98E-01	1.00E+00	7.70E-02	1.00E+00	3.05E-01	1.00E+00	1.95E-01	1.00E+00	4.79E-01	1.00E+00	1.28E-01	1.00E+00	phosphatase inhibitor activity	F
GO:0019213	22	2.20E-01	1.00E+00	3.37E-01	1.00E+00	5.31E-01	1.00E+00	7.96E-01	1.00E+00	1.43E-01	1.00E+00	2.44E-01	1.00E+00	3.90E-01	1.00E+00	1.30E-01	1.00E+00	deacetylase activity	F
GO:0019216	52	9.15E-02	1.00E+00	1.56E-01	1.00E+00	6.31E-02	1.00E+00	3.42E-01	1.00E+00	1.67E-01	1.00E+00	2.28E-01	1.00E+00	1.00E-01	1.00E+00	6.39E-02	1.00E+00	regulation of lipid metabolism	P
GO:0019217	23	2.61E-01	1.00E+00	1.19E-01	1.00E+00	3.80E-01	1.00E+00	1.99E-01	1.00E+00	3.35E-01	1.00E+00	2.24E-01	1.00E+00	1.02E-01	1.00E+00	7.30E-02	1.00E+00	regulation of fatty acid metabolism	P
GO:0019218	18	1.37E-01	1.00E+00	3.20E-01	1.00E+00	7.44E-02	1.00E+00	4.23E-01	1.00E+00	1.92E-01	1.00E+00	3.20E-01	1.00E+00	2.00E-01	1.00E+00	1.98E-01	1.00E+00	regulation of steroid metabolism	P
GO:0019219	2764	1.44E-31	0.00E+00	2.96E-41	0.00E+00	2.61E-13	0.00E+00	6.12E-17	0.00E+00	1.66E-30	0.00E+00	4.71E-37	0.00E+00	1.32E-10	0.00E+00	1.12E-15	0.00E+00	regulation of nucleobase, nucleoside, nucle	P
GO:0019220	124	5.77E-01	1.00E+00	3.15E-01	1.00E+00	1.25E-01	1.00E+00	1.75E-01	1.00E+00	7.04E-01	1.00E+00	3.88E-01	1.00E+00	6.71E-01	1.00E+00	4.86E-01	1.00E+00	regulation of phosphate metabolism	P
GO:0019221	45	6.39E-01	1.00E+00	9.73E-01	1.00E+00	3.69E-01	1.00E+00	8.06E-01	1.00E+00	6.82E-01	1.00E+00	9.38E-01	1.00E+00	7.28E-01	1.00E+00	9.72E-01	1.00E+00	cytokine and chemokine mediated signaling	P
GO:0019222	3207	5.54E-37	0.00E+00	0.00E+00	0.00E+00	1.46E-17	0.00E+00	2.50E-20	0.00E+00	1.35E-34	0.00E+00	5.18E-44	0.00E+00	1.42E-11	0.00E+00	2.85E-19	0.00E+00	regulation of metabolism	P
GO:0019226	363	8.41E-01	1.00E+00	5.64E-01	1.00E+00	6.72E-01	1.00E+00	1.19E-01	1.00E+00	7.74E-01	1.00E+00	6.08E-01	1.00E+00	8.37E-01	1.00E+00	9.24E-01	1.00E+00	transmission of nerve impulse	P
GO:0019229	20	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	5.75E-01	1.00E+00	7.20E-01	1.00E+00	regulation of vasoconstriction	P
GO:0019233	26	9.91E-01	1.00E+00	9.06E-01	1.00E+00	9.64E-01	1.00E+00	4.70E-01	1.00E+00	9.52E-01	1.00E+00	8.95E-01	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	sensory perception of pain	P
GO:0019239	28	3.64E-01	1.00E+00	6.05E-01	1.00E+00	5.58E-01	1.00E+00	8.45E-01	1.00E+00	3.18E-01	1.00E+00	3.87E-01	1.00E+00	4.34E-01	1.00E+00	8.54E-01	1.00E+00	deaminase activity	F
GO:0019290	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	siderophore biosynthesis	P
GO:0019318	179	5.56E-05	1.10E-02	1.50E-03	9.10E-02	1.34E-03	9.80E-02	8.76E-03	7.13E-01	1.20E-04	1.70E-02	1.33E-02	7.39E-01	7.79E-02	1.00E+00	4.05E-03	1.85E-01	hexose metabolism	P
GO:0019319	32	1.76E-01	1.00E+00	1.12E-01	1.00E+00	2.80E-01	1.00E+00	4.34E-01	1.00E+00	1.81E-01	1.00E+00	2.21E-01	1.00E+00	2.93E-01	1.00E+00	3.01E-02	1.00E+00	hexose biosynthesis	P
GO:0019320	88	1.23E-04	2.50E-02	4.88E-04	6.90E-02	1.91E-04	2.40E-02	2.97E-03	1.47E-01	6.06E-04	4.00E-02	4.00E-03	2.70E-01	1.61E-01	1.00E+00	1.99E-02	1.00E+00	hexose catabolism	P
GO:0019321	10	2.91E-01	1.00E+00	3.69E-01	1.00E+00	4.22E-01	1.00E+00	7.54E-01	1.00E+00	2.65E-01	1.00E+00	4.92E-01	1.00E+00	5.65E-01	1.00E+00	1.08E-01	1.00E+00	pentose metabolism	P
GO:0019362	31	2.63E-02	1.00E+00	4.32E-02	1.00E+00	9.72E-03	4.60E-01	1.18E-01	1.00E+00	1.26E-01	1.00E+00	1.23E-01	1.00E+00	4.29E-02	1.00E+00	7.83E-02	1.00E+00	pyridine nucleotide metabolism	P
GO:0019363	13	1.03E-01	1.00E+00	3.36E-01	1.00E+00	9.30E-02	1.00E+00	1.72E-01	1.00E+00	1.61E-01	1.00E+00	4.59E-01	1.00E+00	2.00E-01	1.00E+00	3.88E-01	1.00E+00	pyridine nucleotide biosynthesis	P
GO:0019370	19	1.77E-01	1.00E+00	2.14E-01	1.00E+00	1.14E-01	1.00E+00	5.23E-01	1.00E+00	2.94E-01	1.00E+00	2.12E-01	1.00E+00	3.86E-01	1.00E+00	1.53E-01	1.00E+00	leukotriene biosynthesis	P
GO:0019395	38	1.06E-01	1.00E+00	1.40E-01	1.00E+00	2.06E-01	1.00E+00	4.20E-01	1.00E+00	6.25E-02	1.00E+00	1.75E-01	1.00E+00	2.67E-01	1.00E+00	5.74E-02	1.00E+00	fatty acid oxidation	P
GO:0019438	54	8.18E-01	1.00E+00	4.68E-01	1.00E+00	6.32E-01	1.00E+00	1.35E-01	1.00E+00	8.49E-01	1.00E+00	6.54E-01	1.00E+00	5.23E-01	1.00E+00	3.62E-01	1.00E+00	aromatic compound biosynthesis	P
GO:0019439	18	2.18E-01	1.00E+00	2.31E-01	1.00E+00	1.78E-01	1.00E+00	5.72E-01	1.00E+00	3.75E-01	1.00E+00	1.51E-01	1.00E+00	1.45E-01	1.00E+00	4.20E-01	1.00E+00	aromatic compound catabolism	P

GO:0019538	3787	1.15E-39	0.00E+00	0.00E+00	0.00E+00	8.60E-19	0.00E+00	1.31E-27	0.00E+00	2.90E-37	0.00E+00	0.00E+00	0.00E+00	9.81E-11	0.00E+00	2.77E-20	0.00E+00	protein metabolism	P
GO:0019540	42	7.07E-01	1.00E+00	4.44E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	7.44E-01	1.00E+00	6.19E-01	1.00E+00	5.27E-01	1.00E+00	2.77E-01	1.00E+00	siderophore biosynthesis from catechol	P
GO:0019674	14	3.42E-01	1.00E+00	4.08E-01	1.00E+00	9.69E-02	1.00E+00	4.64E-01	1.00E+00	5.84E-01	1.00E+00	3.50E-01	1.00E+00	3.43E-01	1.00E+00	5.39E-01	1.00E+00	NAD metabolism	P
GO:0019717	53	5.49E-02	1.00E+00	5.54E-02	1.00E+00	1.62E-01	1.00E+00	1.24E-01	1.00E+00	3.89E-02	1.00E+00	4.31E-02	1.00E+00	2.49E-01	1.00E+00	7.53E-01	1.00E+00	synaptosome	C
GO:0019722	47	6.47E-02	1.00E+00	2.21E-01	1.00E+00	3.56E-03	3.27E-01	4.13E-01	1.00E+00	9.02E-02	1.00E+00	1.96E-01	1.00E+00	7.48E-01	1.00E+00	4.87E-01	1.00E+00	calcium-mediated signaling	P
GO:0019724	119	7.45E-01	1.00E+00	5.15E-01	1.00E+00	7.08E-01	1.00E+00	4.97E-01	1.00E+00	6.78E-01	1.00E+00	4.08E-01	1.00E+00	7.53E-01	1.00E+00	9.00E-01	1.00E+00	B cell mediated immunity	P
GO:0019725	317	1.34E-01	1.00E+00	3.40E-02	1.00E+00	1.96E-01	1.00E+00	2.91E-02	1.00E+00	2.39E-01	1.00E+00	2.50E-02	1.00E+00	4.69E-02	1.00E+00	6.32E-01	1.00E+00	cell homeostasis	P
GO:0019748	95	4.72E-02	1.00E+00	5.91E-02	1.00E+00	4.63E-02	1.00E+00	8.80E-02	1.00E+00	6.69E-02	1.00E+00	1.21E-01	1.00E+00	5.28E-01	1.00E+00	8.14E-02	1.00E+00	secondary metabolism	P
GO:0019751	38	2.85E-02	1.00E+00	2.05E-02	1.00E+00	6.18E-02	1.00E+00	6.40E-02	1.00E+00	7.58E-02	1.00E+00	6.88E-02	1.00E+00	9.89E-02	1.00E+00	8.88E-02	1.00E+00	polyol metabolism	P
GO:0019752	667	6.30E-05	1.10E-02	2.01E-06	8.39E-03	6.09E-04	3.60E-02	1.06E-04	1.20E-02	1.73E-04	1.70E-02	3.54E-05	1.20E-02	1.37E-01	1.00E+00	4.66E-03	3.60E-01	carboxylic acid metabolism	P
GO:0019783	81	4.45E-01	1.00E+00	1.29E-02	7.47E-01	5.98E-01	1.00E+00	2.12E-02	1.00E+00	3.82E-01	1.00E+00	2.61E-02	1.00E+00	4.26E-01	1.00E+00	1.95E-01	1.00E+00	small conjugating protein-specific protease	F
GO:0019787	177	2.64E-07	1.95E-03	9.01E-08	4.97E-03	1.01E-04	1.20E-02	2.05E-04	2.70E-02	7.72E-07	2.45E-03	5.06E-07	2.97E-03	9.37E-02	1.00E+00	2.73E-03	1.85E-01	small conjugating protein ligase activity	F
GO:0019825	37	6.38E-01	1.00E+00	9.97E-01	1.00E+00	8.37E-01	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	9.76E-01	1.00E+00	7.17E-02	1.00E+00	8.01E-01	1.00E+00	oxygen binding	F
GO:0019827	14	1.63E-01	1.00E+00	2.71E-01	1.00E+00	6.25E-01	1.00E+00	3.30E-01	1.00E+00	1.09E-01	1.00E+00	1.92E-01	1.00E+00	2.58E-01	1.00E+00	8.50E-01	1.00E+00	stem cell maintenance	P
GO:0019829	48	1.16E-01	1.00E+00	5.23E-01	1.00E+00	5.67E-01	1.00E+00	1.33E-01	1.00E+00	9.09E-02	1.00E+00	5.97E-01	1.00E+00	1.64E-01	1.00E+00	8.92E-01	1.00E+00	cation-transporting ATPase activity	F
GO:0019835	24	4.45E-01	1.00E+00	2.47E-01	1.00E+00	3.05E-01	1.00E+00	7.01E-02	1.00E+00	5.70E-01	1.00E+00	4.78E-01	1.00E+00	3.07E-01	1.00E+00	2.11E-01	1.00E+00	cytolysis	P
GO:0019838	100	9.19E-01	1.00E+00	9.93E-01	1.00E+00	8.77E-01	1.00E+00	9.08E-01	1.00E+00	8.79E-01	1.00E+00	9.85E-01	1.00E+00	8.72E-01	1.00E+00	9.88E-01	1.00E+00	growth factor binding	F
GO:0019840	17	8.12E-01	1.00E+00	6.88E-01	1.00E+00	8.78E-01	1.00E+00	8.09E-01	1.00E+00	8.59E-01	1.00E+00	5.44E-01	1.00E+00	2.25E-01	1.00E+00	5.91E-01	1.00E+00	isoprenoid binding	F
GO:0019841	12	5.27E-01	1.00E+00	5.70E-01	1.00E+00	6.85E-01	1.00E+00	6.85E-01	1.00E+00	6.10E-01	1.00E+00	5.02E-01	1.00E+00	1.18E-01	1.00E+00	3.95E-01	1.00E+00	retinol binding	F
GO:0019842	146	3.04E-02	1.00E+00	1.65E-03	9.10E-02	1.11E-02	5.32E-01	6.05E-02	1.00E+00	9.31E-02	1.00E+00	1.38E-03	6.40E-02	9.97E-02	1.00E+00	2.06E-02	1.00E+00	vitamin binding	F
GO:0019843	20	4.39E-05	1.00E-02	7.89E-04	6.90E-02	1.71E-03	2.48E-01	1.52E-01	1.00E+00	1.59E-04	1.70E-02	3.46E-02	1.00E+00	1.15E-01	1.00E+00	1.74E-02	1.00E+00	rRNA binding	F
GO:0019861	86	6.01E-01	1.00E+00	3.60E-01	1.00E+00	4.18E-01	1.00E+00	3.03E-01	1.00E+00	7.24E-01	1.00E+00	6.32E-01	1.00E+00	2.74E-01	1.00E+00	8.93E-02	1.00E+00	flagellum	C
GO:0019865	16	4.93E-01	1.00E+00	6.36E-01	1.00E+00	7.66E-01	1.00E+00	4.95E-01	1.00E+00	2.75E-01	1.00E+00	6.35E-01	1.00E+00	6.81E-01	1.00E+00	4.53E-01	1.00E+00	immunoglobulin binding	F
GO:0019866	305	3.59E-15	0.00E+00	1.54E-07	4.97E-03	1.33E-06	2.42E-03	7.78E-04	4.70E-02	3.83E-15	0.00E+00	1.10E-07	8.37E-04	8.21E-03	6.30E-01	5.58E-02	1.00E+00	organelle inner membrane	C
GO:0019867	95	4.13E-04	3.37E-02	3.67E-05	9.58E-03	9.69E-03	4.60E-01	3.51E-03	2.02E-01	1.93E-04	1.70E-02	1.51E-04	1.70E-02	3.16E-01	1.00E+00	3.73E-03	1.85E-01	outer membrane	C
GO:0019882	73	8.05E-01	1.00E+00	9.87E-01	1.00E+00	9.39E-01	1.00E+00	8.80E-01	1.00E+00	8.78E-01	1.00E+00	9.79E-01	1.00E+00	8.28E-02	1.00E+00	8.83E-01	1.00E+00	antigen processing and presentation	P
GO:0019883	10	3.32E-01	1.00E+00	3.15E-01	1.00E+00	4.80E-01	1.00E+00	1.77E-01	1.00E+00	2.87E-01	1.00E+00	5.27E-01	1.00E+00	3.71E-01	1.00E+00	6.91E-01	1.00E+00	antigen processing and presentation of end	P
GO:0019884	10	1.44E-01	1.00E+00	4.61E-01	1.00E+00	4.82E-01	1.00E+00	5.68E-01	1.00E+00	1.36E-01	1.00E+00	3.63E-01	1.00E+00	2.07E-01	1.00E+00	7.35E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019887	85	7.00E-01	1.00E+00	7.99E-01	1.00E+00	5.86E-01	1.00E+00	9.10E-01	1.00E+00	6.25E-01	1.00E+00	6.19E-01	1.00E+00	7.81E-01	1.00E+00	8.94E-01	1.00E+00	protein kinase regulator activity	F
GO:0019888	53	2.63E-01	1.00E+00	8.72E-03	5.03E-01	4.03E-01	1.00E+00	1.92E-02	1.00E+00	2.47E-01	1.00E+00	2.48E-02	1.00E+00	3.95E-01	1.00E+00	3.11E-02	1.00E+00	protein phosphatase regulator activity	F
GO:0019897	44	1.01E-01	1.00E+00	7.39E-02	1.00E+00	4.09E-01	1.00E+00	2.67E-01	1.00E+00	1.62E-01	1.00E+00	2.60E-02	1.00E+00	1.71E-02	9.11E-01	7.83E-01	1.00E+00	extrinsic to plasma membrane	C
GO:0019898	83	1.39E-01	1.00E+00	4.08E-02	1.00E+00	1.96E-01	1.00E+00	2.80E-01	1.00E+00	2.28E-01	1.00E+00	1.27E-02	7.39E-01	1.22E-01	1.00E+00	6.58E-01	1.00E+00	extrinsic to membrane	C
GO:0019899	297	8.35E-08	1.84E-03	6.98E-08	4.97E-03	1.08E-04	1.20E-02	2.05E-04	2.70E-02	1.78E-07	1.69E-03	1.22E-06	2.97E-03	2.31E-03	1.95E-01	6.37E-04	9.16E-02	enzyme binding	F
GO:0019900	105	2.27E-03	2.02E-01	1.66E-03	9.10E-02	5.08E-04	3.60E-02	3.23E-02	1.00E+00	6.54E-03	5.39E-01	1.65E-03	1.61E-01	1.76E-01	1.00E+00	1.89E-01	1.00E+00	kinase binding	F
GO:0019901	88	2.85E-03	2.39E-01	1.58E-03	9.10E-02	2.05E-03	2.48E-01	7.67E-02	1.00E+00	3.68E-03	2.85E-01	5.84E-04	5.49E-02	3.34E-01	1.00E+00	2.04E-01	1.00E+00	protein kinase binding	F
GO:0019902	21	1.66E-01	1.00E+00	2.76E-01	1.00E+00	4.02E-01	1.00E+00	1.91E-01	1.00E+00	9.14E-02	1.00E+00	5.45E-01	1.00E+00	3.84E-01	1.00E+00	7.79E-02	1.00E+00	phosphatase binding	F
GO:0019903	16	1.69E-01	1.00E+00	4.50E-01	1.00E+00	1.92E-01	1.00E+00	2.15E-01	1.00E+00	1.30E-01	1.00E+00	8.45E-01	1.00E+00	4.46E-01	1.00E+00	1.09E-01	1.00E+00	protein phosphatase binding	F
GO:0019904	160	1.51E-03	2.02E-01	2.77E-04	4.19E-02	2.51E-03	2.48E-01	5.78E-03	3.46E-01	1.21E-02	5.39E-01	6.11E-04	5.49E-02	1.65E-02	6.63E-01	1.02E-01	1.00E+00	protein domain specific binding	F
GO:0019905	24	2.68E-01	1.00E+00	7.90E-01	1.00E+00	5.55E-02	1.00E+00	5.76E-01	1.00E+00	5.45E-01	1.00E+00	8.35E-01	1.00E+00	1.37E-01	1.00E+00	9.39E-01	1.00E+00	syntaxin binding	F
GO:0019915	12	3.47E-01	1.00E+00	5.48E-01	1.00E+00	5.52E-01	1.00E+00	2.21E-01	1.00E+00	3.48E-01	1.00E+00	7.00E-01	1.00E+00	4.50E-01	1.00E+00	6.17E-01	1.00E+00	sequestering of lipid	P
GO:0019932	282	7.52E-01	1.00E+00	8.72E-01	1.00E+00	6.84E-01	1.00E+00	8.71E-01	1.00E+00	6.10E-01	1.00E+00	8.26E-01	1.00E+00	6.66E-01	1.00E+00	7.23E-01	1.00E+00	second-messenger-mediated signaling	P
GO:0019933	99	9.97E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	9.71E-01	1.00E+00	9.78E-01	1.00E+00	9.70E-01	1.00E+00	5.69E-01	1.00E+00	cAMP-mediated signaling	P
GO:0019935	133	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.69E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.43E-01	1.00E+00	8.61E-01	1.00E+00	cyclic-nucleotide-mediated signaling	P
GO:0019941	233	2.64E-06	1.95E-03	2.02E-10	0.00E+00	6.69E-03	4.60E-01	3.75E-06	8.00E-03	1.70E-05	4.19E-03	5.19E-09	8.37E-04	9.21E-04	7.07E-02	1.43E-04	2.00E-02	modification-dependent protein catabolism	P
GO:0019953	399	9.03E-02	1.00E+00	6.57E-02	1.00E+00	5.22E-01	1.00E+00	1.19E-01	1.00E+00	1.37E-01	1.00E+00	4.04E-02	1.00E+00	9.42E-03	6.30E-01	5.96E-01	1.00E+00	sexual reproduction	P
GO:0019955	137	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.79E-01	1.00E+00	7.18E-01	1.00E+00	9.96E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	cytokine binding	F
GO:0019956	60	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.45E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chemokine binding	F
GO:0019957	41	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	C-C chemokine binding	F
GO:0019958	37	9.56E-01	1.00E+00	9.91E-01	1.00E+00	6.89E-01	1.00E+00	5.57E-01	1.00E+00	9.32E-01	1.00E+00	9.91E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	C-X-C chemokine binding	F
GO:0019959	11	1.00E+00	1.00E+00	8.59E-01	1.00E+00	7.71E-01	1.00E+00	3.17E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	interleukin-8 binding	F
GO:0019965	66	9.78E-01	1.00E+00	9.14E-01	1.00E+00	9.28E-01	1.00E+00	7.82E-01	1.00E+00	9.37E-01	1.00E+00	8.66E-01	1.00E+00	9.98E-01	1.00E+00	9.82E-01	1.00E+00	interleukin binding	F
GO:0019966	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	interleukin-1 binding	F
GO:0019992	65	2.14E-01	1.00E+00	4.16E-03	1.97E-01	2.15E-02	1.00E+00	1.33E-02	8.18E-01	3.74E-01	1.00E+00	5.71E-03	3.51E-01	7.45E-01	1.00E+00	2.18E-01	1.00E+00	diacylglycerol binding	F
GO:0020037	165	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.04E-01	1.00E+00	9.85E-01	1.00E+00	7.43E-01	1.00E+00	7.36E-01	1.00E+00	heme binding	F
GO:0021510	30	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.55E-01	1.00E+00	9.96E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	spinal cord development	P
GO:0021515	22	9.98E-01	1.00E+00	1.00E+00	1.00E+00	5.41E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	cell differentiation in spinal cord	P
GO:0021516	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	dorsal spinal cord development	P
GO:0021517	13	9.06E-01	1.00E+00	9.89E-01	1.00E+00	3.80E-01	1.00E+00	8.89E-01	1.00E+00	9.49E-01	1.00E+00	9.94E-01	1.00E+00	9.87E-01	1.00E+00	7.70E-01	1.00E+00	ventral spinal cord development	P
GO:0021522	11	9.30E-01	1.00E+00	9.59E-01	1.00E+00	3.83E-01	1.00E+00	8.16E-01	1.00E+00	9.76E-01	1.00E+00	9.77E-01	1.00E+00	9.93E-01	1.00E+00	6.22E-01	1.00E+00	spinal cord motor neuron differentiation	P
GO:0021536	24	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.88E-01	1.00E+00	9.09E-01	1.00E+00	9.96E-01	1.00E+00	9.98E-01	1.00E+00	9.95E-01	1.00E+00	9.92E-01	1.00E+00	diencephalon development	P
GO:0021537	38	2.17E-01	1.00E+00	9.36E-01	1.00E+00	3.83E-01	1.00E+00	6.17E-01	1.00E+00	1.84E-01	1.00E+00	9.29E-01	1.00E+00	2.13E-01	1.00E+00	9.64E-01	1.00E+00	telencephalon development	P
GO:0021543	27	6.94E-02	1.00E+00	8.20E-01	1.00E+00	1.02E-01	1.00E+00	4.18E-01	1.00E+00	8.15E-02	1.00E+00	8.30E-01	1.00E+00	1.04E-01	1.00E+00	9.24E-01	1.00E+00	pallium development	P
GO:0021545	10	8.42E-01	1.00E+00	8.40E-01	1.00E+00	9.90E-01	1.00E+00	8.33E-01	1.00E+00	7.21E-01	1.00E+00	7.84E-01	1.00E+00	6.00E-01	1.00E+00	7.94E-01	1.00E+00	cranial nerve development	P
GO:0021549	17	6.82E-01	1.00E+00	8.44E-01	1.00E+00	6.38E-01	1.00E+00	7.25E-01	1.00E+00	6.82E-01	1.00E+00	7.48E-01	1.00E+00	6.02E-01	1.00E+00	9.92E-01	1.00E+00	cerebellum development	P
GO:0021575	12	4.59E-01	1.00E+00	4.80E-01	1.00E+00	2.94E-01	1.00E+00	5.03E-01	1.00E+00	7.03E-01	1.00E+00	4.13E-01	1.00E+00	2.30E-01	1.00E+00	7.97E-01	1.00E+00	hindbrain morphogenesis	P
GO:0021587	11	4.54E-01	1.00E+00	4.58E-01	1.00E+00	3.33E-01	1.00E+00	4.80E-01	1.00E+00	6.34E-01	1.00E+00	4.03E-01	1.00E+00	3.00E-01	1.00E+00	7.88E-01	1.00E+00	cerebellum morphogenesis	P
GO:0021675	16	6.76E-01	1.00E+00	5.57E-01	1.00E+00	4.82E-01	1.00E+00	9.22E-01	1.00E+00	7.89E-01	1.00E+00	5.69E-01	1.00E+00	4.39E-01	1.00E+00	2.05E-01	1.00E+00	nerve development	P
GO:0021695	13	5.43E-01	1.00E+00	5.09E-01	1.00E+00	4.42E-01	1.00E+00	4.72E-01	1.00E+00	6.48E-01	1.00E+00	4.20E-01	1.00E+00	4.10E-01	1.00E+00	9.20E-01	1.00E+00	cerebellar cortex development	P
GO:0021696	11	4.54E-01	1.00E+00	4.58E-01	1.00E+00	3.33E-01	1.00E+00	4.80E-01	1.00E+00	6.34E-01	1.00E+00	4.03E-01	1.00E+00	3.00E-01	1.00E+00	7.88E-01	1.00E+00	cerebellar cortex morphogenesis	P
GO:0021700	86	8.63E-01	1.00E+00	6.80E-01	1.00E+00	4.72E-01	1.00E+00	1.66E-01	1.00E+00	7.09E-01	1.00E+00	7.66E-01	1.00E+00	9.89E-01	1.00E+00	9.43E-01	1.00E+00	developmental maturation	P
GO:0021761	17	1.62E-01	1.00E+00	8.21E-01	1.00E+00	3.61E-01	1.00E+00	2.65E-01	1.00E+00	1.55E-01	1.00E+00	8.87E-01	1.00E+00	2.36E-01	1.00E+00	9.61E-01	1.00E+00	limbic system development	P
GO:0021766	13	4.15E-02	1.00E+00	3.97E-01	1.00E+00	1.34E-01	1.00E+00	5.38E-02	1.00E+00	7.57E-02	1.00E+00	5.70E-01	1.00E+00	1.20E-01	1.00E+00	7.56E-01	1.00E+00	hippocampus development	P
GO:0021782	15	1.06E-01	1.00E+00	9.13E-01	1.00E+00	5.21E-02	1.00E+00	5.16E-01	1.00E+00	1.39E-01	1.00E+00	9.59E-01	1.00E+00	2.28E-01	1.00E+00	9.61E-01	1.00E+00	glial cell development	P
GO:0021795	10	1.32E-01	1.00E+00	7.85E-01	1.00E+00	1.71E-01	1.00E+00	7.99E-01	1.00E+00	9.54E-02	1.00E+00	7.20E-01	1.00E+00	2.00E-01	1.00E+00	8.39E-01	1.00E+00	cerebral cortex cell migration	P
GO:0021872	12	9.93E-01	1.00E+00	9.89E-01	1.00E+00	9.65E-01	1.00E+00	8.82E-01	1.00E+00	9.92E-01	1.00E+00	9.85E-01	1.00E+00	9.93E-01	1.00E+00	9.44E-01	1.00E+00	generation of neurons in the forebrain	P

GO:0021879	10	9.87E-01	1.00E+00	9.67E-01	1.00E+00	8.93E-01	1.00E+00	8.13E-01	1.00E+00	9.87E-01	1.00E+00	9.48E-01	1.00E+00	9.98E-01	1.00E+00	9.73E-01	1.00E+00	forebrain neuron differentiation	P
GO:0021885	12	2.40E-01	1.00E+00	8.69E-01	1.00E+00	3.57E-01	1.00E+00	9.18E-01	1.00E+00	1.72E-01	1.00E+00	8.46E-01	1.00E+00	2.81E-01	1.00E+00	4.08E-01	1.00E+00	forebrain cell migration	P
GO:0021895	10	6.22E-01	1.00E+00	5.53E-01	1.00E+00	7.44E-01	1.00E+00	4.37E-01	1.00E+00	5.24E-01	1.00E+00	5.12E-01	1.00E+00	5.26E-01	1.00E+00	7.45E-01	1.00E+00	cerebral cortex neuron differentiation	P
GO:0021915	48	8.03E-01	1.00E+00	6.69E-01	1.00E+00	4.84E-01	1.00E+00	8.06E-01	1.00E+00	7.26E-01	1.00E+00	6.37E-01	1.00E+00	9.56E-01	1.00E+00	2.35E-01	1.00E+00	neural tube development	P
GO:0021953	27	6.87E-01	1.00E+00	8.73E-01	1.00E+00	5.88E-01	1.00E+00	5.60E-01	1.00E+00	5.92E-01	1.00E+00	8.47E-01	1.00E+00	7.20E-01	1.00E+00	9.46E-01	1.00E+00	central nervous system neuron differentiatic	P
GO:0021954	24	7.15E-01	1.00E+00	9.39E-01	1.00E+00	7.38E-01	1.00E+00	7.12E-01	1.00E+00	5.33E-01	1.00E+00	8.97E-01	1.00E+00	8.28E-01	1.00E+00	9.64E-01	1.00E+00	central nervous system neuron developmer	P
GO:0021955	10	4.95E-01	1.00E+00	7.74E-01	1.00E+00	9.01E-01	1.00E+00	6.12E-01	1.00E+00	3.52E-01	1.00E+00	6.78E-01	1.00E+00	5.35E-01	1.00E+00	9.46E-01	1.00E+00	central nervous system neuron axonogenes	P
GO:0021983	19	9.96E-01	1.00E+00	9.92E-01	1.00E+00	9.50E-01	1.00E+00	8.88E-01	1.00E+00	9.97E-01	1.00E+00	9.92E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	pituitary gland development	P
GO:0021987	20	1.88E-02	1.00E+00	5.72E-01	1.00E+00	2.25E-02	1.00E+00	3.87E-01	1.00E+00	2.22E-02	1.00E+00	5.09E-01	1.00E+00	1.03E-01	1.00E+00	8.07E-01	1.00E+00	cerebral cortex development	P
GO:0022008	420	8.10E-01	1.00E+00	9.70E-01	1.00E+00	5.26E-01	1.00E+00	8.88E-01	1.00E+00	6.47E-01	1.00E+00	9.52E-01	1.00E+00	9.91E-01	1.00E+00	9.11E-01	1.00E+00	neurogenesis	P
GO:0022029	11	1.68E-01	1.00E+00	8.27E-01	1.00E+00	2.61E-01	1.00E+00	8.68E-01	1.00E+00	1.10E-01	1.00E+00	8.00E-01	1.00E+00	2.40E-01	1.00E+00	4.81E-01	1.00E+00	telencephalon cell migration	P
GO:0022037	21	3.03E-01	1.00E+00	7.89E-01	1.00E+00	2.40E-01	1.00E+00	6.68E-01	1.00E+00	3.54E-01	1.00E+00	6.48E-01	1.00E+00	3.71E-01	1.00E+00	9.88E-01	1.00E+00	metencephalon development	P
GO:0030001	613	3.81E-01	1.00E+00	2.55E-01	1.00E+00	4.36E-01	1.00E+00	4.88E-01	1.00E+00	3.13E-01	1.00E+00	1.29E-01	1.00E+00	7.95E-01	1.00E+00	7.16E-01	1.00E+00	metal ion transport	P
GO:0030003	197	3.79E-01	1.00E+00	4.34E-01	1.00E+00	3.54E-01	1.00E+00	2.14E-01	1.00E+00	5.47E-01	1.00E+00	2.88E-01	1.00E+00	8.60E-02	1.00E+00	9.96E-01	1.00E+00	cation homeostasis	P
GO:0030004	18	2.65E-01	1.00E+00	2.42E-01	1.00E+00	4.16E-01	1.00E+00	6.10E-01	1.00E+00	3.00E-01	1.00E+00	1.29E-01	1.00E+00	1.70E-01	1.00E+00	6.45E-01	1.00E+00	monovalent inorganic cation homeostasis	P
GO:0030005	175	4.53E-01	1.00E+00	5.78E-01	1.00E+00	4.27E-01	1.00E+00	3.17E-01	1.00E+00	5.95E-01	1.00E+00	4.34E-01	1.00E+00	1.33E-01	1.00E+00	9.92E-01	1.00E+00	di-, tri-valent inorganic cation homeostasis	P
GO:0030010	11	2.63E-01	1.00E+00	5.62E-01	1.00E+00	4.38E-01	1.00E+00	8.85E-01	1.00E+00	4.63E-01	1.00E+00	5.96E-01	1.00E+00	1.69E-02	9.11E-01	1.69E-01	1.00E+00	establishment of cell polarity	P
GO:0030016	79	8.89E-01	1.00E+00	2.73E-01	1.00E+00	4.90E-01	1.00E+00	2.60E-01	1.00E+00	8.51E-01	1.00E+00	1.99E-01	1.00E+00	9.95E-01	1.00E+00	6.01E-01	1.00E+00	myofibril	C
GO:0030017	74	8.79E-01	1.00E+00	2.96E-01	1.00E+00	6.13E-01	1.00E+00	2.22E-01	1.00E+00	8.16E-01	1.00E+00	2.40E-01	1.00E+00	9.85E-01	1.00E+00	6.41E-01	1.00E+00	sarcomere	C
GO:0030018	26	6.48E-01	1.00E+00	4.29E-01	1.00E+00	5.58E-01	1.00E+00	4.47E-01	1.00E+00	5.67E-01	1.00E+00	5.40E-01	1.00E+00	9.40E-01	1.00E+00	1.75E-01	1.00E+00	Z disc	C
GO:0030027	55	1.87E-02	1.00E+00	3.64E-02	1.00E+00	5.94E-03	4.60E-01	1.18E-01	1.00E+00	7.27E-02	1.00E+00	1.24E-01	1.00E+00	1.95E-01	1.00E+00	7.77E-03	4.81E-01	lamellipodium	C
GO:0030029	262	2.87E-03	2.39E-01	3.47E-03	1.97E-01	1.18E-03	9.80E-02	3.02E-02	1.00E+00	7.77E-03	5.39E-01	4.00E-03	2.70E-01	3.39E-01	1.00E+00	8.67E-02	1.00E+00	actin filament-based process	P
GO:0030030	317	7.29E-01	1.00E+00	7.11E-01	1.00E+00	4.10E-01	1.00E+00	7.55E-01	1.00E+00	6.52E-01	1.00E+00	6.92E-01	1.00E+00	8.95E-01	1.00E+00	3.88E-01	1.00E+00	cell projection organization and biogenesis	P
GO:0030031	80	3.24E-02	1.00E+00	2.78E-02	1.00E+00	1.04E-01	1.00E+00	2.55E-01	1.00E+00	3.13E-02	1.00E+00	2.04E-02	1.00E+00	1.59E-01	1.00E+00	9.17E-02	1.00E+00	cell projection biogenesis	P
GO:0030032	13	1.09E-01	1.00E+00	1.08E-01	1.00E+00	1.16E-01	1.00E+00	4.76E-01	1.00E+00	1.41E-01	1.00E+00	1.01E-01	1.00E+00	1.94E-01	1.00E+00	2.00E-01	1.00E+00	lamellipodium biogenesis	P
GO:0030035	18	1.79E-01	1.00E+00	1.30E-01	1.00E+00	1.06E-01	1.00E+00	1.47E-01	1.00E+00	2.19E-01	1.00E+00	1.17E-01	1.00E+00	1.56E-01	1.00E+00	3.83E-01	1.00E+00	microspike biogenesis	P
GO:0030036	236	2.47E-03	2.02E-01	4.21E-03	1.97E-01	1.79E-03	2.48E-01	3.58E-02	1.00E+00	4.75E-03	4.18E-01	6.23E-03	3.51E-01	3.24E-01	1.00E+00	4.96E-02	1.00E+00	actin cytoskeleton organization and biogene	P
GO:0030041	37	7.27E-02	1.00E+00	1.02E-01	1.00E+00	2.78E-01	1.00E+00	2.73E-01	1.00E+00	3.97E-02	1.00E+00	8.42E-02	1.00E+00	5.06E-01	1.00E+00	3.80E-01	1.00E+00	actin filament polymerization	P
GO:0030042	25	8.95E-02	1.00E+00	4.27E-01	1.00E+00	3.53E-02	1.00E+00	2.51E-01	1.00E+00	1.82E-01	1.00E+00	5.37E-01	1.00E+00	7.18E-01	1.00E+00	5.94E-01	1.00E+00	actin filament depolymerization	P
GO:0030048	20	2.85E-01	1.00E+00	1.46E-01	1.00E+00	1.56E-01	1.00E+00	1.34E-01	1.00E+00	3.91E-01	1.00E+00	1.15E-01	1.00E+00	4.72E-01	1.00E+00	5.39E-01	1.00E+00	actin filament-based movement	P
GO:0030054	455	3.45E-01	1.00E+00	1.63E-01	1.00E+00	1.62E-01	1.00E+00	1.83E-01	1.00E+00	1.98E-01	1.00E+00	1.02E-01	1.00E+00	9.66E-01	1.00E+00	7.44E-01	1.00E+00	cell junction	C
GO:0030055	47	4.26E-01	1.00E+00	2.81E-01	1.00E+00	1.99E-02	1.00E+00	9.61E-02	1.00E+00	5.37E-01	1.00E+00	2.38E-01	1.00E+00	9.91E-01	1.00E+00	9.95E-01	1.00E+00	cell-matrix junction	C
GO:0030072	40	8.17E-01	1.00E+00	6.70E-01	1.00E+00	4.69E-01	1.00E+00	8.19E-01	1.00E+00	7.88E-01	1.00E+00	5.70E-01	1.00E+00	9.72E-01	1.00E+00	6.50E-01	1.00E+00	peptide hormone secretion	P
GO:0030073	34	7.85E-01	1.00E+00	6.32E-01	1.00E+00	5.01E-01	1.00E+00	7.63E-01	1.00E+00	7.72E-01	1.00E+00	5.70E-01	1.00E+00	9.32E-01	1.00E+00	4.86E-01	1.00E+00	insulin secretion	P
GO:0030097	229	8.56E-02	1.00E+00	1.32E-01	1.00E+00	3.31E-01	1.00E+00	1.58E-01	1.00E+00	3.62E-02	1.00E+00	2.35E-01	1.00E+00	5.60E-01	1.00E+00	1.11E-01	1.00E+00	hemopoiesis	P
GO:0030098	102	2.20E-01	1.00E+00	2.42E-01	1.00E+00	2.17E-01	1.00E+00	3.53E-01	1.00E+00	1.82E-01	1.00E+00	2.87E-01	1.00E+00	7.05E-01	1.00E+00	1.65E-01	1.00E+00	lymphocyte differentiation	P
GO:0030099	105	1.53E-01	1.00E+00	1.99E-01	1.00E+00	3.99E-01	1.00E+00	2.48E-01	1.00E+00	1.19E-01	1.00E+00	2.70E-01	1.00E+00	4.30E-01	1.00E+00	2.58E-01	1.00E+00	myeloid cell differentiation	P
GO:0030100	41	1.81E-02	1.00E+00	4.59E-05	9.58E-03	1.23E-01	1.00E+00	9.54E-03	7.13E-01	5.76E-03	5.39E-01	1.47E-05	7.63E-03	4.24E-01	1.00E+00	1.41E-01	1.00E+00	regulation of endocytosis	P
GO:0030101	19	9.33E-01	1.00E+00	8.65E-01	1.00E+00	9.84E-01	1.00E+00	9.54E-01	1.00E+00	9.30E-01	1.00E+00	7.91E-01	1.00E+00	1.52E-01	1.00E+00	4.87E-01	1.00E+00	natural killer cell activation	P
GO:0030111	32	9.80E-02	1.00E+00	8.31E-02	1.00E+00	5.93E-01	1.00E+00	1.50E-01	1.00E+00	7.11E-02	1.00E+00	4.92E-02	1.00E+00	1.20E-01	1.00E+00	8.42E-01	1.00E+00	regulation of Wnt receptor signaling pathwa	P
GO:0030117	65	1.44E-06	1.95E-03	1.82E-05	9.58E-03	1.43E-04	1.50E-02	1.42E-01	1.00E+00	1.01E-05	4.00E-03	1.67E-06	2.97E-03	6.87E-04	6.50E-02	8.89E-02	1.00E+00	membrane coat	C
GO:0030118	39	3.40E-04	3.37E-02	2.47E-04	4.19E-02	1.57E-03	2.48E-01	2.26E-01	1.00E+00	1.58E-03	1.76E-01	9.66E-06	4.88E-03	5.32E-03	3.57E-01	4.59E-01	1.00E+00	clathrin coat	C
GO:0030119	30	5.80E-04	3.37E-02	7.88E-03	3.60E-01	5.76E-04	3.60E-02	2.42E-01	1.00E+00	1.76E-03	1.76E-01	1.29E-03	6.40E-02	3.42E-02	1.00E+00	5.67E-01	1.00E+00	membrane coat adaptor complex	C
GO:0030120	35	3.80E-04	3.37E-02	4.89E-04	6.90E-02	9.76E-03	4.60E-01	1.18E-01	1.00E+00	5.14E-04	2.20E-02	2.68E-04	2.60E-02	3.63E-02	1.00E+00	1.32E-01	1.00E+00	vesicle coat	C
GO:0030125	19	2.84E-02	1.00E+00	4.11E-03	1.97E-01	9.17E-02	1.00E+00	1.51E-01	1.00E+00	3.66E-02	1.00E+00	3.05E-03	2.39E-01	8.81E-02	1.00E+00	7.12E-01	1.00E+00	clathrin vesicle coat	C
GO:0030130	13	6.58E-02	1.00E+00	4.42E-02	1.00E+00	2.20E-01	1.00E+00	3.04E-01	1.00E+00	5.75E-02	1.00E+00	3.66E-02	1.00E+00	8.94E-02	1.00E+00	7.55E-01	1.00E+00	clathrin coat of trans-Golgi network vesicle	C
GO:0030131	29	4.03E-04	3.37E-02	4.90E-03	3.60E-01	3.00E-04	3.60E-02	2.36E-01	1.00E+00	1.70E-03	1.76E-01	7.06E-04	5.49E-02	2.49E-02	1.00E+00	5.25E-01	1.00E+00	clathrin adaptor complex	C
GO:0030132	10	2.10E-02	1.00E+00	7.96E-03	3.60E-01	1.59E-01	1.00E+00	7.47E-01	1.00E+00	1.68E-02	1.00E+00	3.87E-03	2.70E-01	1.32E-01	1.00E+00	2.50E-01	1.00E+00	clathrin coat of coated pit	C
GO:0030133	51	6.05E-02	1.00E+00	6.00E-02	1.00E+00	1.77E-01	1.00E+00	1.95E-01	1.00E+00	6.21E-02	1.00E+00	5.98E-02	1.00E+00	1.87E-01	1.00E+00	4.97E-01	1.00E+00	transport vesicle	C
GO:0030135	135	6.02E-04	3.37E-02	5.55E-03	3.60E-01	2.46E-03	2.48E-01	7.73E-02	1.00E+00	1.23E-03	7.80E-02	3.05E-03	2.39E-01	6.34E-02	1.00E+00	2.68E-01	1.00E+00	coated vesicle	C
GO:0030136	114	1.47E-02	6.67E-01	4.30E-02	1.00E+00	2.47E-02	1.00E+00	1.04E-01	1.00E+00	2.52E-02	1.00E+00	2.71E-02	1.00E+00	1.07E-01	1.00E+00	6.17E-01	1.00E+00	clathrin-coated vesicle	C
GO:0030137	12	8.32E-04	8.30E-02	6.97E-02	1.00E+00	7.29E-02	1.00E+00	5.64E-01	1.00E+00	2.53E-04	1.70E-02	3.38E-02	1.00E+00	1.94E-01	1.00E+00	9.07E-02	1.00E+00	COPI-coated vesicle	C
GO:0030139	32	3.00E-02	1.00E+00	1.01E-01	1.00E+00	1.03E-01	1.00E+00	2.41E-01	1.00E+00	2.00E-02	1.00E+00	7.31E-02	1.00E+00	1.68E-01	1.00E+00	3.73E-01	1.00E+00	endocytic vesicle	C
GO:0030140	23	5.59E-02	1.00E+00	1.05E-01	1.00E+00	2.98E-01	1.00E+00	5.20E-01	1.00E+00	5.69E-02	1.00E+00	7.79E-02	1.00E+00	6.73E-02	1.00E+00	4.61E-01	1.00E+00	trans-Golgi network transport vesicle	C
GO:0030141	90	4.84E-01	1.00E+00	3.48E-01	1.00E+00	5.50E-01	1.00E+00	3.23E-01	1.00E+00	4.08E-01	1.00E+00	3.59E-01	1.00E+00	5.37E-01	1.00E+00	4.84E-01	1.00E+00	secretory granule	C
GO:0030145	151	4.13E-02	1.00E+00	1.10E-03	9.10E-02	3.62E-02	1.00E+00	2.23E-03	1.24E-01	4.65E-02	1.00E+00	2.52E-03	2.39E-01	6.71E-01	1.00E+00	1.93E-01	1.00E+00	manganese ion binding	F
GO:0030148	22	1.16E-01	1.00E+00	1.33E-02	7.47E-01	1.24E-01	1.00E+00	2.23E-01	1.00E+00	1.13E-01	1.00E+00	8.35E-03	7.39E-01	3.68E-01	1.00E+00	1.37E-01	1.00E+00	sphingolipid biosynthesis	P
GO:0030149	16	4.52E-02	1.00E+00	2.16E-01	1.00E+00	2.76E-01	1.00E+00	5.69E-01	1.00E+00	4.62E-02	1.00E+00	2.64E-01	1.00E+00	1.20E-01	1.00E+00	1.34E-01	1.00E+00	sphingolipid catabolism	P
GO:0030154	1370	5.91E-01	1.00E+00	8.71E-01	1.00E+00	6.18E-01	1.00E+00	6.33E-01	1.00E+00	4.20E-01	1.00E+00	8.91E-01	1.00E+00	9.06E-01	1.00E+00	7.44E-01	1.00E+00	cell differentiation	P
GO:0030155	71	2.17E-01	1.00E+00	8.75E-02	1.00E+00	4.45E-01	1.00E+00	9.96E-02	1.00E+00	1.63E-01	1.00E+00	2.02E-01	1.00E+00	2.04E-01	1.00E+00	7.82E-02	1.00E+00	regulation of cell adhesion	P
GO:0030159	19	2.18E-01	1.00E+00	1.47E-01	1.00E+00	5.75E-02	1.00E+00	1.90E-01	1.00E+00	2.32E-01	1.00E+00	1.33E-01	1.00E+00	9.84E-01	1.00E+00	5.18E-01	1.00E+00	receptor signaling complex scaffold activity	F
GO:0030162	19	7.20E-01	1.00E+00	1.83E-01	1.00E+00	6.66E-01	1.00E+00	3.71E-01	1.00E+00	6.69E-01	1.00E+00	1.42E-01	1.00E+00	5.43E-01	1.00E+00	3.59E-01	1.00E+00	regulation of proteolysis	P
GO:0030163	296	4.63E-07	1.95E-03	1.87E-12	0.00E+00	2.62E-04	3.60E-02	3.76E-07	1.96E-03	1.70E-05	4.19E-03	2.98E-11	0.00E+00	6.64E-04	6.50E-02	1.08E-04	2.00E-02	protein catabolism	P
GO:0030165	28	5.56E-01	1.00E+00	4.53E-01	1.00E+00	7.84E-01	1.00E+00	6.64E-01	1.00E+00	4.58E-01	1.00E+00	2.59E-01	1.00E+00	4.32E-01	1.00E+00	6.11E-01	1.00E+00	PDZ domain binding	F
GO:0030166	24	9.96E-01	1.00E+00	9.67E-01	1.00E+00	3.76E-01	1.00E+00	9.71E-01	1.00E+00	9.99E-01	1.00E+00	9.46E-01	1.00E+00	9.75E-01	1.00E+00	8.84E-01	1.00E+00	proteoglycan biosynthesis	P
GO:0030168	22	2.26E-01	1.00E+00	2.85E-01	1.00E+00	3.36E-01	1.00E+00	1.41E-01	1.00E+00	2.75E-01	1.00E+00	3.40E-01	1.00E+00	1.53E-01	1.00E+00	6.31E-01	1.00E+00	platelet activation	P
GO:0030169	17	1.36E-01	1.00E+00	2.52E-01	1.00E+00	8.92E-01	1.00E+00	6.66E-01	1.00E+00	4.86E-02	1.00E+00	2.27E-01	1.00E+00	1.53E-01	1.00E+00	1.22E-01	1.00E+00	low-density lipoprotein binding	F
GO:0030170	58	3.26E-02	1.00E+00	1.59E-01	1.00E+00	8.68E-03	4.60E-01	2.20E-01	1.00E+00	1.12E-01	1.00E+00	2.43E-01	1.00E+00	1.40E-01	1.00E+00	1.34E-01	1.00E+00	pyridoxal phosphate binding	F
GO:0030173	40	4.43E-01	1.00E+00	7.28E-02	1.00E+00	3.95E-01	1.00E+00	2.75E-01	1.00E+00	4.60E-01	1.00E+00	4.51E-02	1.00E+00	2.66E-01	1.00E+00	2.17E-01	1.00E+00	integral to Golgi membrane	C
GO:0030175	17	8.36E-02	1.00E+00	2.25E-03	1.77E-01	1.26E-01	1.00E+00	1.28E-01	1.00E+00	6.99E-02	1.00E+00	3.07E-03	2.39E-01	4.53E-01	1.00E+00	1.22E-02	6.47E-01	filopodium	C
GO:0030176	38	1.59E-01	1.00E+00	1.37E-03	9.10E-02	2.16E-01	1.00E+00	1.94E-01	1.00E+00	1.52E-01	1.00E+00	9.45E-04	5.49E-02	6.61E-01	1.00E+00	1.34E-01	1.00E+00	integral to endoplasmic reticulum membran	C
GO:0030178	20	3.18E-01	1.00E+00	4.74E-01	1.00E+00	5.08E-01	1.00E+00	2.28E-01	1.00E+00	4.43E-01	1.00E+00	4.49E-01	1.00E+00	1.62E-01	1.00E+00	9.31E-01	1.00E+00	negative regulation of Wnt receptor signalin	P
GO:0030182	346	9.92E-01	1.00E+00	9.97E-01	1.00E+00	9.04E-01	1.00E+00	9.80E-01	1.00E+00	9.43E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	neuron differentiation	P
GO:0030183	52	3.97E-01	1.00E+00	8.76E-01	1.00E+00	3.55E-01	1.00E+00	8.73E-01	1.00E+00	3.55E-01	1.00E+00	6.92E-01	1.00E+00	6.69E-01	1.00E+00	9.89E-01	1.00E+00	B cell differentiation	P
GO:0030193	19	3.63E-02	1.00E+00	1.87E-01	1.00E+00	2.23E-02	1.00E+00	2.72E-01	1.00E+00	1.02E-01	1.00E+00	1.23E-01	1.00E+00	8.23E-02	1.00E+00	6.18E-01	1.00E+00	regulation of blood coagulation	P

GO:0030195	15	5.21E-02	1.00E+00	9.50E-02	1.00E+00	5.93E-02	1.00E+00	1.31E-01	1.00E+00	6.51E-02	1.00E+00	7.71E-02	1.00E+00	2.54E-01	1.00E+00	4.06E-01	1.00E+00	negative regulation of blood coagulation	P
GO:0030198	95	9.82E-01	1.00E+00	7.52E-01	1.00E+00	4.16E-01	1.00E+00	7.44E-02	1.00E+00	9.87E-01	1.00E+00	8.54E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	extracellular matrix organization and biogen	P
GO:0030199	16	9.98E-01	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	8.61E-01	1.00E+00	9.63E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	4.66E-01	1.00E+00	collagen fibril organization	P
GO:0030201	13	9.77E-01	1.00E+00	9.57E-01	1.00E+00	9.50E-01	1.00E+00	4.08E-01	1.00E+00	7.69E-01	1.00E+00	9.78E-01	1.00E+00	8.30E-01	1.00E+00	9.98E-01	1.00E+00	heparan sulfate proteoglycan metabolism	P
GO:0030203	47	6.26E-01	1.00E+00	3.64E-01	1.00E+00	4.12E-01	1.00E+00	2.44E-01	1.00E+00	6.49E-01	1.00E+00	5.84E-01	1.00E+00	7.12E-01	1.00E+00	1.69E-01	1.00E+00	glycosaminoglycan metabolism	P
GO:0030216	39	7.59E-01	1.00E+00	8.91E-01	1.00E+00	8.03E-01	1.00E+00	9.47E-01	1.00E+00	6.31E-01	1.00E+00	8.62E-01	1.00E+00	9.15E-01	1.00E+00	4.89E-01	1.00E+00	keratinocyte differentiation	P
GO:0030217	62	2.45E-01	1.00E+00	7.24E-02	1.00E+00	1.82E-01	1.00E+00	1.05E-01	1.00E+00	1.96E-01	1.00E+00	1.63E-01	1.00E+00	8.43E-01	1.00E+00	3.77E-02	1.00E+00	T cell differentiation	P
GO:0030218	44	2.12E-01	1.00E+00	3.34E-01	1.00E+00	4.27E-01	1.00E+00	4.98E-01	1.00E+00	1.96E-01	1.00E+00	3.64E-01	1.00E+00	2.70E-01	1.00E+00	2.65E-01	1.00E+00	erythrocyte differentiation	P
GO:0030225	15	8.40E-01	1.00E+00	4.38E-01	1.00E+00	7.92E-01	1.00E+00	3.88E-01	1.00E+00	7.12E-01	1.00E+00	4.61E-01	1.00E+00	1.00E+00	1.00E+00	5.24E-01	1.00E+00	macrophage differentiation	P
GO:0030228	13	2.73E-01	1.00E+00	1.46E-01	1.00E+00	9.35E-01	1.00E+00	6.96E-01	1.00E+00	1.75E-01	1.00E+00	7.09E-02	1.00E+00	1.82E-01	1.00E+00	1.50E-01	1.00E+00	lipoprotein receptor activity	F
GO:0030234	885	4.25E-03	3.28E-01	1.05E-03	9.10E-02	1.93E-02	1.00E+00	1.29E-02	8.18E-01	3.85E-03	2.85E-01	2.57E-03	2.39E-01	1.89E-01	1.00E+00	2.61E-02	1.00E+00	enzyme regulator activity	F
GO:0030239	16	8.56E-01	1.00E+00	6.97E-02	1.00E+00	2.67E-01	1.00E+00	3.82E-02	1.00E+00	9.77E-01	1.00E+00	1.20E-01	1.00E+00	9.92E-01	1.00E+00	7.71E-01	1.00E+00	myofibril assembly	P
GO:0030246	330	9.87E-01	1.00E+00	7.23E-01	1.00E+00	9.39E-01	1.00E+00	8.91E-01	1.00E+00	9.78E-01	1.00E+00	5.18E-01	1.00E+00	8.86E-01	1.00E+00	7.45E-01	1.00E+00	carbohydrate binding	F
GO:0030247	114	9.54E-01	1.00E+00	9.75E-01	1.00E+00	5.70E-01	1.00E+00	9.40E-01	1.00E+00	9.64E-01	1.00E+00	9.24E-01	1.00E+00	9.26E-01	1.00E+00	9.64E-01	1.00E+00	polysaccharide binding	F
GO:0030258	37	2.83E-01	1.00E+00	1.15E-02	6.77E-01	5.00E-01	1.00E+00	3.18E-02	1.00E+00	4.36E-01	1.00E+00	3.58E-02	1.00E+00	1.09E-02	6.30E-01	1.84E-02	1.00E+00	lipid modification	P
GO:0030260	11	6.16E-01	1.00E+00	2.35E-01	1.00E+00	9.19E-01	1.00E+00	3.58E-01	1.00E+00	5.71E-01	1.00E+00	2.09E-01	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	entry into host cell	P
GO:0030261	23	3.79E-03	3.28E-01	7.34E-03	3.60E-01	3.72E-01	1.00E+00	7.87E-04	4.70E-02	2.60E-02	1.00E+00	3.15E-01	1.00E+00	7.57E-03	5.44E-01	4.59E-03	3.60E-01	chromosome condensation	P
GO:0030262	23	1.31E-01	1.00E+00	4.34E-02	1.00E+00	2.57E-01	1.00E+00	7.64E-03	4.55E-01	1.39E-01	1.00E+00	1.42E-01	1.00E+00	4.08E-01	1.00E+00	5.51E-01	1.00E+00	apoptotic nuclear changes	P
GO:0030278	34	9.82E-01	1.00E+00	3.09E-01	1.00E+00	9.63E-01	1.00E+00	5.33E-01	1.00E+00	9.41E-01	1.00E+00	3.49E-01	1.00E+00	9.66E-01	1.00E+00	1.45E-01	1.00E+00	regulation of ossification	P
GO:0030279	11	8.86E-01	1.00E+00	2.27E-01	1.00E+00	4.63E-01	1.00E+00	4.02E-01	1.00E+00	8.91E-01	1.00E+00	2.04E-01	1.00E+00	1.00E+00	1.00E+00	4.38E-01	1.00E+00	negative regulation of ossification	P
GO:0030282	39	8.91E-01	1.00E+00	7.59E-01	1.00E+00	8.62E-01	1.00E+00	7.67E-01	1.00E+00	7.78E-01	1.00E+00	8.31E-01	1.00E+00	9.86E-01	1.00E+00	2.63E-01	1.00E+00	bone mineralization	P
GO:0030286	33	6.33E-01	1.00E+00	5.02E-01	1.00E+00	1.75E-01	1.00E+00	5.30E-01	1.00E+00	8.90E-01	1.00E+00	3.77E-01	1.00E+00	5.47E-01	1.00E+00	6.67E-01	1.00E+00	dynein complex	C
GO:0030288	27	7.65E-01	1.00E+00	8.82E-01	1.00E+00	5.81E-01	1.00E+00	9.92E-01	1.00E+00	8.53E-01	1.00E+00	7.19E-01	1.00E+00	4.16E-01	1.00E+00	7.03E-01	1.00E+00	periplasmic space (sensu Proteobacteria)	C
GO:0030295	14	2.72E-01	1.00E+00	6.83E-01	1.00E+00	1.80E-01	1.00E+00	1.00E+00	1.00E+00	2.30E-01	1.00E+00	4.05E-01	1.00E+00	9.88E-01	1.00E+00	8.62E-01	1.00E+00	protein kinase activator activity	F
GO:0030301	15	7.88E-02	1.00E+00	3.03E-01	1.00E+00	5.12E-02	1.00E+00	1.88E-01	1.00E+00	7.98E-02	1.00E+00	3.85E-01	1.00E+00	5.04E-01	1.00E+00	5.08E-01	1.00E+00	cholesterol transport	P
GO:0030308	64	6.87E-02	1.00E+00	7.21E-03	3.60E-01	6.93E-02	1.00E+00	3.35E-02	1.00E+00	4.32E-02	1.00E+00	1.58E-02	7.63E-01	7.03E-01	1.00E+00	6.42E-02	1.00E+00	negative regulation of cell growth	P
GO:0030312	31	8.42E-01	1.00E+00	9.31E-01	1.00E+00	6.14E-01	1.00E+00	9.89E-01	1.00E+00	9.24E-01	1.00E+00	8.24E-01	1.00E+00	4.25E-01	1.00E+00	7.92E-01	1.00E+00	external encapsulating structure	C
GO:0030313	28	7.70E-01	1.00E+00	9.12E-01	1.00E+00	5.82E-01	1.00E+00	9.96E-01	1.00E+00	8.64E-01	1.00E+00	7.63E-01	1.00E+00	3.85E-01	1.00E+00	7.45E-01	1.00E+00	cell envelope	C
GO:0030315	13	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.46E-01	1.00E+00	9.44E-01	1.00E+00	1.00E+00	1.00E+00	8.33E-01	1.00E+00	1.00E+00	1.00E+00	T-tubule	C
GO:0030316	17	9.15E-01	1.00E+00	7.97E-01	1.00E+00	9.60E-01	1.00E+00	9.18E-01	1.00E+00	8.25E-01	1.00E+00	7.75E-01	1.00E+00	9.34E-01	1.00E+00	2.60E-01	1.00E+00	osteoclast differentiation	P
GO:0030317	26	6.47E-01	1.00E+00	9.98E-01	1.00E+00	5.51E-01	1.00E+00	9.14E-01	1.00E+00	7.34E-01	1.00E+00	9.94E-01	1.00E+00	3.77E-01	1.00E+00	9.93E-01	1.00E+00	sperm motility	P
GO:0030318	17	4.13E-01	1.00E+00	3.88E-01	1.00E+00	7.97E-01	1.00E+00	6.58E-01	1.00E+00	4.16E-01	1.00E+00	4.35E-01	1.00E+00	1.58E-01	1.00E+00	1.50E-01	1.00E+00	melanocyte differentiation	P
GO:0030323	74	8.05E-01	1.00E+00	8.85E-01	1.00E+00	9.87E-01	1.00E+00	9.73E-01	1.00E+00	5.87E-01	1.00E+00	8.71E-01	1.00E+00	7.43E-01	1.00E+00	3.32E-01	1.00E+00	respiratory tube development	P
GO:0030324	71	8.52E-01	1.00E+00	8.96E-01	1.00E+00	9.89E-01	1.00E+00	9.64E-01	1.00E+00	6.50E-01	1.00E+00	8.96E-01	1.00E+00	7.98E-01	1.00E+00	3.59E-01	1.00E+00	lung development	P
GO:0030326	70	9.98E-01	1.00E+00	9.84E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	4.86E-01	1.00E+00	9.72E-01	1.00E+00	embryonic limb morphogenesis	P
GO:0030330	17	3.28E-02	1.00E+00	2.66E-01	1.00E+00	1.36E-01	1.00E+00	3.75E-01	1.00E+00	4.41E-02	1.00E+00	3.10E-01	1.00E+00	4.21E-02	1.00E+00	3.03E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0030334	87	3.78E-01	1.00E+00	6.56E-01	1.00E+00	1.57E-01	1.00E+00	4.97E-01	1.00E+00	3.89E-01	1.00E+00	7.17E-01	1.00E+00	7.14E-01	1.00E+00	5.73E-01	1.00E+00	regulation of cell migration	P
GO:0030335	35	7.30E-01	1.00E+00	8.27E-01	1.00E+00	2.62E-01	1.00E+00	6.94E-01	1.00E+00	8.32E-01	1.00E+00	8.63E-01	1.00E+00	9.00E-01	1.00E+00	4.03E-01	1.00E+00	positive regulation of cell migration	P
GO:0030336	26	1.78E-01	1.00E+00	2.88E-01	1.00E+00	3.09E-01	1.00E+00	1.85E-01	1.00E+00	1.38E-01	1.00E+00	4.54E-01	1.00E+00	2.36E-01	1.00E+00	1.69E-01	1.00E+00	negative regulation of cell migration	P
GO:0030374	28	8.13E-02	1.00E+00	2.68E-02	1.00E+00	2.07E-02	1.00E+00	2.91E-02	1.00E+00	1.07E-01	1.00E+00	2.95E-02	1.00E+00	5.20E-01	1.00E+00	3.88E-01	1.00E+00	ligand-dependent nuclear receptor transcrip	F
GO:0030375	11	8.81E-01	1.00E+00	2.08E-01	1.00E+00	7.56E-01	1.00E+00	2.87E-01	1.00E+00	7.73E-01	1.00E+00	2.03E-01	1.00E+00	9.99E-01	1.00E+00	3.36E-01	1.00E+00	thyroid hormone receptor coactivator activit	F
GO:0030384	65	8.79E-04	8.30E-02	2.44E-03	1.77E-01	3.83E-02	1.00E+00	1.17E-02	8.18E-01	1.50E-03	1.76E-01	1.10E-02	7.39E-01	2.51E-02	1.00E+00	1.47E-02	8.49E-01	phosphoinositide metabolism	P
GO:0030414	183	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.23E-01	1.00E+00	1.00E+00	1.00E+00	protease inhibitor activity	F
GO:0030424	68	9.61E-01	1.00E+00	8.29E-01	1.00E+00	6.91E-01	1.00E+00	4.23E-01	1.00E+00	9.38E-01	1.00E+00	7.59E-01	1.00E+00	9.97E-01	1.00E+00	9.83E-01	1.00E+00	axon	C
GO:0030425	71	9.16E-01	1.00E+00	5.90E-01	1.00E+00	5.77E-01	1.00E+00	2.25E-01	1.00E+00	9.38E-01	1.00E+00	5.75E-01	1.00E+00	8.20E-01	1.00E+00	9.71E-01	1.00E+00	dendrite	C
GO:0030426	29	9.42E-01	1.00E+00	9.76E-01	1.00E+00	9.11E-01	1.00E+00	9.77E-01	1.00E+00	8.40E-01	1.00E+00	7.98E-01	1.00E+00	9.45E-01	1.00E+00	9.99E-01	1.00E+00	growth cone	C
GO:0030427	30	8.20E-01	1.00E+00	9.07E-01	1.00E+00	8.86E-01	1.00E+00	9.59E-01	1.00E+00	7.17E-01	1.00E+00	7.23E-01	1.00E+00	6.87E-01	1.00E+00	8.11E-01	1.00E+00	site of polarized growth	C
GO:0030433	18	2.10E-02	1.00E+00	2.66E-06	8.39E-03	7.48E-02	1.00E+00	4.69E-02	1.00E+00	7.63E-02	1.00E+00	5.44E-05	1.70E-02	3.98E-02	1.00E+00	8.88E-03	4.81E-01	ER-associated protein catabolism	P
GO:0030496	12	9.25E-03	6.67E-01	1.64E-02	1.00E+00	2.63E-01	1.00E+00	3.06E-01	1.00E+00	1.11E-02	5.39E-01	2.00E-02	1.00E+00	3.37E-01	1.00E+00	3.94E-02	1.00E+00	midbody	C
GO:0030500	23	9.78E-01	1.00E+00	3.23E-01	1.00E+00	9.42E-01	1.00E+00	4.80E-01	1.00E+00	9.62E-01	1.00E+00	4.38E-01	1.00E+00	7.88E-01	1.00E+00	1.17E-01	1.00E+00	regulation of bone mineralization	P
GO:0030501	14	9.72E-01	1.00E+00	5.19E-01	1.00E+00	9.90E-01	1.00E+00	4.95E-01	1.00E+00	9.04E-01	1.00E+00	7.72E-01	1.00E+00	6.77E-01	1.00E+00	1.16E-01	1.00E+00	positive regulation of bone mineralization	P
GO:0030509	52	7.51E-01	1.00E+00	7.49E-01	1.00E+00	7.13E-01	1.00E+00	3.45E-01	1.00E+00	6.69E-01	1.00E+00	8.84E-01	1.00E+00	7.46E-01	1.00E+00	4.54E-01	1.00E+00	BMP signaling pathway	P
GO:0030510	19	7.82E-01	1.00E+00	8.90E-01	1.00E+00	4.27E-01	1.00E+00	8.01E-01	1.00E+00	7.20E-01	1.00E+00	8.47E-01	1.00E+00	9.99E-01	1.00E+00	7.15E-01	1.00E+00	regulation of BMP signaling pathway	P
GO:0030514	13	5.69E-01	1.00E+00	6.97E-01	1.00E+00	3.31E-01	1.00E+00	6.64E-01	1.00E+00	5.52E-01	1.00E+00	6.89E-01	1.00E+00	9.85E-01	1.00E+00	5.80E-01	1.00E+00	negative regulation of BMP signaling pathw	P
GO:0030516	15	6.16E-01	1.00E+00	5.92E-01	1.00E+00	4.72E-01	1.00E+00	2.31E-01	1.00E+00	6.14E-01	1.00E+00	5.79E-01	1.00E+00	5.84E-01	1.00E+00	9.90E-01	1.00E+00	regulation of axon extension	P
GO:0030518	51	4.23E-03	3.28E-01	4.36E-04	6.90E-02	4.58E-03	3.27E-01	8.64E-03	7.13E-01	1.99E-02	1.00E+00	1.47E-03	1.61E-01	3.18E-01	1.00E+00	4.65E-02	1.00E+00	steroid hormone receptor signaling pathway	P
GO:0030520	10	2.21E-02	1.00E+00	1.79E-05	9.58E-03	2.90E-02	1.00E+00	1.18E-03	1.15E-01	1.43E-01	1.00E+00	9.02E-04	5.49E-02	7.39E-02	1.00E+00	1.21E-04	2.00E-02	estrogen receptor signaling pathway	P
GO:0030521	35	1.56E-02	6.67E-01	1.00E-02	5.18E-01	1.05E-02	5.32E-01	1.99E-01	1.00E+00	3.62E-02	1.00E+00	7.70E-03	5.30E-01	5.16E-01	1.00E+00	1.00E-01	1.00E+00	androgen receptor signaling pathway	P
GO:0030522	61	1.53E-02	6.67E-01	2.24E-03	1.77E-01	1.24E-02	5.32E-01	1.93E-02	1.00E+00	4.99E-02	1.00E+00	6.61E-03	5.30E-01	3.70E-01	1.00E+00	5.57E-02	1.00E+00	intracellular receptor-mediated signaling pa	P
GO:0030528	1585	1.53E-09	8.06E-04	9.32E-09	4.97E-03	6.60E-06	2.66E-03	5.97E-05	1.20E-02	5.41E-09	9.64E-04	2.95E-07	9.41E-04	8.91E-03	6.30E-01	1.18E-04	2.00E-02	transcription regulator activity	F
GO:0030529	572	1.26E-22	0.00E+00	1.79E-14	0.00E+00	7.22E-12	0.00E+00	1.55E-05	8.00E-03	2.93E-18	0.00E+00	1.33E-12	0.00E+00	2.29E-09	0.00E+00	3.83E-07	1.88E-03	ribonucleoprotein complex	C
GO:0030530	17	8.22E-10	8.06E-04	1.66E-05	9.58E-03	5.43E-03	4.19E-01	7.64E-04	4.70E-02	4.63E-09	9.64E-04	2.27E-04	2.60E-02	8.42E-03	6.30E-01	3.00E-03	1.85E-01	heterogeneous nuclear ribonucleoprotein c	C
GO:0030532	24	1.03E-03	9.60E-02	6.08E-04	6.90E-02	5.03E-03	4.19E-01	2.92E-02	1.00E+00	5.91E-03	5.39E-01	5.01E-04	4.10E-02	4.08E-02	1.00E+00	1.52E-01	1.00E+00	small nuclear ribonucleoprotein complex	C
GO:0030534	67	4.40E-01	1.00E+00	6.94E-01	1.00E+00	6.19E-01	1.00E+00	2.49E-01	1.00E+00	3.74E-01	1.00E+00	8.66E-01	1.00E+00	4.64E-01	1.00E+00	3.24E-01	1.00E+00	adult behavior	P
GO:0030539	12	1.00E+00	1.00E+00	8.68E-01	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	8.01E-01	1.00E+00	1.00E+00	1.00E+00	7.36E-01	1.00E+00	male genitalia development	P
GO:0030545	16	9.99E-01	1.00E+00	7.12E-01	1.00E+00	9.98E-01	1.00E+00	8.50E-01	1.00E+00	9.99E-01	1.00E+00	6.54E-01	1.00E+00	6.89E-01	1.00E+00	6.54E-01	1.00E+00	receptor regulator activity	F
GO:0030547	12	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	7.73E-01	1.00E+00	9.72E-01	1.00E+00	receptor inhibitor activity	F
GO:0030551	29	9.04E-01	1.00E+00	9.04E-01	1.00E+00	7.69E-01	1.00E+00	5.89E-01	1.00E+00	9.28E-01	1.00E+00	8.67E-01	1.00E+00	5.47E-01	1.00E+00	9.80E-01	1.00E+00	cyclic nucleotide binding	F
GO:0030552	20	6.35E-01	1.00E+00	7.77E-01	1.00E+00	4.97E-01	1.00E+00	4.06E-01	1.00E+00	6.47E-01	1.00E+00	7.80E-01	1.00E+00	6.91E-01	1.00E+00	9.63E-01	1.00E+00	cAMP binding	F
GO:0030554	1679	6.35E-23	0.00E+00	1.56E-32	0.00E+00	5.10E-14	0.00E+00	1.39E-16	0.00E+00	1.17E-19	0.00E+00	2.76E-29	0.00E+00	5.75E-06	2.00E-03	3.96E-08	7.71E-04	adenyl nucleotide binding	F
GO:0030574	20	8.70E-01	1.00E+00	8.39E-01	1.00E+00	1.82E-01	1.00E+00	6.52E-01	1.00E+00	9.74E-01	1.00E+00	7.84E-01	1.00E+00	9.79E-01	1.00E+00	8.05E-01	1.00E+00	collagen catabolism	P
GO:0030593	15	3.23E-01	1.00E+00	4.78E-01	1.00E+00	5.69E-01	1.00E+00	1.28E-01	1.00E+00	3.51E-01	1.00E+00	6.66E-01	1.00E+00	1.18E-01	1.00E+00	5.28E-01	1.00E+00	neutrophil chemotaxis	P
GO:0030594	263	9.23E-01	1.00E+00	1.00E+00	1.00E+00	5.99E-01	1.00E+00	9.93E-01	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	5.95E-01	1.00E+00	7.34E-01	1.00E+00	neurotransmitter receptor activity	F
GO:0030595	28	2.89E-01	1.00E+00	2.87E-01	1.00E+00	2.53E-01	1.00E+00	8.16E-02	1.00E+00	3.64E-01	1.00E+00	5.11E-01	1.00E+00	1.88E-01	1.00E+00	1.88E-01	1.00E+00	leukocyte chemotaxis	P
GO:0030641	14	1.78E-01	1.00E+00	1.52E-01	1.00E+00	4.32E-01	1.00E+00	5.09E-01	1.00E+00	1.71E-01	1.00E+00	9.37E-02	1.00E+00	1.43E-01	1.00E+00	4.42E-01	1.00E+00	hydrogen ion homeostasis	P

GO:0030658	21	2.76E-02	1.00E+00	1.71E-02	1.00E+00	8.32E-02	1.00E+00	2.98E-01	1.00E+00	4.25E-02	1.00E+00	2.14E-02	1.00E+00	5.27E-02	1.00E+00	2.56E-01	1.00E+00	transport vesicle membrane	C
GO:0030659	110	4.37E-05	1.00E-02	1.10E-04	1.50E-02	8.55E-04	7.56E-02	6.32E-03	3.64E-01	5.00E-05	6.35E-03	2.47E-04	2.60E-02	4.06E-02	1.00E+00	1.90E-01	1.00E+00	cytoplasmic vesicle membrane	C
GO:0030660	23	1.09E-02	6.67E-01	1.86E-02	1.00E+00	7.39E-02	1.00E+00	3.48E-01	1.00E+00	1.52E-02	1.00E+00	1.95E-02	1.00E+00	3.58E-02	1.00E+00	2.72E-01	1.00E+00	Golgi-associated vesicle membrane	C
GO:0030662	39	6.56E-04	3.44E-02	4.74E-04	6.90E-02	2.05E-02	1.00E+00	1.09E-01	1.00E+00	6.97E-04	4.00E-02	2.30E-04	2.60E-02	2.89E-02	1.00E+00	6.51E-02	1.00E+00	coated vesicle membrane	C
GO:0030665	23	3.36E-02	1.00E+00	4.80E-03	3.60E-01	1.58E-01	1.00E+00	1.40E-01	1.00E+00	3.85E-02	1.00E+00	2.71E-03	2.39E-01	6.48E-02	1.00E+00	3.19E-01	1.00E+00	clathrin coated vesicle membrane	C
GO:0030666	11	4.18E-02	1.00E+00	1.69E-01	1.00E+00	1.36E-01	1.00E+00	5.61E-01	1.00E+00	2.49E-02	1.00E+00	1.05E-01	1.00E+00	1.72E-01	1.00E+00	2.85E-01	1.00E+00	endocytic vesicle membrane	C
GO:0030667	17	1.58E-01	1.00E+00	1.93E-02	1.00E+00	8.46E-02	1.00E+00	7.45E-02	1.00E+00	1.54E-01	1.00E+00	3.93E-02	1.00E+00	8.39E-01	1.00E+00	4.25E-01	1.00E+00	secretory granule membrane	C
GO:0030672	10	4.36E-01	1.00E+00	6.29E-01	1.00E+00	3.66E-01	1.00E+00	5.70E-01	1.00E+00	4.01E-01	1.00E+00	7.84E-01	1.00E+00	7.17E-01	1.00E+00	3.21E-01	1.00E+00	synaptic vesicle membrane	C
GO:0030674	83	9.96E-02	1.00E+00	6.16E-02	1.00E+00	2.54E-01	1.00E+00	2.94E-02	1.00E+00	7.68E-02	1.00E+00	9.16E-02	1.00E+00	4.23E-01	1.00E+00	1.92E-01	1.00E+00	protein binding, bridging	F
GO:0030693	21	4.87E-01	1.00E+00	5.12E-01	1.00E+00	2.44E-01	1.00E+00	3.33E-01	1.00E+00	4.42E-01	1.00E+00	6.13E-01	1.00E+00	9.59E-01	1.00E+00	6.39E-01	1.00E+00	caspase activity	F
GO:0030695	410	1.82E-04	2.50E-02	1.02E-05	9.58E-03	7.07E-05	1.20E-02	7.78E-04	4.70E-02	7.44E-04	4.00E-02	2.54E-04	2.60E-02	5.80E-01	1.00E+00	5.84E-03	3.60E-01	GTPase regulator activity	F
GO:0030705	132	1.99E-04	2.50E-02	1.53E-02	1.00E+00	8.14E-03	4.60E-01	2.02E-02	1.00E+00	2.08E-04	1.70E-02	1.36E-02	7.39E-01	2.07E-02	9.11E-01	7.48E-01	1.00E+00	cytoskeleton-dependent intracellular transp	P
GO:0030742	10	6.67E-02	1.00E+00	3.27E-02	1.00E+00	1.48E-01	1.00E+00	2.48E-03	1.47E-01	5.48E-02	1.00E+00	6.71E-02	1.00E+00	6.12E-02	1.00E+00	3.15E-01	1.00E+00	GTP-dependent protein binding	F
GO:0030799	14	2.60E-01	1.00E+00	2.06E-01	1.00E+00	2.29E-01	1.00E+00	2.61E-01	1.00E+00	2.38E-01	1.00E+00	1.53E-01	1.00E+00	5.42E-01	1.00E+00	5.35E-01	1.00E+00	regulation of cyclic nucleotide metabolism	P
GO:0030802	10	2.17E-01	1.00E+00	4.11E-01	1.00E+00	2.26E-01	1.00E+00	3.59E-01	1.00E+00	2.38E-01	1.00E+00	4.03E-01	1.00E+00	2.85E-01	1.00E+00	4.84E-01	1.00E+00	regulation of cyclic nucleotide biosynthesis	P
GO:0030808	10	2.17E-01	1.00E+00	4.11E-01	1.00E+00	2.26E-01	1.00E+00	3.59E-01	1.00E+00	2.38E-01	1.00E+00	4.03E-01	1.00E+00	2.85E-01	1.00E+00	4.84E-01	1.00E+00	regulation of nucleotide biosynthesis	P
GO:0030832	58	1.09E-02	6.67E-01	1.08E-01	1.00E+00	2.28E-02	1.00E+00	3.29E-01	1.00E+00	1.35E-02	1.00E+00	1.03E-01	1.00E+00	5.16E-01	1.00E+00	2.22E-01	1.00E+00	regulation of actin filament length	P
GO:0030833	27	2.84E-02	1.00E+00	5.47E-02	1.00E+00	1.59E-01	1.00E+00	4.33E-01	1.00E+00	1.01E-02	5.39E-01	3.64E-02	1.00E+00	6.01E-01	1.00E+00	2.54E-01	1.00E+00	regulation of actin filament polymerization	P
GO:0030834	25	8.95E-02	1.00E+00	4.27E-01	1.00E+00	3.53E-02	1.00E+00	2.51E-01	1.00E+00	1.82E-01	1.00E+00	5.37E-01	1.00E+00	7.18E-01	1.00E+00	5.94E-01	1.00E+00	regulation of actin filament depolymerizatio	P
GO:0030835	23	7.53E-02	1.00E+00	3.25E-01	1.00E+00	4.52E-02	1.00E+00	1.61E-01	1.00E+00	1.50E-01	1.00E+00	5.25E-01	1.00E+00	7.10E-01	1.00E+00	4.85E-01	1.00E+00	negative regulation of actin filament depoly	P
GO:0030855	55	9.82E-01	1.00E+00	9.04E-01	1.00E+00	9.21E-01	1.00E+00	8.53E-01	1.00E+00	9.79E-01	1.00E+00	8.45E-01	1.00E+00	7.38E-01	1.00E+00	9.44E-01	1.00E+00	epithelial cell differentiation	P
GO:0030856	12	9.87E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.53E-01	1.00E+00	9.77E-01	1.00E+00	9.70E-01	1.00E+00	4.68E-01	1.00E+00	1.00E+00	1.00E+00	regulation of epithelial cell differentiation	P
GO:0030863	32	2.67E-02	1.00E+00	7.93E-03	3.60E-01	4.69E-03	3.27E-01	1.90E-01	1.00E+00	7.15E-02	1.00E+00	7.39E-03	5.30E-01	2.35E-01	1.00E+00	6.41E-02	1.00E+00	cortical cytoskeleton	C
GO:0030864	22	7.56E-02	1.00E+00	2.91E-02	1.00E+00	2.12E-02	1.00E+00	3.31E-01	1.00E+00	1.46E-01	1.00E+00	2.42E-02	1.00E+00	3.83E-01	1.00E+00	8.10E-02	1.00E+00	cortical actin cytoskeleton	C
GO:0030865	11	2.03E-02	1.00E+00	9.52E-03	5.18E-01	5.37E-01	1.00E+00	1.07E-01	1.00E+00	6.38E-03	5.39E-01	5.09E-03	2.70E-01	2.09E-01	1.00E+00	1.28E-01	1.00E+00	cortical cytoskeleton organization and biogе	P
GO:0030866	10	5.36E-02	1.00E+00	2.79E-02	1.00E+00	6.46E-01	1.00E+00	1.03E-01	1.00E+00	2.00E-02	1.00E+00	1.22E-02	7.39E-01	2.63E-01	1.00E+00	1.72E-01	1.00E+00	cortical actin cytoskeleton organization and	P
GO:0030867	11	3.19E-01	1.00E+00	7.39E-02	1.00E+00	4.40E-01	1.00E+00	2.50E-01	1.00E+00	4.09E-01	1.00E+00	6.79E-02	1.00E+00	6.39E-02	1.00E+00	1.12E-01	1.00E+00	rough endoplasmic reticulum membrane	C
GO:0030878	10	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	thyroid gland development	P
GO:0030879	28	9.92E-01	1.00E+00	9.83E-01	1.00E+00	9.86E-01	1.00E+00	9.36E-01	1.00E+00	9.48E-01	1.00E+00	9.74E-01	1.00E+00	9.58E-01	1.00E+00	9.72E-01	1.00E+00	mammary gland development	P
GO:0030880	26	4.66E-02	1.00E+00	1.08E-02	6.77E-01	2.85E-01	1.00E+00	1.99E-02	1.00E+00	1.22E-01	1.00E+00	2.49E-02	1.00E+00	6.22E-03	3.57E-01	4.64E-01	1.00E+00	RNA polymerase complex	C
GO:0030888	18	8.23E-01	1.00E+00	5.36E-01	1.00E+00	6.93E-01	1.00E+00	3.61E-01	1.00E+00	7.34E-01	1.00E+00	6.66E-01	1.00E+00	9.46E-01	1.00E+00	3.97E-01	1.00E+00	regulation of B cell proliferation	P
GO:0030890	14	6.74E-01	1.00E+00	4.52E-01	1.00E+00	4.31E-01	1.00E+00	2.51E-01	1.00E+00	6.69E-01	1.00E+00	6.54E-01	1.00E+00	8.10E-01	1.00E+00	2.99E-01	1.00E+00	positive regulation of B cell proliferation	P
GO:0030894	14	2.92E-03	2.39E-01	2.49E-03	1.77E-01	1.54E-01	1.00E+00	4.56E-02	1.00E+00	1.64E-03	1.76E-01	2.81E-03	2.39E-01	1.41E-01	1.00E+00	5.79E-02	1.00E+00	replisome	C
GO:0030900	112	9.26E-01	1.00E+00	9.65E-01	1.00E+00	7.85E-01	1.00E+00	5.95E-01	1.00E+00	9.24E-01	1.00E+00	9.73E-01	1.00E+00	8.76E-01	1.00E+00	9.85E-01	1.00E+00	forebrain development	P
GO:0030901	12	9.66E-01	1.00E+00	9.93E-01	1.00E+00	5.78E-01	1.00E+00	8.37E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	midbrain development	P
GO:0030902	42	8.56E-01	1.00E+00	9.70E-01	1.00E+00	6.34E-01	1.00E+00	9.48E-01	1.00E+00	9.31E-01	1.00E+00	8.99E-01	1.00E+00	6.42E-01	1.00E+00	9.97E-01	1.00E+00	hindbrain development	P
GO:0030955	125	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	9.35E-01	1.00E+00	potassium ion binding	F
GO:0030968	17	4.09E-01	1.00E+00	7.56E-02	1.00E+00	4.00E-01	1.00E+00	6.62E-01	1.00E+00	4.20E-01	1.00E+00	1.82E-02	8.81E-01	5.93E-01	1.00E+00	6.17E-01	1.00E+00	unfolded protein response	P
GO:0030983	22	4.35E-04	3.37E-02	3.19E-05	9.58E-03	7.55E-02	1.00E+00	1.77E-03	1.24E-01	2.75E-04	1.70E-02	5.54E-05	1.70E-02	2.73E-02	1.00E+00	6.28E-01	1.00E+00	mismatched DNA binding	F
GO:0031012	352	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.58E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	extracellular matrix	C
GO:0031016	21	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	pancreas development	P
GO:0031018	13	1.00E+00	1.00E+00	9.58E-01	1.00E+00	9.19E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	8.62E-01	1.00E+00	endocrine pancreas development	P
GO:0031023	19	2.41E-02	1.00E+00	7.24E-02	1.00E+00	4.81E-02	1.00E+00	1.01E-01	1.00E+00	1.72E-02	1.00E+00	1.15E-01	1.00E+00	6.23E-01	1.00E+00	1.71E-01	1.00E+00	microtubule organizing center organization	P
GO:0031032	12	4.60E-01	1.00E+00	2.27E-01	1.00E+00	1.64E-01	1.00E+00	1.56E-01	1.00E+00	5.86E-01	1.00E+00	2.61E-01	1.00E+00	6.28E-01	1.00E+00	4.82E-01	1.00E+00	actomyosin structure organization and biog	P
GO:0031047	14	2.18E-02	1.00E+00	5.98E-03	3.60E-01	3.15E-02	1.00E+00	5.92E-02	1.00E+00	5.89E-02	1.00E+00	5.26E-02	1.00E+00	7.11E-02	1.00E+00	1.66E-02	8.49E-01	RNA-mediated gene silencing	P
GO:0031069	15	9.90E-01	1.00E+00	8.50E-01	1.00E+00	9.79E-01	1.00E+00	8.34E-01	1.00E+00	9.38E-01	1.00E+00	8.31E-01	1.00E+00	1.00E+00	1.00E+00	5.74E-01	1.00E+00	hair follicle morphogenesis	P
GO:0031072	66	1.05E-01	1.00E+00	1.48E-03	9.10E-02	5.84E-02	1.00E+00	2.42E-02	1.00E+00	1.60E-01	1.00E+00	1.99E-03	1.61E-01	5.45E-01	1.00E+00	2.91E-01	1.00E+00	heat shock protein binding	F
GO:0031090	1517	1.66E-24	0.00E+00	2.81E-23	0.00E+00	1.03E-11	0.00E+00	6.09E-10	0.00E+00	1.01E-22	0.00E+00	1.46E-21	0.00E+00	1.38E-07	8.55E-04	2.22E-07	1.88E-03	organelle membrane	C
GO:0031091	45	9.10E-01	1.00E+00	9.15E-01	1.00E+00	6.82E-01	1.00E+00	9.18E-01	1.00E+00	9.36E-01	1.00E+00	8.99E-01	1.00E+00	6.67E-01	1.00E+00	7.17E-01	1.00E+00	platelet alpha granule	C
GO:0031092	10	4.31E-01	1.00E+00	1.73E-01	1.00E+00	1.75E-01	1.00E+00	5.76E-01	1.00E+00	4.47E-01	1.00E+00	1.88E-01	1.00E+00	9.61E-01	1.00E+00	2.05E-01	1.00E+00	platelet alpha granule membrane	C
GO:0031093	33	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.49E-01	1.00E+00	9.41E-01	1.00E+00	9.84E-01	1.00E+00	9.97E-01	1.00E+00	6.46E-01	1.00E+00	9.91E-01	1.00E+00	platelet alpha granule lumen	C
GO:0031098	79	1.40E-02	6.67E-01	2.13E-02	1.00E+00	4.00E-02	1.00E+00	2.23E-02	1.00E+00	1.14E-02	5.39E-01	9.98E-02	1.00E+00	4.00E-01	1.00E+00	6.17E-03	3.60E-01	stress-activated protein kinase signaling pa	P
GO:0031099	28	1.27E-01	1.00E+00	1.12E-01	1.00E+00	2.08E-01	1.00E+00	4.78E-01	1.00E+00	1.70E-01	1.00E+00	7.42E-02	1.00E+00	2.70E-01	1.00E+00	1.61E-01	1.00E+00	regeneration	P
GO:0031105	12	3.44E-02	1.00E+00	1.49E-04	1.50E-02	7.97E-02	1.00E+00	2.18E-01	1.00E+00	6.56E-02	1.00E+00	1.19E-03	6.40E-02	5.59E-02	1.00E+00	4.02E-01	1.00E+00	septin complex	C
GO:0031109	32	1.94E-01	1.00E+00	9.64E-01	1.00E+00	3.21E-02	1.00E+00	7.89E-01	1.00E+00	4.11E-01	1.00E+00	9.50E-01	1.00E+00	2.29E-01	1.00E+00	9.13E-01	1.00E+00	microtubule polymerization or depolymeriza	P
GO:0031110	29	1.27E-01	1.00E+00	8.92E-01	1.00E+00	2.00E-02	1.00E+00	7.05E-01	1.00E+00	2.85E-01	1.00E+00	8.77E-01	1.00E+00	2.52E-01	1.00E+00	8.33E-01	1.00E+00	regulation of microtubule polymerization or	P
GO:0031111	18	6.41E-02	1.00E+00	5.17E-01	1.00E+00	3.95E-03	3.27E-01	5.36E-01	1.00E+00	1.32E-01	1.00E+00	4.01E-01	1.00E+00	4.66E-01	1.00E+00	7.98E-01	1.00E+00	negative regulation of microtubule polymeri	P
GO:0031112	12	6.96E-01	1.00E+00	9.16E-01	1.00E+00	4.13E-01	1.00E+00	6.90E-01	1.00E+00	8.27E-01	1.00E+00	8.94E-01	1.00E+00	2.53E-01	1.00E+00	7.94E-01	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031113	13	2.84E-01	1.00E+00	6.37E-01	1.00E+00	4.30E-01	1.00E+00	6.86E-01	1.00E+00	4.92E-01	1.00E+00	7.25E-01	1.00E+00	1.41E-01	1.00E+00	4.23E-01	1.00E+00	regulation of microtubule polymerization	P
GO:0031114	16	1.29E-01	1.00E+00	7.33E-01	1.00E+00	5.44E-03	4.19E-01	5.44E-01	1.00E+00	2.27E-01	1.00E+00	5.09E-01	1.00E+00	5.93E-01	1.00E+00	9.99E-01	1.00E+00	regulation of microtubule depolymerization	P
GO:0031116	11	6.79E-01	1.00E+00	8.66E-01	1.00E+00	5.49E-01	1.00E+00	6.92E-01	1.00E+00	8.08E-01	1.00E+00	8.45E-01	1.00E+00	1.83E-01	1.00E+00	7.38E-01	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031123	16	9.34E-02	1.00E+00	9.52E-05	1.50E-02	8.95E-02	1.00E+00	1.27E-02	8.18E-01	8.48E-02	1.00E+00	1.01E-04	1.70E-02	7.15E-01	1.00E+00	3.83E-02	1.00E+00	RNA 3'-end processing	P
GO:0031124	13	2.24E-01	1.00E+00	1.20E-03	9.10E-02	2.25E-01	1.00E+00	3.53E-02	1.00E+00	2.19E-01	1.00E+00	1.23E-03	6.40E-02	6.22E-01	1.00E+00	3.75E-02	1.00E+00	mRNA 3'-end processing	P
GO:0031128	14	8.33E-01	1.00E+00	9.96E-01	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	6.16E-01	1.00E+00	9.75E-01	1.00E+00	9.49E-01	1.00E+00	9.83E-01	1.00E+00	induction	P
GO:0031145	65	1.75E-04	2.50E-02	2.49E-04	4.19E-02	1.53E-01	1.00E+00	3.16E-02	1.00E+00	7.88E-05	1.70E-02	8.51E-04	5.49E-02	1.07E-02	6.30E-01	2.70E-03	1.85E-01	anaphase-promoting complex-dependent p	P
GO:0031175	222	9.30E-01	1.00E+00	9.09E-01	1.00E+00	6.36E-01	1.00E+00	9.21E-01	1.00E+00	9.02E-01	1.00E+00	8.94E-01	1.00E+00	9.57E-01	1.00E+00	5.23E-01	1.00E+00	neurite development	P
GO:0031177	18	3.69E-01	1.00E+00	4.14E-02	1.00E+00	6.85E-01	1.00E+00	9.34E-03	7.13E-01	3.12E-01	1.00E+00	8.71E-02	1.00E+00	3.32E-01	1.00E+00	4.35E-02	1.00E+00	phosphopantetheine binding	F
GO:0031201	11	8.85E-01	1.00E+00	3.73E-01	1.00E+00	9.03E-01	1.00E+00	6.22E-01	1.00E+00	7.82E-01	1.00E+00	2.80E-01	1.00E+00	9.32E-01	1.00E+00	4.63E-01	1.00E+00	SNARE complex	C
GO:0031202	24	1.41E-06	1.95E-03	3.26E-05	9.58E-03	6.26E-04	3.60E-02	6.72E-04	4.70E-02	4.56E-05	6.35E-03	9.60E-04	5.49E-02	5.53E-03	3.57E-01	2.53E-04	2.70E-02	RNA splicing factor activity, transesterificati	F
GO:0031214	145	4.83E-01	1.00E+00	6.39E-01	1.00E+00	5.69E-01	1.00E+00	3.87E-01	1.00E+00	3.14E-01	1.00E+00	6.90E-01	1.00E+00	9.48E-01	1.00E+00	6.46E-01	1.00E+00	biomineral formation	P
GO:0031224	5572	9.79E-01	1.00E+00	6.41E-01	1.00E+00	9.61E-01	1.00E+00	9.63E-01	1.00E+00	8.96E-01	1.00E+00	3.09E-01	1.00E+00	9.87E-01	1.00E+00	7.05E-01	1.00E+00	intrinsic to membrane	C
GO:0031225	127	6.67E-01	1.00E+00	9.82E-01	1.00E+00	3.09E-01	1.00E+00	8.36E-01	1.00E+00	5.28E-01	1.00E+00	9.92E-01	1.00E+00	9.80E-01	1.00E+00	6.90E-01	1.00E+00	anchored to membrane	C
GO:0031226	1245	9.98E-01	1.00E+00	9.47E-01	1.00E+00	9.86E-01	1.00E+00	9.96E-01	1.00E+00	9.72E-01	1.00E+00	7.71E-01	1.00E+00	9.99E-01	1.00E+00	8.42E-01	1.00E+00	intrinsic to plasma membrane	C
GO:0031227	47	2.24E-01	1.00E+00	3.73E-02	1.00E+00	1.34E-01	1.00E+00	5.29E-01	1.00E+00	2.62E-01	1.00E+00	1.39E-02	7.39E-01	6.14E-01	1.00E+00	3.46E-01	1.00E+00	intrinsic to endoplasmic reticulum membran	C
GO:0031228	43	4.32E-01	1.00E+00	6.47E-02	1.00E+00	4.50E-01	1.00E+00	2.79E-01	1.00E+00	4.22E-01	1.00E+00	3.13E-02	1.00E+00	3.14E-01	1.00E+00	3.34E-01	1.00E+00	intrinsic to Golgi membrane	C

GO:0031231	12	4.28E-02	1.00E+00	4.11E-01	1.00E+00	5.89E-02	1.00E+00	2.28E-01	1.00E+00	8.79E-02	1.00E+00	3.88E-01	1.00E+00	1.25E-01	1.00E+00	9.14E-01	1.00E+00	intrinsic to peroxisomal membrane	C
GO:0031252	91	3.76E-03	3.28E-01	5.29E-03	3.60E-01	7.44E-03	4.60E-01	5.00E-02	1.00E+00	8.79E-03	5.39E-01	2.00E-02	1.00E+00	1.21E-01	1.00E+00	3.21E-03	1.85E-01	leading edge	C
GO:0031253	16	9.09E-01	1.00E+00	3.06E-01	1.00E+00	7.44E-01	1.00E+00	4.37E-01	1.00E+00	9.16E-01	1.00E+00	3.13E-01	1.00E+00	7.53E-01	1.00E+00	3.69E-01	1.00E+00	cell projection membrane	C
GO:0031267	75	1.42E-01	1.00E+00	2.82E-02	1.00E+00	3.27E-01	1.00E+00	3.95E-01	1.00E+00	1.33E-01	1.00E+00	6.20E-02	1.00E+00	3.31E-01	1.00E+00	3.70E-03	1.85E-01	small GTPase binding	F
GO:0031279	46	9.32E-01	1.00E+00	7.87E-01	1.00E+00	9.58E-01	1.00E+00	5.16E-01	1.00E+00	8.68E-01	1.00E+00	8.61E-01	1.00E+00	8.01E-01	1.00E+00	3.78E-01	1.00E+00	regulation of cyclase activity	P
GO:0031280	16	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	negative regulation of cyclase activity	P
GO:0031281	28	6.55E-01	1.00E+00	5.67E-01	1.00E+00	5.56E-01	1.00E+00	1.90E-01	1.00E+00	7.19E-01	1.00E+00	8.38E-01	1.00E+00	3.89E-01	1.00E+00	1.54E-01	1.00E+00	positive regulation of cyclase activity	P
GO:0031290	10	9.81E-01	1.00E+00	9.85E-01	1.00E+00	9.96E-01	1.00E+00	9.39E-01	1.00E+00	9.26E-01	1.00E+00	9.92E-01	1.00E+00	6.86E-01	1.00E+00	6.77E-01	1.00E+00	retinal ganglion cell axon guidance	P
GO:0031300	114	9.56E-02	1.00E+00	1.59E-03	9.10E-02	1.05E-01	1.00E+00	1.11E-01	1.00E+00	1.33E-01	1.00E+00	4.51E-04	4.10E-02	3.28E-01	1.00E+00	2.85E-01	1.00E+00	intrinsic to organelle membrane	C
GO:0031301	100	9.28E-02	1.00E+00	2.35E-04	4.19E-02	1.30E-01	1.00E+00	3.57E-02	1.00E+00	1.27E-01	1.00E+00	1.43E-04	1.70E-02	3.11E-01	1.00E+00	1.24E-01	1.00E+00	integral to organelle membrane	C
GO:0031323	3030	1.71E-32	0.00E+00	0.00E+00	0.00E+00	4.50E-15	0.00E+00	5.41E-19	0.00E+00	1.17E-30	0.00E+00	4.48E-41	0.00E+00	1.42E-10	0.00E+00	3.53E-18	0.00E+00	regulation of cellular metabolism	P
GO:0031324	455	1.14E-09	8.06E-04	1.57E-08	4.97E-03	7.93E-06	2.66E-03	1.48E-04	1.70E-02	6.21E-09	9.64E-04	1.18E-07	9.20E-04	1.32E-02	6.30E-01	2.48E-04	2.70E-02	negative regulation of cellular metabolism	P
GO:0031325	530	2.78E-02	1.00E+00	1.93E-03	1.29E-01	6.25E-03	4.60E-01	5.81E-03	3.46E-01	8.06E-02	1.00E+00	4.66E-03	2.70E-01	2.57E-01	1.00E+00	1.19E-01	1.00E+00	positive regulation of cellular metabolism	P
GO:0031326	212	4.07E-05	1.00E-02	5.12E-06	8.39E-03	1.84E-06	2.42E-03	1.24E-04	1.30E-02	2.94E-03	2.85E-01	4.12E-05	1.20E-02	1.00E-02	6.30E-01	5.74E-03	3.60E-01	regulation of cellular biosynthesis	P
GO:0031327	48	4.95E-02	1.00E+00	5.76E-02	1.00E+00	1.41E-02	6.93E-01	2.93E-01	1.00E+00	2.43E-01	1.00E+00	6.91E-02	1.00E+00	4.45E-02	1.00E+00	3.66E-02	1.00E+00	negative regulation of cellular biosynthesis	P
GO:0031328	76	1.03E-01	1.00E+00	5.72E-02	1.00E+00	1.05E-02	5.32E-01	4.15E-02	1.00E+00	4.01E-01	1.00E+00	1.30E-01	1.00E+00	1.08E-01	1.00E+00	6.77E-02	1.00E+00	positive regulation of cellular biosynthesis	P
GO:0031341	12	9.66E-01	1.00E+00	9.18E-01	1.00E+00	9.50E-01	1.00E+00	3.45E-01	1.00E+00	9.17E-01	1.00E+00	9.19E-01	1.00E+00	6.51E-01	1.00E+00	9.89E-01	1.00E+00	regulation of cell killing	P
GO:0031365	11	8.58E-04	8.30E-02	6.12E-10	0.00E+00	6.45E-04	3.60E-02	2.21E-04	2.70E-02	1.59E-02	1.00E+00	1.24E-03	6.40E-02	3.00E-01	1.00E+00	7.17E-02	1.00E+00	N-terminal protein amino acid modification	P
GO:0031396	13	6.53E-01	1.00E+00	9.40E-01	1.00E+00	3.92E-01	1.00E+00	9.45E-01	1.00E+00	7.17E-01	1.00E+00	8.18E-01	1.00E+00	6.50E-01	1.00E+00	9.15E-01	1.00E+00	regulation of protein ubiquitination	P
GO:0031399	15	3.29E-01	1.00E+00	9.54E-01	1.00E+00	3.95E-01	1.00E+00	9.75E-01	1.00E+00	3.06E-01	1.00E+00	8.55E-01	1.00E+00	6.58E-01	1.00E+00	8.00E-01	1.00E+00	regulation of protein modification	P
GO:0031402	114	9.99E-01	1.00E+00	9.22E-01	1.00E+00	9.80E-01	1.00E+00	8.74E-01	1.00E+00	9.88E-01	1.00E+00	8.70E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	sodium ion binding	F
GO:0031404	67	9.81E-01	1.00E+00	9.99E-01	1.00E+00	9.67E-01	1.00E+00	9.66E-01	1.00E+00	9.77E-01	1.00E+00	9.99E-01	1.00E+00	7.29E-01	1.00E+00	9.57E-01	1.00E+00	chloride ion binding	F
GO:0031406	12	3.74E-01	1.00E+00	7.37E-01	1.00E+00	3.63E-01	1.00E+00	9.07E-01	1.00E+00	3.83E-01	1.00E+00	5.78E-01	1.00E+00	4.09E-01	1.00E+00	7.26E-01	1.00E+00	carboxylic acid binding	F
GO:0031410	490	7.18E-08	1.84E-03	6.79E-08	4.97E-03	1.22E-04	1.50E-02	1.00E-04	1.20E-02	3.89E-07	1.69E-03	4.46E-08	8.37E-04	3.31E-04	3.40E-02	6.96E-02	1.00E+00	cytoplasmic vesicle	C
GO:0031418	20	3.85E-01	1.00E+00	4.71E-02	1.00E+00	1.34E-01	1.00E+00	2.17E-01	1.00E+00	5.70E-01	1.00E+00	2.62E-02	1.00E+00	2.63E-01	1.00E+00	1.64E-01	1.00E+00	L-ascorbic acid binding	F
GO:0031420	222	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	alkali metal ion binding	F
GO:0031424	47	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	keratinization	P
GO:0031461	13	8.88E-02	1.00E+00	5.11E-02	1.00E+00	3.55E-01	1.00E+00	4.79E-02	1.00E+00	2.16E-01	1.00E+00	6.09E-02	1.00E+00	1.26E-02	6.30E-01	1.27E-01	1.00E+00	cullin-RING ubiquitin ligase complex	C
GO:0031497	191	6.13E-03	5.17E-01	1.87E-02	1.00E+00	9.75E-01	1.00E+00	8.75E-01	1.00E+00	1.21E-04	1.70E-02	1.36E-02	7.39E-01	3.98E-02	1.00E+00	1.88E-03	1.40E-01	chromatin assembly	P
GO:0031507	13	7.22E-03	6.34E-01	2.29E-02	1.00E+00	1.38E-01	1.00E+00	7.05E-02	1.00E+00	1.79E-03	1.76E-01	4.10E-02	1.00E+00	8.64E-02	1.00E+00	1.34E-02	6.47E-01	heterochromatin formation	P
GO:0031513	18	9.05E-01	1.00E+00	3.93E-01	1.00E+00	4.31E-01	1.00E+00	9.81E-01	1.00E+00	9.12E-01	1.00E+00	2.08E-01	1.00E+00	9.89E-01	1.00E+00	2.37E-01	1.00E+00	nonmotile primary cilium	C
GO:0031519	10	2.98E-02	1.00E+00	8.13E-02	1.00E+00	5.55E-01	1.00E+00	2.01E-01	1.00E+00	2.76E-02	1.00E+00	8.14E-02	1.00E+00	1.13E-01	1.00E+00	8.71E-02	1.00E+00	PcG protein complex	C
GO:0031526	12	8.89E-01	1.00E+00	2.33E-01	1.00E+00	7.73E-01	1.00E+00	5.71E-01	1.00E+00	8.78E-01	1.00E+00	2.55E-01	1.00E+00	6.53E-01	1.00E+00	2.17E-01	1.00E+00	brush border membrane	C
GO:0031532	12	4.60E-01	1.00E+00	1.34E-01	1.00E+00	1.09E-01	1.00E+00	6.04E-01	1.00E+00	6.54E-01	1.00E+00	1.14E-01	1.00E+00	6.95E-01	1.00E+00	8.54E-02	1.00E+00	actin cytoskeleton reorganization	P
GO:0031570	36	3.46E-03	2.73E-01	7.93E-03	3.60E-01	1.37E-02	6.93E-01	1.93E-02	1.00E+00	1.60E-02	1.00E+00	9.70E-03	7.39E-01	2.10E-01	1.00E+00	1.71E-01	1.00E+00	DNA integrity checkpoint	P
GO:0031589	121	2.61E-01	1.00E+00	7.37E-02	1.00E+00	2.90E-01	1.00E+00	1.64E-01	1.00E+00	2.91E-01	1.00E+00	1.05E-01	1.00E+00	2.99E-01	1.00E+00	1.31E-01	1.00E+00	cell-substrate adhesion	P
GO:0031594	15	6.86E-01	1.00E+00	2.56E-01	1.00E+00	8.32E-01	1.00E+00	1.70E-01	1.00E+00	5.61E-01	1.00E+00	1.93E-01	1.00E+00	4.99E-01	1.00E+00	7.63E-01	1.00E+00	neuromuscular junction	C
GO:0031625	13	2.08E-02	1.00E+00	8.09E-02	1.00E+00	1.34E-01	1.00E+00	6.48E-02	1.00E+00	1.36E-01	1.00E+00	9.24E-02	1.00E+00	1.17E-02	6.30E-01	3.40E-01	1.00E+00	ubiquitin protein ligase binding	F
GO:0031644	75	1.97E-01	1.00E+00	6.54E-01	1.00E+00	4.10E-01	1.00E+00	4.08E-01	1.00E+00	8.04E-02	1.00E+00	5.92E-01	1.00E+00	7.06E-01	1.00E+00	9.33E-01	1.00E+00	regulation of neurophysiological process	P
GO:0031645	14	8.15E-01	1.00E+00	9.97E-01	1.00E+00	9.11E-01	1.00E+00	9.85E-01	1.00E+00	5.55E-01	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	negative regulation of neurophysiological pr	P
GO:0031646	21	7.81E-02	1.00E+00	2.20E-01	1.00E+00	1.36E-01	1.00E+00	2.51E-01	1.00E+00	6.03E-02	1.00E+00	2.78E-01	1.00E+00	2.84E-01	1.00E+00	2.56E-01	1.00E+00	positive regulation of neurophysiological pro	P
GO:0031647	28	7.61E-02	1.00E+00	1.67E-01	1.00E+00	2.39E-01	1.00E+00	2.65E-01	1.00E+00	8.21E-02	1.00E+00	1.01E-01	1.00E+00	2.11E-01	1.00E+00	5.99E-01	1.00E+00	regulation of protein stability	P
GO:0031663	10	4.52E-02	1.00E+00	4.68E-02	1.00E+00	3.53E-02	1.00E+00	1.30E-02	8.18E-01	6.29E-02	1.00E+00	6.11E-02	1.00E+00	2.34E-01	1.00E+00	2.14E-01	1.00E+00	lipopolysaccharide-mediated signaling path	P
GO:0031667	81	8.82E-02	1.00E+00	2.30E-02	1.00E+00	3.97E-01	1.00E+00	5.87E-01	1.00E+00	7.26E-02	1.00E+00	8.60E-03	7.39E-01	1.40E-01	1.00E+00	6.76E-02	1.00E+00	response to nutrient levels	P
GO:0031668	15	4.67E-01	1.00E+00	6.40E-01	1.00E+00	4.22E-01	1.00E+00	9.31E-01	1.00E+00	4.59E-01	1.00E+00	4.09E-01	1.00E+00	3.39E-01	1.00E+00	6.24E-01	1.00E+00	cellular response to extracellular stimulus	P
GO:0031669	13	4.21E-01	1.00E+00	4.79E-01	1.00E+00	5.06E-01	1.00E+00	8.66E-01	1.00E+00	4.15E-01	1.00E+00	3.29E-01	1.00E+00	2.26E-01	1.00E+00	4.21E-01	1.00E+00	cellular response to nutrient levels	P
GO:0031672	23	9.97E-01	1.00E+00	4.02E-01	1.00E+00	9.47E-01	1.00E+00	2.88E-01	1.00E+00	9.81E-01	1.00E+00	3.21E-01	1.00E+00	9.98E-01	1.00E+00	7.56E-01	1.00E+00	A band	C
GO:0031901	22	2.84E-01	1.00E+00	2.88E-02	1.00E+00	2.77E-01	1.00E+00	3.22E-01	1.00E+00	2.99E-01	1.00E+00	4.16E-02	1.00E+00	5.79E-01	1.00E+00	1.57E-02	8.49E-01	early endosome membrane	C
GO:0031902	34	1.42E-02	6.67E-01	2.60E-02	1.00E+00	1.16E-01	1.00E+00	2.96E-02	1.00E+00	2.29E-02	1.00E+00	1.89E-01	1.00E+00	1.48E-01	1.00E+00	3.18E-02	1.00E+00	late endosome membrane	C
GO:0031903	42	2.90E-03	2.39E-01	1.83E-01	1.00E+00	4.91E-02	1.00E+00	1.68E-01	1.00E+00	3.56E-03	2.85E-01	1.62E-01	1.00E+00	4.25E-03	3.57E-01	4.58E-01	1.00E+00	microbody membrane	C
GO:0031941	14	8.48E-02	1.00E+00	1.26E-02	7.47E-01	1.72E-02	6.93E-01	8.86E-04	5.90E-02	2.41E-01	1.00E+00	3.84E-01	1.00E+00	1.66E-01	1.00E+00	3.06E-01	1.00E+00	filamentous actin	C
GO:0031965	154	3.34E-09	8.06E-04	2.25E-12	0.00E+00	4.79E-05	1.20E-02	2.29E-05	8.00E-03	2.64E-08	9.64E-04	3.57E-11	0.00E+00	3.23E-03	1.95E-01	5.82E-05	9.00E-03	nuclear membrane	C
GO:0031966	380	7.49E-16	0.00E+00	3.63E-10	0.00E+00	2.51E-08	9.68E-04	1.04E-05	8.00E-03	4.09E-15	0.00E+00	1.85E-09	0.00E+00	2.94E-03	1.95E-01	2.56E-03	1.85E-01	mitochondrial membrane	C
GO:0031967	584	3.27E-22	0.00E+00	3.53E-18	0.00E+00	3.75E-11	0.00E+00	7.92E-09	9.71E-04	6.95E-21	0.00E+00	2.75E-16	0.00E+00	1.59E-04	2.50E-02	3.10E-06	1.88E-03	organelle envelope	C
GO:0031968	91	4.89E-04	3.37E-02	1.99E-05	9.58E-03	7.20E-03	4.60E-01	3.06E-03	1.47E-01	2.44E-04	1.70E-02	7.61E-05	1.70E-02	4.04E-01	1.00E+00	3.73E-03	1.85E-01	organelle outer membrane	C
GO:0031970	34	3.20E-01	1.00E+00	3.98E-01	1.00E+00	8.15E-01	1.00E+00	5.06E-01	1.00E+00	1.18E-01	1.00E+00	3.60E-01	1.00E+00	6.10E-01	1.00E+00	4.97E-01	1.00E+00	organelle envelope lumen	C
GO:0031974	1245	1.22E-34	0.00E+00	8.57E-29	0.00E+00	2.95E-19	0.00E+00	3.50E-15	0.00E+00	5.58E-31	0.00E+00	4.56E-26	0.00E+00	2.70E-08	8.55E-04	4.48E-06	1.88E-03	membrane-enclosed lumen	C
GO:0031975	611	3.27E-20	0.00E+00	1.40E-16	0.00E+00	2.06E-10	9.34E-04	9.14E-08	9.71E-04	6.56E-19	0.00E+00	2.52E-15	0.00E+00	1.89E-04	3.40E-02	6.73E-06	1.88E-03	envelope	C
GO:0031980	196	1.41E-04	2.50E-02	4.52E-03	3.60E-01	2.06E-04	2.40E-02	5.56E-03	3.46E-01	2.62E-03	2.85E-01	1.00E-02	7.39E-01	1.97E-02	9.11E-01	3.85E-01	1.00E+00	mitochondrial lumen	C
GO:0031981	905	3.19E-34	0.00E+00	7.22E-30	0.00E+00	6.25E-17	0.00E+00	1.72E-14	0.00E+00	8.62E-32	0.00E+00	6.18E-27	0.00E+00	2.89E-08	8.55E-04	2.44E-07	1.88E-03	nuclear lumen	C
GO:0031982	506	1.06E-07	1.85E-03	7.36E-08	4.97E-03	1.64E-04	1.50E-02	6.09E-05	1.20E-02	6.33E-07	2.45E-03	5.66E-08	8.37E-04	2.69E-04	3.40E-02	7.41E-02	1.00E+00	vesicle	C
GO:0031988	418	1.37E-06	1.95E-03	1.61E-06	8.39E-03	1.86E-03	2.48E-01	3.41E-04	4.20E-02	1.31E-06	2.60E-03	1.34E-06	2.97E-03	4.56E-03	3.57E-01	1.06E-01	1.00E+00	membrane-bound vesicle	C
GO:0032011	16	1.23E-01	1.00E+00	3.54E-01	1.00E+00	8.78E-02	1.00E+00	1.32E-01	1.00E+00	2.26E-01	1.00E+00	4.07E-01	1.00E+00	7.83E-01	1.00E+00	9.77E-01	1.00E+00	ARF protein signal transduction	P
GO:0032012	16	1.23E-01	1.00E+00	3.54E-01	1.00E+00	8.78E-02	1.00E+00	1.32E-01	1.00E+00	2.26E-01	1.00E+00	4.07E-01	1.00E+00	7.83E-01	1.00E+00	9.77E-01	1.00E+00	regulation of ARF protein signal transductio	P
GO:0032039	13	2.00E-02	1.00E+00	1.17E-01	1.00E+00	1.32E-01	1.00E+00	1.46E-01	1.00E+00	1.73E-02	1.00E+00	1.01E-01	1.00E+00	8.09E-02	1.00E+00	6.26E-01	1.00E+00	integrator complex	C
GO:0032040	10	1.84E-01	1.00E+00	4.82E-01	1.00E+00	8.30E-01	1.00E+00	4.46E-01	1.00E+00	2.16E-01	1.00E+00	4.53E-01	1.00E+00	5.17E-02	1.00E+00	9.45E-01	1.00E+00	small subunit processome	C
GO:0032094	10	6.34E-01	1.00E+00	8.10E-01	1.00E+00	1.24E-01	1.00E+00	6.55E-01	1.00E+00	9.16E-01	1.00E+00	8.12E-01	1.00E+00	5.99E-01	1.00E+00	8.27E-01	1.00E+00	response to food	P
GO:0032147	65	2.65E-01	1.00E+00	3.36E-01	1.00E+00	3.59E-01	1.00E+00	8.49E-01	1.00E+00	2.09E-01	1.00E+00	1.89E-01	1.00E+00	4.28E-01	1.00E+00	2.95E-01	1.00E+00	activation of protein kinase activity	P
GO:0032156	12	3.44E-02	1.00E+00	1.49E-04	1.50E-02	7.97E-02	1.00E+00	2.18E-01	1.00E+00	6.56E-02	1.00E+00	1.19E-03	6.40E-02	5.59E-02	1.00E+00	4.02E-01	1.00E+00	septin cytoskeleton	C
GO:0032182	13	4.94E-03	3.28E-01	1.75E-01	1.00E+00	2.48E-02	1.00E+00	3.15E-01	1.00E+00	1.60E-02	1.00E+00	1.07E-01	1.00E+00	2.39E-02	1.00E+00	3.08E-01	1.00E+00	small conjugating protein binding	F
GO:0032200	28	2.75E-02	1.00E+00	1.08E-01	1.00E+00	1.70E-02	6.93E-01	7.87E-01	1.00E+00	9.41E-02	1.00E+00	5.27E-02	1.00E+00	2.11E-01	1.00E+00	3.50E-01	1.00E+00	telomere organization and biogenesis	P
GO:0032259	70	3.99E-03	3.28E-01	7.22E-05	1.00E-02	3.53E-01	1.00E+00	2.04E-03	1.24E-01	1.00E-03	4.40E-02	3.58E-04	3.07E-02	2.46E-01	1.00E+00	3.32E-02	1.00E+00	methylation	P
GO:0032312	31	9.92E-03	6.67E-01	1.74E-01	1.00E+00	1.41E-02	6.93E-01	3.89E-01	1.00E+00	1.07E-02	5.39E-01	2.05E-01	1.00E+00	3.66E-01	1.00E+00	1.92E-01	1.00E+00	regulation of ARF GTPase activity	P
GO:0032313	56	1.29E-01	1.00E+00	7.75E-02	1.00E+00	1.95E-01	1.00E+00	5.39E-01	1.00E+00	2.46E-01	1.00E+00	1.24E-01	1.00E+00	6.32E-02	1.00E+00	7.17E-02	1.00E+00	regulation of Rab GTPase activity	P
GO:0032318	101	1.51E-02	6.67E-01	5.75E-02	1.00E+00	2.37E-02	1.00E+00	5.01E-01	1.00E+00	4.21E-02	1.00E+00	9.38E-02	1.00E+00	5.27E-02	1.00E+00	3.25E-02	1.00E+00	regulation of Ras GTPase activity	P

GO:0032319	12	4.30E-01	1.00E+00	3.59E-01	1.00E+00	3.60E-01	1.00E+00	5.41E-01	1.00E+00	4.78E-01	1.00E+00	3.49E-01	1.00E+00	3.98E-01	1.00E+00	2.05E-01	1.00E+00	regulation of Rho GTPase activity	P
GO:0032392	13	9.33E-03	6.67E-01	2.02E-01	1.00E+00	1.19E-01	1.00E+00	1.88E-01	1.00E+00	8.96E-04	4.40E-02	2.01E-01	1.00E+00	2.41E-01	1.00E+00	9.06E-01	1.00E+00	DNA geometric change	P
GO:0032393	14	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.94E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.99E-01	1.00E+00	4.57E-01	1.00E+00	MHC class I receptor activity	F
GO:0032403	112	7.58E-01	1.00E+00	8.33E-01	1.00E+00	3.56E-01	1.00E+00	4.55E-01	1.00E+00	7.08E-01	1.00E+00	8.33E-01	1.00E+00	9.92E-01	1.00E+00	9.45E-01	1.00E+00	protein complex binding	F
GO:0032432	19	3.87E-02	1.00E+00	3.19E-02	1.00E+00	4.84E-02	1.00E+00	1.16E-01	1.00E+00	1.65E-02	1.00E+00	3.43E-02	1.00E+00	9.45E-01	1.00E+00	6.55E-01	1.00E+00	actin filament bundle	C
GO:0035004	12	5.15E-02	1.00E+00	2.02E-01	1.00E+00	2.77E-02	1.00E+00	7.62E-02	1.00E+00	1.82E-01	1.00E+00	3.95E-01	1.00E+00	5.55E-02	1.00E+00	2.10E-01	1.00E+00	phosphoinositide 3-kinase activity	F
GO:0035014	10	2.27E-01	1.00E+00	2.48E-01	1.00E+00	1.46E-01	1.00E+00	2.61E-01	1.00E+00	3.29E-01	1.00E+00	2.46E-01	1.00E+00	1.64E-01	1.00E+00	2.85E-01	1.00E+00	phosphoinositide 3-kinase regulator activity	F
GO:0035023	78	4.89E-01	1.00E+00	2.28E-01	1.00E+00	2.57E-01	1.00E+00	6.16E-01	1.00E+00	4.92E-01	1.00E+00	1.92E-01	1.00E+00	7.79E-01	1.00E+00	1.99E-01	1.00E+00	regulation of Rho protein signal transductio	P
GO:0035036	18	4.02E-01	1.00E+00	1.82E-01	1.00E+00	3.05E-01	1.00E+00	3.86E-02	1.00E+00	4.91E-01	1.00E+00	2.88E-01	1.00E+00	5.31E-01	1.00E+00	8.67E-01	1.00E+00	sperm-egg recognition	P
GO:0035050	11	4.55E-01	1.00E+00	9.99E-01	1.00E+00	8.43E-01	1.00E+00	9.50E-01	1.00E+00	5.00E-01	1.00E+00	9.99E-01	1.00E+00	1.33E-01	1.00E+00	9.10E-01	1.00E+00	embryonic heart tube development	P
GO:0035051	15	8.40E-01	1.00E+00	9.98E-01	1.00E+00	6.51E-01	1.00E+00	9.66E-01	1.00E+00	8.62E-01	1.00E+00	9.85E-01	1.00E+00	5.72E-01	1.00E+00	9.98E-01	1.00E+00	cardiac cell differentiation	P
GO:0035088	12	2.17E-01	1.00E+00	2.64E-01	1.00E+00	5.50E-01	1.00E+00	4.65E-01	1.00E+00	2.50E-01	1.00E+00	3.23E-01	1.00E+00	6.45E-02	1.00E+00	1.82E-01	1.00E+00	establishment and/or maintenance of apical	P
GO:0035091	85	3.35E-03	2.73E-01	1.89E-04	1.50E-02	5.42E-02	1.00E+00	1.21E-02	8.18E-01	1.38E-02	1.00E+00	9.23E-05	1.70E-02	3.51E-02	1.00E+00	8.46E-02	1.00E+00	phosphoinositide binding	F
GO:0035094	11	7.63E-01	1.00E+00	7.62E-01	1.00E+00	4.58E-01	1.00E+00	6.86E-01	1.00E+00	8.08E-01	1.00E+00	8.83E-01	1.00E+00	7.75E-01	1.00E+00	1.82E-01	1.00E+00	response to nicotine	P
GO:0035107	77	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	5.68E-01	1.00E+00	9.86E-01	1.00E+00	appendage morphogenesis	P
GO:0035108	77	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	5.68E-01	1.00E+00	9.86E-01	1.00E+00	limb morphogenesis	P
GO:0035113	70	9.98E-01	1.00E+00	9.84E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	4.86E-01	1.00E+00	9.72E-01	1.00E+00	embryonic appendage morphogenesis	P
GO:0035115	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	embryonic forelimb morphogenesis	P
GO:0035116	14	6.21E-01	1.00E+00	7.14E-01	1.00E+00	6.85E-01	1.00E+00	9.73E-01	1.00E+00	8.25E-01	1.00E+00	5.29E-01	1.00E+00	1.25E-01	1.00E+00	7.62E-01	1.00E+00	embryonic hindlimb morphogenesis	P
GO:0035136	18	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.98E-01	1.00E+00	forelimb morphogenesis	P
GO:0035137	21	7.92E-01	1.00E+00	9.03E-01	1.00E+00	8.06E-01	1.00E+00	9.89E-01	1.00E+00	9.15E-01	1.00E+00	7.90E-01	1.00E+00	2.85E-01	1.00E+00	8.40E-01	1.00E+00	hindlimb morphogenesis	P
GO:0035239	96	9.98E-01	1.00E+00	9.69E-01	1.00E+00	8.96E-01	1.00E+00	9.56E-01	1.00E+00	9.97E-01	1.00E+00	9.33E-01	1.00E+00	9.98E-01	1.00E+00	9.28E-01	1.00E+00	tube morphogenesis	P
GO:0035240	74	1.15E-01	1.00E+00	5.68E-01	1.00E+00	1.16E-02	5.32E-01	7.81E-01	1.00E+00	3.91E-01	1.00E+00	7.51E-01	1.00E+00	2.70E-01	1.00E+00	1.27E-02	6.47E-01	dopamine binding	F
GO:0035249	19	9.15E-01	1.00E+00	1.00E+00	1.00E+00	9.01E-01	1.00E+00	9.71E-01	1.00E+00	9.16E-01	1.00E+00	1.00E+00	1.00E+00	4.07E-01	1.00E+00	7.41E-01	1.00E+00	synaptic transmission, glutamatergic	P
GO:0035250	21	9.59E-01	1.00E+00	7.77E-01	1.00E+00	3.74E-01	1.00E+00	3.76E-01	1.00E+00	9.90E-01	1.00E+00	7.16E-01	1.00E+00	9.29E-01	1.00E+00	9.98E-01	1.00E+00	UDP-galactosyltransferase activity	F
GO:0035257	67	1.25E-02	6.67E-01	6.80E-04	6.90E-02	9.91E-03	4.60E-01	3.56E-02	1.00E+00	1.58E-02	1.00E+00	1.12E-03	5.49E-02	8.58E-01	1.00E+00	4.31E-02	1.00E+00	nuclear hormone receptor binding	F
GO:0035258	33	6.83E-02	1.00E+00	7.31E-02	1.00E+00	4.18E-02	1.00E+00	3.52E-01	1.00E+00	1.04E-01	1.00E+00	8.90E-02	1.00E+00	8.73E-01	1.00E+00	1.35E-01	1.00E+00	steroid hormone receptor binding	F
GO:0035264	57	5.98E-01	1.00E+00	8.21E-01	1.00E+00	2.57E-01	1.00E+00	5.83E-01	1.00E+00	7.59E-01	1.00E+00	8.35E-01	1.00E+00	6.31E-01	1.00E+00	8.41E-01	1.00E+00	body growth	P
GO:0035265	20	5.42E-01	1.00E+00	8.48E-01	1.00E+00	2.54E-01	1.00E+00	3.13E-01	1.00E+00	7.45E-01	1.00E+00	9.43E-01	1.00E+00	3.12E-01	1.00E+00	9.70E-01	1.00E+00	organ growth	P
GO:0035270	46	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	endocrine system development	P
GO:0035272	15	3.20E-01	1.00E+00	9.98E-01	1.00E+00	7.42E-01	1.00E+00	9.94E-01	1.00E+00	1.63E-01	1.00E+00	9.95E-01	1.00E+00	8.67E-01	1.00E+00	3.67E-01	1.00E+00	exocrine system development	P
GO:0035282	41	9.72E-01	1.00E+00	9.61E-01	1.00E+00	8.93E-01	1.00E+00	9.82E-01	1.00E+00	8.77E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	6.94E-01	1.00E+00	segmentation	P
GO:0035295	165	9.71E-01	1.00E+00	9.87E-01	1.00E+00	9.72E-01	1.00E+00	9.90E-01	1.00E+00	9.19E-01	1.00E+00	9.78E-01	1.00E+00	9.40E-01	1.00E+00	7.35E-01	1.00E+00	tube development	P
GO:0035315	19	9.46E-01	1.00E+00	9.46E-01	1.00E+00	7.36E-01	1.00E+00	9.77E-01	1.00E+00	9.54E-01	1.00E+00	8.71E-01	1.00E+00	9.45E-01	1.00E+00	7.51E-01	1.00E+00	hair cell differentiation	P
GO:0040007	355	1.99E-02	1.00E+00	2.81E-02	1.00E+00	4.33E-03	3.27E-01	7.84E-03	4.55E-01	4.27E-02	1.00E+00	5.76E-02	1.00E+00	4.83E-01	1.00E+00	2.15E-01	1.00E+00	growth	P
GO:0040008	244	1.03E-01	1.00E+00	7.54E-02	1.00E+00	7.81E-03	4.60E-01	9.20E-03	7.13E-01	2.36E-01	1.00E+00	1.80E-01	1.00E+00	5.80E-01	1.00E+00	2.43E-01	1.00E+00	regulation of growth	P
GO:0040011	524	6.93E-01	1.00E+00	4.59E-01	1.00E+00	1.70E-01	1.00E+00	1.99E-01	1.00E+00	8.28E-01	1.00E+00	6.71E-01	1.00E+00	5.95E-01	1.00E+00	2.92E-01	1.00E+00	locomotion	P
GO:0040012	103	2.85E-01	1.00E+00	7.49E-01	1.00E+00	1.10E-01	1.00E+00	3.51E-01	1.00E+00	3.00E-01	1.00E+00	8.63E-01	1.00E+00	6.87E-01	1.00E+00	6.40E-01	1.00E+00	regulation of locomotion	P
GO:0040013	33	1.01E-01	1.00E+00	3.50E-01	1.00E+00	1.52E-01	1.00E+00	8.93E-02	1.00E+00	6.43E-02	1.00E+00	5.80E-01	1.00E+00	3.36E-01	1.00E+00	4.19E-01	1.00E+00	negative regulation of locomotion	P
GO:0040014	46	6.16E-01	1.00E+00	8.23E-01	1.00E+00	2.76E-01	1.00E+00	4.22E-01	1.00E+00	7.92E-01	1.00E+00	8.84E-01	1.00E+00	4.88E-01	1.00E+00	7.98E-01	1.00E+00	regulation of body size	P
GO:0040017	40	4.94E-01	1.00E+00	7.26E-01	1.00E+00	1.82E-01	1.00E+00	6.11E-01	1.00E+00	5.80E-01	1.00E+00	8.52E-01	1.00E+00	8.24E-01	1.00E+00	1.72E-01	1.00E+00	positive regulation of locomotion	P
GO:0040018	21	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	8.08E-01	1.00E+00	9.99E-01	1.00E+00	positive regulation of body size	P
GO:0040029	54	1.67E-03	2.02E-01	1.96E-03	1.29E-01	1.31E-01	1.00E+00	7.23E-02	1.00E+00	7.78E-04	4.04E-02	1.24E-03	6.40E-02	5.95E-02	1.00E+00	5.92E-02	1.00E+00	regulation of gene expression, epigenetic	P
GO:0042033	12	8.25E-02	1.00E+00	1.31E-01	1.00E+00	7.66E-02	1.00E+00	2.23E-01	1.00E+00	1.50E-01	1.00E+00	2.31E-01	1.00E+00	1.66E-01	1.00E+00	1.88E-02	1.00E+00	chemokine biosynthesis	P
GO:0042035	71	6.34E-01	1.00E+00	2.18E-01	1.00E+00	2.32E-01	1.00E+00	3.69E-01	1.00E+00	7.92E-01	1.00E+00	2.67E-01	1.00E+00	6.56E-01	1.00E+00	1.21E-01	1.00E+00	regulation of cytokine biosynthesis	P
GO:0042036	18	5.36E-01	1.00E+00	9.55E-01	1.00E+00	6.90E-01	1.00E+00	9.84E-01	1.00E+00	5.67E-01	1.00E+00	9.17E-01	1.00E+00	3.33E-01	1.00E+00	5.81E-01	1.00E+00	negative regulation of cytokine biosynthesis	P
GO:0042044	11	2.56E-01	1.00E+00	1.20E-01	1.00E+00	1.81E-01	1.00E+00	2.40E-01	1.00E+00	1.60E-01	1.00E+00	9.59E-02	1.00E+00	9.65E-01	1.00E+00	2.77E-01	1.00E+00	fluid transport	P
GO:0042054	35	9.36E-06	7.00E-03	8.07E-07	8.39E-03	2.53E-02	1.00E+00	1.69E-04	2.70E-02	1.32E-05	4.00E-03	1.16E-05	4.88E-03	2.82E-02	1.00E+00	3.30E-03	1.85E-01	histone methyltransferase activity	F
GO:0042060	199	7.07E-01	1.00E+00	2.43E-01	1.00E+00	6.39E-01	1.00E+00	1.18E-01	1.00E+00	5.27E-01	1.00E+00	2.91E-01	1.00E+00	9.08E-01	1.00E+00	4.48E-01	1.00E+00	wound healing	P
GO:0042063	48	2.58E-01	1.00E+00	8.45E-01	1.00E+00	7.00E-02	1.00E+00	6.99E-01	1.00E+00	3.84E-01	1.00E+00	8.60E-01	1.00E+00	3.18E-01	1.00E+00	6.82E-01	1.00E+00	gliogenesis	P
GO:0042088	14	2.02E-01	1.00E+00	1.92E-01	1.00E+00	7.81E-02	1.00E+00	1.55E-01	1.00E+00	2.67E-01	1.00E+00	1.93E-01	1.00E+00	7.81E-01	1.00E+00	6.09E-01	1.00E+00	T-helper 1 type immune response	P
GO:0042089	82	5.40E-01	1.00E+00	4.00E-01	1.00E+00	2.98E-01	1.00E+00	5.32E-01	1.00E+00	6.42E-01	1.00E+00	4.32E-01	1.00E+00	5.85E-01	1.00E+00	2.93E-01	1.00E+00	cytokine biosynthesis	P
GO:0042092	11	3.61E-01	1.00E+00	7.78E-01	1.00E+00	3.02E-01	1.00E+00	5.15E-01	1.00E+00	3.75E-01	1.00E+00	9.30E-01	1.00E+00	9.01E-01	1.00E+00	6.50E-01	1.00E+00	T-helper 2 type immune response	P
GO:0042093	13	5.38E-01	1.00E+00	2.98E-01	1.00E+00	2.53E-01	1.00E+00	5.03E-01	1.00E+00	6.23E-01	1.00E+00	2.03E-01	1.00E+00	8.54E-01	1.00E+00	8.19E-01	1.00E+00	T-helper cell differentiation	P
GO:0042094	18	9.93E-01	1.00E+00	9.43E-01	1.00E+00	9.74E-01	1.00E+00	7.24E-01	1.00E+00	9.18E-01	1.00E+00	9.80E-01	1.00E+00	9.91E-01	1.00E+00	5.84E-01	1.00E+00	interleukin-2 biosynthesis	P
GO:0042095	14	8.89E-01	1.00E+00	4.42E-01	1.00E+00	6.45E-01	1.00E+00	6.22E-01	1.00E+00	9.59E-01	1.00E+00	3.77E-01	1.00E+00	5.37E-01	1.00E+00	4.86E-01	1.00E+00	interferon-gamma biosynthesis	P
GO:0042098	56	6.23E-01	1.00E+00	3.18E-01	1.00E+00	2.48E-01	1.00E+00	4.23E-01	1.00E+00	8.02E-01	1.00E+00	3.54E-01	1.00E+00	4.10E-01	1.00E+00	3.33E-01	1.00E+00	T cell proliferation	P
GO:0042100	26	5.86E-01	1.00E+00	7.03E-01	1.00E+00	6.97E-01	1.00E+00	5.57E-01	1.00E+00	4.85E-01	1.00E+00	7.91E-01	1.00E+00	6.72E-01	1.00E+00	4.30E-01	1.00E+00	B cell proliferation	P
GO:0042101	13	4.03E-02	1.00E+00	9.44E-01	1.00E+00	1.14E-02	5.32E-01	4.45E-01	1.00E+00	3.25E-01	1.00E+00	1.00E+00	1.00E+00	3.98E-01	1.00E+00	4.78E-01	1.00E+00	T cell receptor complex	C
GO:0042102	32	5.15E-01	1.00E+00	4.91E-01	1.00E+00	1.14E-01	1.00E+00	8.40E-01	1.00E+00	7.09E-01	1.00E+00	4.97E-01	1.00E+00	5.65E-01	1.00E+00	3.25E-01	1.00E+00	positive regulation of T cell proliferation	P
GO:0042107	83	5.89E-01	1.00E+00	4.41E-01	1.00E+00	3.30E-01	1.00E+00	5.72E-01	1.00E+00	6.80E-01	1.00E+00	4.72E-01	1.00E+00	6.23E-01	1.00E+00	3.18E-01	1.00E+00	cytokine metabolism	P
GO:0042108	46	3.13E-01	1.00E+00	1.20E-01	1.00E+00	5.97E-02	1.00E+00	2.08E-01	1.00E+00	5.14E-01	1.00E+00	1.64E-01	1.00E+00	6.38E-01	1.00E+00	7.73E-02	1.00E+00	positive regulation of cytokine biosynthesis	P
GO:0042110	135	1.67E-01	1.00E+00	7.33E-02	1.00E+00	1.46E-01	1.00E+00	7.89E-02	1.00E+00	2.02E-01	1.00E+00	1.63E-01	1.00E+00	3.60E-01	1.00E+00	7.07E-02	1.00E+00	T cell activation	P
GO:0042113	100	1.68E-01	1.00E+00	3.18E-01	1.00E+00	2.10E-01	1.00E+00	4.73E-01	1.00E+00	1.06E-01	1.00E+00	1.91E-01	1.00E+00	8.83E-01	1.00E+00	8.00E-01	1.00E+00	B cell activation	P
GO:0042116	12	2.46E-01	1.00E+00	7.06E-02	1.00E+00	3.77E-01	1.00E+00	4.84E-02	1.00E+00	1.56E-01	1.00E+00	1.39E-01	1.00E+00	6.17E-01	1.00E+00	1.32E-01	1.00E+00	macrophage activation	P
GO:0042127	593	1.60E-01	1.00E+00	3.33E-01	1.00E+00	1.78E-01	1.00E+00	8.30E-01	1.00E+00	1.24E-01	1.00E+00	3.10E-01	1.00E+00	3.80E-01	1.00E+00	8.08E-02	1.00E+00	regulation of cell proliferation	P
GO:0042129	44	6.53E-01	1.00E+00	4.50E-01	1.00E+00	2.03E-01	1.00E+00	8.70E-01	1.00E+00	8.43E-01	1.00E+00	3.70E-01	1.00E+00	5.07E-01	1.00E+00	4.29E-01	1.00E+00	regulation of T cell proliferation	P
GO:0042130	16	8.16E-01	1.00E+00	5.03E-01	1.00E+00	5.83E-01	1.00E+00	8.92E-01	1.00E+00	9.11E-01	1.00E+00	4.18E-01	1.00E+00	4.80E-01	1.00E+00	4.64E-01	1.00E+00	negative regulation of T cell proliferation	P
GO:0042133	39	8.62E-01	1.00E+00	2.71E-01	1.00E+00	4.92E-01	1.00E+00	6.00E-02	1.00E+00	8.63E-01	1.00E+00	4.25E-01	1.00E+00	9.01E-01	1.00E+00	7.59E-01	1.00E+00	neurotransmitter metabolism	P
GO:0042135	10	2.50E-01	1.00E+00	2.40E-01	1.00E+00	5.81E-01	1.00E+00	1.60E-01	1.00E+00	1.92E-01	1.00E+00	4.39E-01	1.00E+00	5.77E-01	1.00E+00	5.07E-01	1.00E+00	neurotransmitter catabolism	P
GO:0042136	17	1.00E+00	1.00E+00	9.31E-01	1.00E+00	9.71E-01	1.00E+00	6.97E-01	1.00E+00	1.00E+00	1.00E+00	8.97E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	neurotransmitter biosynthesis	P
GO:0042147	10	9.12E-01	1.00E+00	4.91E-01	1.00E+00	9.70E-01	1.00E+00	5.72E-01	1.00E+00	6.39E-01	1.00E+00	5.27E-01	1.00E+00	9.98E-01	1.00E+00	7.08E-01	1.00E+00	retrograde transport, endosome to Golgi	P
GO:0042157	73	1.46E-03	2.02E-01	1.71E-02	1.00E+00	5.11E-02	1.00E+00	8.15E-02	1.00E+00	1.51E-03	1.76E-01	2.05E-02	1.00E+00	7.88E-02	1.00E+00	2.50E-01	1.00E+00	lipoprotein metabolism	P
GO:0042158	57	9.57E-04	8.30E-02	7.66E-02	1.00E+00	6.51E-02	1.00E+00	5.07E-01	1.00E+00	7.81E-04	4.04E-02	3.12E-02	1.00E+00	5.98E-02	1.00E+00	4.22E-01	1.00E+00	lipoprotein biosynthesis	P
GO:0042162	11	3.71E-02	1.00E+00	2.64E-01	1.00E+00	5.06E-02	1.00E+00	3.67E-01	1.00E+00	6.33E-02	1.00E+00	1.97E-01	1.00E+00	9.09E-02	1.00E+00	6.57E-01	1.00E+00	telomeric DNA binding	F

GO:0042165	267	8.70E-01	1.00E+00	9.99E-01	1.00E+00	5.23E-01	1.00E+00	9.88E-01	1.00E+00	9.37E-01	1.00E+00	9.99E-01	1.00E+00	6.27E-01	1.00E+00	7.87E-01	1.00E+00	neurotransmitter binding	F
GO:0042166	36	4.76E-01	1.00E+00	9.37E-01	1.00E+00	6.32E-01	1.00E+00	5.91E-01	1.00E+00	3.18E-01	1.00E+00	9.89E-01	1.00E+00	6.86E-01	1.00E+00	5.93E-01	1.00E+00	acetylcholine binding	F
GO:0042168	19	1.05E-02	6.67E-01	3.88E-03	1.97E-01	6.31E-03	4.60E-01	2.12E-02	1.00E+00	2.94E-02	1.00E+00	1.04E-02	7.39E-01	4.88E-01	1.00E+00	1.88E-01	1.00E+00	heme metabolism	P
GO:0042169	19	1.49E-01	1.00E+00	2.57E-02	1.00E+00	1.02E-01	1.00E+00	5.91E-02	1.00E+00	1.92E-01	1.00E+00	4.08E-02	1.00E+00	3.91E-01	1.00E+00	2.03E-01	1.00E+00	SH2 domain binding	F
GO:0042175	517	1.87E-03	2.02E-01	1.75E-04	1.50E-02	4.92E-02	1.00E+00	8.10E-02	1.00E+00	3.70E-03	2.85E-01	1.85E-04	2.60E-02	2.43E-02	1.00E+00	2.68E-03	1.85E-01	nuclear envelope-endoplasmic reticulum ne	C
GO:0042176	25	2.66E-01	1.00E+00	3.26E-01	1.00E+00	2.88E-01	1.00E+00	9.05E-01	1.00E+00	4.18E-01	1.00E+00	1.67E-01	1.00E+00	2.16E-01	1.00E+00	3.72E-01	1.00E+00	regulation of protein catabolism	P
GO:0042219	18	7.68E-02	1.00E+00	2.48E-01	1.00E+00	2.07E-01	1.00E+00	4.03E-01	1.00E+00	1.30E-01	1.00E+00	1.22E-01	1.00E+00	5.97E-02	1.00E+00	9.30E-01	1.00E+00	amino acid derivative catabolism	P
GO:0042221	768	8.46E-02	1.00E+00	4.50E-03	3.60E-01	1.03E-01	1.00E+00	4.92E-02	1.00E+00	4.96E-02	1.00E+00	2.05E-03	1.61E-01	6.85E-01	1.00E+00	3.83E-01	1.00E+00	response to chemical stimulus	P
GO:0042226	15	7.28E-01	1.00E+00	7.06E-01	1.00E+00	5.62E-01	1.00E+00	5.47E-01	1.00E+00	9.03E-01	1.00E+00	5.74E-01	1.00E+00	8.89E-02	1.00E+00	1.00E+00	1.00E+00	interleukin-6 biosynthesis	P
GO:0042228	10	2.42E-01	1.00E+00	7.55E-01	1.00E+00	2.28E-01	1.00E+00	3.06E-01	1.00E+00	2.68E-01	1.00E+00	7.51E-01	1.00E+00	6.56E-01	1.00E+00	9.67E-01	1.00E+00	interleukin-8 biosynthesis	P
GO:0042246	23	1.99E-01	1.00E+00	7.10E-02	1.00E+00	2.56E-01	1.00E+00	3.59E-01	1.00E+00	2.26E-01	1.00E+00	4.97E-02	1.00E+00	4.33E-01	1.00E+00	1.55E-01	1.00E+00	tissue regeneration	P
GO:0042254	103	1.62E-04	2.50E-02	2.93E-02	1.00E+00	1.01E-02	4.60E-01	2.60E-01	1.00E+00	2.93E-04	1.70E-02	6.82E-02	1.00E+00	3.22E-02	1.00E+00	6.99E-02	1.00E+00	ribosome biogenesis and assembly	P
GO:0042267	16	7.90E-01	1.00E+00	4.29E-01	1.00E+00	6.82E-01	1.00E+00	6.47E-01	1.00E+00	8.04E-01	1.00E+00	3.42E-01	1.00E+00	3.19E-01	1.00E+00	6.64E-01	1.00E+00	natural killer cell mediated cytotoxicity	P
GO:0042277	486	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide binding	F
GO:0042278	10	1.08E-01	1.00E+00	5.79E-02	1.00E+00	4.58E-01	1.00E+00	4.81E-02	1.00E+00	8.86E-02	1.00E+00	6.94E-02	1.00E+00	1.34E-01	1.00E+00	2.93E-01	1.00E+00	purine nucleoside metabolism	P
GO:0042287	29	7.16E-01	1.00E+00	8.04E-01	1.00E+00	9.99E-01	1.00E+00	3.54E-01	1.00E+00	5.16E-01	1.00E+00	9.52E-01	1.00E+00	2.66E-01	1.00E+00	4.47E-01	1.00E+00	MHC protein binding	F
GO:0042288	16	3.78E-01	1.00E+00	3.63E-01	1.00E+00	9.98E-01	1.00E+00	1.46E-01	1.00E+00	2.41E-01	1.00E+00	5.76E-01	1.00E+00	2.67E-01	1.00E+00	3.40E-01	1.00E+00	MHC class I protein binding	F
GO:0042303	34	9.86E-01	1.00E+00	9.72E-01	1.00E+00	9.89E-01	1.00E+00	9.70E-01	1.00E+00	9.62E-01	1.00E+00	9.69E-01	1.00E+00	9.79E-01	1.00E+00	3.61E-01	1.00E+00	molting cycle	P
GO:0042306	31	2.67E-02	1.00E+00	5.89E-03	3.60E-01	2.69E-01	1.00E+00	1.94E-01	1.00E+00	9.54E-03	5.39E-01	2.01E-02	1.00E+00	3.10E-01	1.00E+00	1.22E-02	6.47E-01	regulation of protein import into nucleus	P
GO:0042307	15	9.31E-02	1.00E+00	5.49E-02	1.00E+00	3.16E-01	1.00E+00	6.93E-01	1.00E+00	5.22E-02	1.00E+00	1.15E-01	1.00E+00	2.31E-01	1.00E+00	1.32E-02	6.47E-01	positive regulation of protein import into nuc	P
GO:0042308	13	5.25E-01	1.00E+00	1.34E-01	1.00E+00	7.76E-01	1.00E+00	3.39E-01	1.00E+00	4.01E-01	1.00E+00	1.97E-01	1.00E+00	5.42E-01	1.00E+00	1.89E-01	1.00E+00	negative regulation of protein import into nu	P
GO:0042309	215	8.99E-02	1.00E+00	2.27E-01	1.00E+00	8.47E-03	4.60E-01	1.32E-01	1.00E+00	2.97E-01	1.00E+00	2.45E-01	1.00E+00	2.05E-01	1.00E+00	7.43E-01	1.00E+00	homoiothermy	P
GO:0042310	28	9.76E-01	1.00E+00	9.96E-01	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.97E-01	1.00E+00	5.23E-01	1.00E+00	7.36E-01	1.00E+00	vasoconstriction	P
GO:0042311	30	9.10E-01	1.00E+00	6.25E-01	1.00E+00	7.40E-01	1.00E+00	3.93E-01	1.00E+00	9.68E-01	1.00E+00	6.95E-01	1.00E+00	1.58E-01	1.00E+00	5.72E-01	1.00E+00	vasodilation	P
GO:0042312	14	9.20E-01	1.00E+00	9.11E-01	1.00E+00	5.69E-01	1.00E+00	8.20E-01	1.00E+00	9.91E-01	1.00E+00	9.18E-01	1.00E+00	4.11E-01	1.00E+00	5.70E-01	1.00E+00	regulation of vasodilation	P
GO:0042325	116	7.55E-01	1.00E+00	5.58E-01	1.00E+00	1.92E-01	1.00E+00	2.73E-01	1.00E+00	8.21E-01	1.00E+00	6.19E-01	1.00E+00	8.65E-01	1.00E+00	7.03E-01	1.00E+00	regulation of phosphorylation	P
GO:0042326	17	6.05E-02	1.00E+00	3.13E-02	1.00E+00	2.17E-02	1.00E+00	7.77E-02	1.00E+00	7.99E-02	1.00E+00	9.50E-02	1.00E+00	3.11E-01	1.00E+00	1.11E-01	1.00E+00	negative regulation of phosphorylation	P
GO:0042327	37	9.90E-01	1.00E+00	9.88E-01	1.00E+00	5.26E-01	1.00E+00	7.22E-01	1.00E+00	9.95E-01	1.00E+00	9.96E-01	1.00E+00	9.80E-01	1.00E+00	9.56E-01	1.00E+00	positive regulation of phosphorylation	P
GO:0042330	198	6.58E-01	1.00E+00	1.97E-01	1.00E+00	5.20E-01	1.00E+00	1.79E-01	1.00E+00	6.79E-01	1.00E+00	1.83E-01	1.00E+00	5.72E-01	1.00E+00	5.42E-01	1.00E+00	taxis	P
GO:0042345	16	5.26E-02	1.00E+00	2.59E-03	1.77E-01	4.71E-01	1.00E+00	5.94E-02	1.00E+00	2.54E-02	1.00E+00	1.98E-02	1.00E+00	5.65E-01	1.00E+00	1.18E-01	1.00E+00	regulation of NF-kappaB import into nucleus	P
GO:0042348	16	5.26E-02	1.00E+00	2.59E-03	1.77E-01	4.71E-01	1.00E+00	5.94E-02	1.00E+00	2.54E-02	1.00E+00	1.98E-02	1.00E+00	5.65E-01	1.00E+00	1.18E-01	1.00E+00	NF-kappaB import into nucleus	P
GO:0042354	11	3.52E-02	1.00E+00	2.40E-02	1.00E+00	4.48E-01	1.00E+00	8.29E-02	1.00E+00	1.14E-02	5.39E-01	3.76E-02	1.00E+00	1.81E-01	1.00E+00	2.28E-02	1.00E+00	L-fucose metabolism	P
GO:0042364	24	1.17E-01	1.00E+00	2.38E-01	1.00E+00	6.01E-02	1.00E+00	2.23E-01	1.00E+00	2.23E-01	1.00E+00	2.85E-01	1.00E+00	3.79E-01	1.00E+00	3.12E-01	1.00E+00	water-soluble vitamin biosynthesis	P
GO:0042375	11	1.57E-02	6.67E-01	1.12E-03	9.10E-02	3.39E-01	1.00E+00	1.71E-04	2.70E-02	1.87E-02	1.00E+00	1.30E-02	7.39E-01	4.09E-02	1.00E+00	2.58E-01	1.00E+00	quinone cofactor metabolism	P
GO:0042379	55	9.21E-01	1.00E+00	9.39E-01	1.00E+00	7.47E-01	1.00E+00	6.72E-01	1.00E+00	9.56E-01	1.00E+00	8.55E-01	1.00E+00	6.68E-01	1.00E+00	1.00E+00	1.00E+00	chemokine receptor binding	F
GO:0042383	20	4.74E-01	1.00E+00	3.46E-01	1.00E+00	4.06E-01	1.00E+00	9.17E-01	1.00E+00	4.61E-01	1.00E+00	2.22E-01	1.00E+00	7.52E-01	1.00E+00	1.46E-01	1.00E+00	sarcolemma	C
GO:0042384	22	5.75E-01	1.00E+00	9.59E-01	1.00E+00	5.04E-01	1.00E+00	1.00E+00	1.00E+00	4.72E-01	1.00E+00	8.29E-01	1.00E+00	9.34E-01	1.00E+00	7.24E-01	1.00E+00	cilium biogenesis	P
GO:0042391	46	4.09E-01	1.00E+00	4.70E-01	1.00E+00	1.66E-01	1.00E+00	2.09E-01	1.00E+00	6.75E-01	1.00E+00	5.49E-01	1.00E+00	3.08E-01	1.00E+00	6.84E-01	1.00E+00	regulation of membrane potential	P
GO:0042393	16	2.66E-03	2.39E-01	6.95E-03	3.60E-01	4.23E-02	1.00E+00	1.21E-02	8.18E-01	3.10E-03	2.85E-01	4.85E-02	1.00E+00	2.42E-01	1.00E+00	3.78E-02	1.00E+00	histone binding	F
GO:0042398	39	5.20E-01	1.00E+00	3.31E-01	1.00E+00	6.54E-01	1.00E+00	2.41E-01	1.00E+00	7.30E-01	1.00E+00	3.99E-01	1.00E+00	7.24E-02	1.00E+00	1.61E-01	1.00E+00	amino acid derivative biosynthesis	P
GO:0042401	31	9.34E-01	1.00E+00	5.17E-01	1.00E+00	9.57E-01	1.00E+00	2.87E-01	1.00E+00	9.55E-01	1.00E+00	5.97E-01	1.00E+00	4.28E-01	1.00E+00	2.92E-01	1.00E+00	biogenic amine biosynthesis	P
GO:0042402	15	1.84E-01	1.00E+00	6.95E-01	1.00E+00	3.10E-01	1.00E+00	7.78E-01	1.00E+00	2.65E-01	1.00E+00	4.10E-01	1.00E+00	1.07E-01	1.00E+00	9.70E-01	1.00E+00	biogenic amine catabolism	P
GO:0042403	12	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.11E-01	1.00E+00	8.80E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	thyroid hormone metabolism	P
GO:0042417	18	9.23E-01	1.00E+00	4.56E-01	1.00E+00	6.83E-01	1.00E+00	1.79E-01	1.00E+00	9.60E-01	1.00E+00	6.01E-01	1.00E+00	8.05E-01	1.00E+00	3.16E-01	1.00E+00	dopamine metabolism	P
GO:0042423	12	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.73E-01	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.93E-01	1.00E+00	9.93E-01	1.00E+00	catecholamine biosynthesis	P
GO:0042430	11	2.45E-01	1.00E+00	4.27E-01	1.00E+00	1.96E-01	1.00E+00	7.02E-01	1.00E+00	6.42E-01	1.00E+00	2.32E-01	1.00E+00	7.19E-02	1.00E+00	7.27E-01	1.00E+00	indole and derivative metabolism	P
GO:0042434	11	2.45E-01	1.00E+00	4.27E-01	1.00E+00	1.96E-01	1.00E+00	7.02E-01	1.00E+00	6.42E-01	1.00E+00	2.32E-01	1.00E+00	7.19E-02	1.00E+00	7.27E-01	1.00E+00	indole derivative metabolism	P
GO:0042440	44	4.24E-03	3.28E-01	5.95E-03	3.60E-01	2.34E-02	1.00E+00	7.10E-02	1.00E+00	4.78E-03	4.18E-01	1.64E-02	8.60E-01	4.39E-01	1.00E+00	3.44E-02	1.00E+00	pigment metabolism	P
GO:0042445	103	9.98E-01	1.00E+00	9.97E-01	1.00E+00	8.00E-01	1.00E+00	8.33E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	4.16E-01	1.00E+00	9.99E-01	1.00E+00	hormone metabolism	P
GO:0042446	45	8.15E-01	1.00E+00	8.94E-01	1.00E+00	4.23E-01	1.00E+00	5.59E-01	1.00E+00	9.49E-01	1.00E+00	9.36E-01	1.00E+00	2.73E-01	1.00E+00	8.49E-01	1.00E+00	hormone biosynthesis	P
GO:0042461	11	6.56E-01	1.00E+00	7.31E-01	1.00E+00	1.30E-01	1.00E+00	8.45E-01	1.00E+00	8.05E-01	1.00E+00	8.39E-01	1.00E+00	7.18E-01	1.00E+00	2.29E-01	1.00E+00	photoreceptor cell development	P
GO:0042470	80	4.87E-09	8.06E-04	4.66E-07	8.39E-03	3.33E-02	1.00E+00	2.78E-03	1.47E-01	2.59E-09	9.64E-04	6.61E-08	8.37E-04	3.57E-03	3.57E-01	5.90E-02	1.00E+00	melanosome	C
GO:0042471	53	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	ear morphogenesis	P
GO:0042472	45	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.85E-01	1.00E+00	inner ear morphogenesis	P
GO:0042474	10	8.92E-01	1.00E+00	9.95E-01	1.00E+00	4.71E-01	1.00E+00	8.99E-01	1.00E+00	9.59E-01	1.00E+00	9.99E-01	1.00E+00	8.45E-01	1.00E+00	7.46E-01	1.00E+00	middle ear morphogenesis	P
GO:0042475	36	8.45E-01	1.00E+00	9.50E-01	1.00E+00	9.54E-01	1.00E+00	9.76E-01	1.00E+00	8.77E-01	1.00E+00	9.60E-01	1.00E+00	2.74E-01	1.00E+00	5.88E-01	1.00E+00	odontogenesis (sensu Vertebrata)	P
GO:0042476	43	9.33E-01	1.00E+00	9.55E-01	1.00E+00	9.85E-01	1.00E+00	9.96E-01	1.00E+00	9.47E-01	1.00E+00	9.53E-01	1.00E+00	3.37E-01	1.00E+00	5.28E-01	1.00E+00	odontogenesis	P
GO:0042490	19	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.46E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	mechanoreceptor differentiation	P
GO:0042491	16	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	9.78E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	auditory receptor cell differentiation	P
GO:0042493	129	6.69E-01	1.00E+00	1.50E-01	1.00E+00	2.63E-01	1.00E+00	3.40E-01	1.00E+00	6.81E-01	1.00E+00	1.21E-01	1.00E+00	8.89E-01	1.00E+00	3.11E-01	1.00E+00	response to drug	P
GO:0042503	10	6.02E-02	1.00E+00	1.20E-01	1.00E+00	2.65E-02	1.00E+00	5.53E-02	1.00E+00	9.22E-02	1.00E+00	3.82E-01	1.00E+00	3.10E-01	1.00E+00	2.51E-01	1.00E+00	tyrosine phosphorylation of Stat3 protein	P
GO:0042506	10	3.19E-01	1.00E+00	5.18E-01	1.00E+00	1.26E-01	1.00E+00	2.68E-01	1.00E+00	3.88E-01	1.00E+00	6.57E-01	1.00E+00	7.13E-01	1.00E+00	7.13E-01	1.00E+00	tyrosine phosphorylation of Stat5 protein	P
GO:0042509	20	2.33E-01	1.00E+00	3.14E-01	1.00E+00	9.20E-02	1.00E+00	8.20E-02	1.00E+00	2.43E-01	1.00E+00	5.83E-01	1.00E+00	7.74E-01	1.00E+00	5.86E-01	1.00E+00	regulation of tyrosine phosphorylation of ST	P
GO:0042531	13	7.90E-01	1.00E+00	7.50E-01	1.00E+00	3.97E-01	1.00E+00	2.96E-01	1.00E+00	8.35E-01	1.00E+00	8.83E-01	1.00E+00	8.00E-01	1.00E+00	9.02E-01	1.00E+00	positive regulation of tyrosine phosphorylati	P
GO:0042542	28	1.55E-02	6.67E-01	5.47E-02	1.00E+00	2.87E-01	1.00E+00	9.74E-02	1.00E+00	2.84E-03	2.85E-01	8.18E-02	1.00E+00	3.97E-01	1.00E+00	7.19E-02	1.00E+00	response to hydrogen peroxide	P
GO:0042551	19	7.62E-01	1.00E+00	7.29E-01	1.00E+00	6.97E-01	1.00E+00	7.33E-01	1.00E+00	4.24E-01	1.00E+00	5.80E-01	1.00E+00	1.00E+00	1.00E+00	8.72E-01	1.00E+00	neuron maturation	P
GO:0042552	34	1.51E-01	1.00E+00	4.22E-01	1.00E+00	4.18E-02	1.00E+00	2.76E-01	1.00E+00	3.95E-01	1.00E+00	4.25E-01	1.00E+00	2.00E-01	1.00E+00	6.45E-01	1.00E+00	myelination	P
GO:0042558	15	3.71E-01	1.00E+00	1.84E-01	1.00E+00	2.68E-01	1.00E+00	8.17E-02	1.00E+00	4.77E-01	1.00E+00	2.73E-01	1.00E+00	3.37E-01	1.00E+00	2.70E-01	1.00E+00	pteridine and derivative metabolism	P
GO:0042559	12	7.21E-01	1.00E+00	3.26E-01	1.00E+00	3.67E-01	1.00E+00	1.32E-01	1.00E+00	8.50E-01	1.00E+00	4.61E-01	1.00E+00	4.92E-01	1.00E+00	4.22E-01	1.00E+00	pteridine and derivative biosynthesis	P
GO:0042562	31	5.48E-01	1.00E+00	7.92E-01	1.00E+00	6.00E-01	1.00E+00	5.26E-01	1.00E+00	5.95E-01	1.00E+00	8.09E-01	1.00E+00	2.11E-01	1.00E+00	7.24E-01	1.00E+00	hormone binding	F
GO:0042577	14	1.81E-01	1.00E+00	2.04E-01	1.00E+00	6.47E-01	1.00E+00	2.05E-01	1.00E+00	1.38E-01	1.00E+00	2.36E-01	1.00E+00	5.10E-02	1.00E+00	3.83E-01	1.00E+00	lipid phosphatase activity	F
GO:0042578	356	1.03E-03	9.60E-02	9.66E-06	9.58E-03	2.21E-02	1.00E+00	5.93E-04	4.70E-02	3.61E-03	2.85E-01	3.71E-05	1.20E-02	1.08E-02	6.30E-01	4.72E-03	3.60E-01	phosphoric ester hydrolase activity	F
GO:0042579	98	6.28E-04	3.44E-02	4.39E-02	1.00E+00	2.23E-02	1.00E+00	3.68E-02	1.00E+00	7.84E-04	4.04E-02	4.26E-02	1.00E+00	2.14E-02	9.11E-01	5.34E-01	1.00E+00	microbody	C
GO:0042592	668	3.55E-02	1.00E+00	4.87E-02	1.00E+00	1.71E-02	6.93E-01	9.40E-03	7.13E-01	9.91E-02	1.00E+00	4.44E-02	1.00E+00	6.96E-02	1.00E+00	8.05E-01	1.00E+00	homeostasis	P
GO:0042593	37	1.86E-01	1.00E+00	1.22E-01	1.00E+00	1.61E-01	1.00E+00	4.06E-02	1.00E+00	2.86E-01	1.00E+00	1.86E-01	1.00E+00	1.11E-01	1.00E+00	4.90E-01	1.00E+00	glucose homeostasis	P

GO:0042594	16	7.70E-01	1.00E+00	6.54E-01	1.00E+00	8.04E-01	1.00E+00	9.68E-01	1.00E+00	7.05E-01	1.00E+00	4.43E-01	1.00E+00	6.24E-01	1.00E+00	4.49E-01	1.00E+00	response to starvation	P
GO:0042596	15	9.04E-01	1.00E+00	6.23E-01	1.00E+00	4.06E-01	1.00E+00	8.49E-01	1.00E+00	9.88E-01	1.00E+00	6.42E-01	1.00E+00	8.64E-01	1.00E+00	1.53E-01	1.00E+00	fear response	P
GO:0042597	28	7.55E-01	1.00E+00	8.83E-01	1.00E+00	5.33E-01	1.00E+00	9.96E-01	1.00E+00	8.78E-01	1.00E+00	6.88E-01	1.00E+00	3.40E-01	1.00E+00	7.45E-01	1.00E+00	periplasmic space	C
GO:0042598	188	3.50E-01	1.00E+00	5.13E-01	1.00E+00	4.31E-01	1.00E+00	7.67E-01	1.00E+00	4.55E-01	1.00E+00	3.69E-01	1.00E+00	8.78E-02	1.00E+00	6.76E-01	1.00E+00	vesicular fraction	C
GO:0042605	17	8.63E-01	1.00E+00	7.40E-01	1.00E+00	9.97E-01	1.00E+00	5.26E-01	1.00E+00	8.78E-01	1.00E+00	7.47E-01	1.00E+00	2.04E-01	1.00E+00	7.38E-01	1.00E+00	peptide antigen binding	F
GO:0042611	43	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	3.14E-01	1.00E+00	8.49E-01	1.00E+00	MHC protein complex	C
GO:0042612	27	7.82E-01	1.00E+00	9.96E-01	1.00E+00	8.48E-01	1.00E+00	8.69E-01	1.00E+00	8.01E-01	1.00E+00	9.94E-01	1.00E+00	2.36E-01	1.00E+00	8.86E-01	1.00E+00	MHC class I protein complex	C
GO:0042613	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.19E-01	1.00E+00	6.04E-01	1.00E+00	MHC class II protein complex	C
GO:0042623	275	7.18E-06	7.00E-03	1.96E-05	9.58E-03	2.22E-03	2.48E-01	1.64E-03	1.24E-01	1.51E-05	4.00E-03	3.76E-05	1.20E-02	1.25E-01	1.00E+00	5.34E-02	1.00E+00	ATPase activity, coupled	F
GO:0042625	88	1.08E-01	1.00E+00	2.01E-01	1.00E+00	4.80E-01	1.00E+00	2.87E-01	1.00E+00	3.97E-02	1.00E+00	2.71E-01	1.00E+00	5.59E-01	1.00E+00	1.70E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042626	128	1.11E-01	1.00E+00	2.70E-01	1.00E+00	5.91E-01	1.00E+00	2.28E-01	1.00E+00	3.07E-02	1.00E+00	3.77E-01	1.00E+00	7.21E-01	1.00E+00	3.40E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042627	10	2.54E-02	1.00E+00	4.21E-02	1.00E+00	2.88E-02	1.00E+00	2.06E-01	1.00E+00	7.38E-02	1.00E+00	1.51E-02	7.39E-01	8.29E-02	1.00E+00	7.70E-01	1.00E+00	chylomicron	C
GO:0042632	28	1.23E-01	1.00E+00	2.73E-01	1.00E+00	6.53E-02	1.00E+00	1.70E-01	1.00E+00	1.94E-01	1.00E+00	2.99E-01	1.00E+00	2.56E-01	1.00E+00	6.90E-01	1.00E+00	cholesterol homeostasis	P
GO:0042633	34	9.86E-01	1.00E+00	9.72E-01	1.00E+00	9.89E-01	1.00E+00	9.70E-01	1.00E+00	9.62E-01	1.00E+00	9.69E-01	1.00E+00	9.79E-01	1.00E+00	3.61E-01	1.00E+00	hair cycle	P
GO:0042692	76	9.96E-01	1.00E+00	8.92E-01	1.00E+00	9.45E-01	1.00E+00	7.48E-01	1.00E+00	9.94E-01	1.00E+00	8.56E-01	1.00E+00	8.91E-01	1.00E+00	7.68E-01	1.00E+00	muscle cell differentiation	P
GO:0042698	37	4.64E-01	1.00E+00	6.32E-01	1.00E+00	2.19E-01	1.00E+00	4.24E-01	1.00E+00	5.58E-01	1.00E+00	7.14E-01	1.00E+00	7.34E-01	1.00E+00	4.09E-01	1.00E+00	menstrual cycle	P
GO:0042730	12	5.62E-02	1.00E+00	1.55E-02	1.00E+00	9.16E-02	1.00E+00	2.58E-02	1.00E+00	4.09E-02	1.00E+00	2.81E-02	1.00E+00	3.80E-01	1.00E+00	1.34E-01	1.00E+00	fibrinolysis	P
GO:0042733	16	9.42E-01	1.00E+00	7.47E-01	1.00E+00	8.39E-01	1.00E+00	7.05E-01	1.00E+00	9.68E-01	1.00E+00	6.59E-01	1.00E+00	5.78E-01	1.00E+00	8.78E-01	1.00E+00	embryonic digit morphogenesis	P
GO:0042734	25	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.64E-01	1.00E+00	8.60E-01	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	presynaptic membrane	C
GO:0042742	111	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	defense response to bacterium	P
GO:0042743	20	3.61E-02	1.00E+00	7.89E-02	1.00E+00	5.00E-01	1.00E+00	2.11E-01	1.00E+00	1.55E-02	1.00E+00	6.96E-02	1.00E+00	9.51E-02	1.00E+00	1.46E-01	1.00E+00	hydrogen peroxide metabolism	P
GO:0042744	15	1.25E-01	1.00E+00	1.21E-01	1.00E+00	7.48E-01	1.00E+00	2.38E-01	1.00E+00	4.61E-02	1.00E+00	1.42E-01	1.00E+00	3.14E-01	1.00E+00	9.08E-02	1.00E+00	hydrogen peroxide catabolism	P
GO:0042755	10	8.46E-01	1.00E+00	8.68E-01	1.00E+00	7.49E-01	1.00E+00	3.92E-01	1.00E+00	6.52E-01	1.00E+00	8.10E-01	1.00E+00	8.54E-01	1.00E+00	9.99E-01	1.00E+00	eating behavior	P
GO:0042770	55	3.70E-03	3.28E-01	5.43E-03	3.60E-01	2.16E-02	1.00E+00	1.74E-03	1.24E-01	1.42E-02	1.00E+00	3.03E-02	1.00E+00	6.67E-02	1.00E+00	5.84E-02	1.00E+00	DNA damage response, signal transduction	P
GO:0042773	52	5.82E-04	3.37E-02	2.28E-02	1.00E+00	4.52E-02	1.00E+00	1.57E-01	1.00E+00	1.52E-03	1.76E-01	4.09E-02	1.00E+00	2.28E-02	1.00E+00	1.09E-01	1.00E+00	ATP synthesis coupled electron transport	P
GO:0042775	46	1.36E-04	2.50E-02	1.54E-02	1.00E+00	2.35E-02	1.00E+00	9.58E-02	1.00E+00	4.72E-04	2.20E-02	2.95E-02	1.00E+00	2.13E-02	9.11E-01	1.46E-01	1.00E+00	ATP synthesis coupled electron transport (s	P
GO:0042802	452	2.12E-08	9.77E-04	8.17E-08	4.97E-03	1.91E-04	2.40E-02	1.43E-07	1.96E-03	8.27E-09	9.64E-04	1.37E-06	2.97E-03	3.57E-03	3.57E-01	2.66E-02	1.00E+00	identical protein binding	F
GO:0042803	218	6.91E-04	3.44E-02	4.96E-04	6.90E-02	9.85E-02	1.00E+00	1.92E-04	2.70E-02	1.58E-04	1.70E-02	2.16E-03	1.61E-01	5.74E-02	1.00E+00	1.85E-01	1.00E+00	protein homodimerization activity	F
GO:0042809	20	7.33E-02	1.00E+00	5.62E-02	1.00E+00	5.74E-02	1.00E+00	1.08E-01	1.00E+00	7.00E-02	1.00E+00	3.93E-02	1.00E+00	4.24E-01	1.00E+00	3.50E-01	1.00E+00	vitamin D receptor binding	F
GO:0042826	11	2.98E-01	1.00E+00	6.14E-01	1.00E+00	9.36E-02	1.00E+00	9.68E-01	1.00E+00	3.83E-01	1.00E+00	3.42E-01	1.00E+00	6.62E-01	1.00E+00	8.33E-01	1.00E+00	histone deacetylase binding	F
GO:0042895	27	4.42E-01	1.00E+00	2.06E-01	1.00E+00	4.40E-02	1.00E+00	6.96E-01	1.00E+00	6.43E-01	1.00E+00	1.53E-01	1.00E+00	9.27E-01	1.00E+00	2.00E-01	1.00E+00	antibiotic transporter activity	F
GO:0042923	145	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.94E-01	1.00E+00	9.98E-01	1.00E+00	neuropeptide binding	F
GO:0042974	16	4.52E-01	1.00E+00	2.66E-01	1.00E+00	3.65E-01	1.00E+00	4.65E-01	1.00E+00	2.85E-01	1.00E+00	2.52E-01	1.00E+00	9.90E-01	1.00E+00	3.03E-01	1.00E+00	retinoic acid receptor binding	F
GO:0042981	606	7.18E-09	8.06E-04	1.06E-10	0.00E+00	1.14E-06	2.42E-03	1.49E-07	1.96E-03	5.28E-08	1.69E-03	2.16E-08	8.37E-04	1.05E-03	7.07E-02	5.73E-05	9.00E-03	regulation of apoptosis	P
GO:0042982	12	2.52E-01	1.00E+00	3.29E-01	1.00E+00	4.26E-01	1.00E+00	3.15E-01	1.00E+00	1.54E-01	1.00E+00	4.49E-01	1.00E+00	9.80E-01	1.00E+00	3.19E-01	1.00E+00	amyloid precursor protein metabolism	P
GO:0042990	25	1.39E-02	6.67E-01	3.20E-03	1.97E-01	2.84E-01	1.00E+00	1.28E-01	1.00E+00	4.65E-03	4.18E-01	2.88E-02	1.00E+00	1.91E-01	1.00E+00	1.00E-02	4.81E-01	regulation of transcription factor import into	P
GO:0042991	25	1.39E-02	6.67E-01	3.20E-03	1.97E-01	2.84E-01	1.00E+00	1.28E-01	1.00E+00	4.65E-03	4.18E-01	2.88E-02	1.00E+00	1.91E-01	1.00E+00	1.00E-02	4.81E-01	transcription factor import into nucleus	P
GO:0042992	11	4.54E-01	1.00E+00	1.05E-01	1.00E+00	7.28E-01	1.00E+00	2.62E-01	1.00E+00	3.23E-01	1.00E+00	2.10E-01	1.00E+00	5.40E-01	1.00E+00	1.62E-01	1.00E+00	negative regulation of transcription factor im	P
GO:0042993	11	2.48E-02	1.00E+00	1.64E-02	1.00E+00	2.07E-01	1.00E+00	4.62E-01	1.00E+00	1.36E-02	1.00E+00	6.33E-02	1.00E+00	1.01E-01	1.00E+00	2.18E-02	1.00E+00	positive regulation of transcription factor imp	P
GO:0042995	498	5.20E-01	1.00E+00	6.16E-02	1.00E+00	7.81E-02	1.00E+00	2.27E-01	1.00E+00	7.46E-01	1.00E+00	6.12E-02	1.00E+00	4.76E-01	1.00E+00	1.80E-01	1.00E+00	cell projection	C
GO:0043005	151	9.51E-01	1.00E+00	8.29E-01	1.00E+00	4.45E-01	1.00E+00	4.01E-01	1.00E+00	9.71E-01	1.00E+00	7.55E-01	1.00E+00	8.73E-01	1.00E+00	9.93E-01	1.00E+00	neuron projection	C
GO:0043009	193	3.33E-01	1.00E+00	7.94E-01	1.00E+00	6.50E-01	1.00E+00	6.80E-01	1.00E+00	3.17E-01	1.00E+00	7.40E-01	1.00E+00	1.79E-01	1.00E+00	8.51E-01	1.00E+00	embryonic development (sensu Vertebrata)	P
GO:0043010	59	5.69E-01	1.00E+00	8.40E-01	1.00E+00	5.13E-01	1.00E+00	6.04E-01	1.00E+00	4.54E-01	1.00E+00	9.01E-01	1.00E+00	8.38E-01	1.00E+00	4.60E-01	1.00E+00	eye development (sensu Vertebrata)	P
GO:0043021	19	7.63E-03	6.34E-01	4.04E-05	9.58E-03	6.37E-02	1.00E+00	7.37E-02	1.00E+00	1.90E-02	1.00E+00	7.89E-05	1.70E-02	1.51E-02	6.47E-01	5.05E-03	3.60E-01	ribonucleoprotein binding	F
GO:0043025	77	8.86E-01	1.00E+00	6.13E-01	1.00E+00	3.15E-01	1.00E+00	1.68E-01	1.00E+00	9.81E-01	1.00E+00	6.06E-01	1.00E+00	6.13E-01	1.00E+00	9.46E-01	1.00E+00	cell soma	C
GO:0043028	22	2.08E-05	8.00E-03	3.69E-02	1.00E+00	1.23E-03	9.80E-02	3.21E-01	1.00E+00	6.87E-04	4.00E-02	7.47E-02	1.00E+00	8.40E-03	6.30E-01	1.80E-02	1.00E+00	caspase regulator activity	F
GO:0043029	16	1.54E-01	1.00E+00	1.37E-01	1.00E+00	2.79E-01	1.00E+00	1.67E-01	1.00E+00	1.20E-01	1.00E+00	7.36E-02	1.00E+00	2.80E-01	1.00E+00	4.49E-01	1.00E+00	T cell homeostasis	P
GO:0043037	254	3.39E-18	0.00E+00	7.80E-16	0.00E+00	8.72E-08	2.42E-03	4.11E-06	8.00E-03	2.88E-17	0.00E+00	3.15E-13	0.00E+00	3.08E-06	1.95E-03	2.89E-08	7.71E-04	translation	P
GO:0043038	72	3.30E-03	2.73E-01	6.83E-03	3.60E-01	2.18E-02	1.00E+00	1.04E-01	1.00E+00	4.97E-03	4.18E-01	8.80E-03	7.39E-01	1.50E-01	1.00E+00	1.12E-01	1.00E+00	amino acid activation	P
GO:0043039	72	3.30E-03	2.73E-01	6.83E-03	3.60E-01	2.18E-02	1.00E+00	1.04E-01	1.00E+00	4.97E-03	4.18E-01	8.80E-03	7.39E-01	1.50E-01	1.00E+00	1.12E-01	1.00E+00	tRNA aminoacylation	P
GO:0043043	10	4.14E-01	1.00E+00	1.00E+00	1.00E+00	2.96E-01	1.00E+00	1.00E+00	1.00E+00	3.69E-01	1.00E+00	1.00E+00	1.00E+00	7.38E-01	1.00E+00	1.00E+00	1.00E+00	peptide biosynthesis	P
GO:0043062	95	9.82E-01	1.00E+00	7.52E-01	1.00E+00	4.16E-01	1.00E+00	7.44E-02	1.00E+00	9.87E-01	1.00E+00	8.54E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	extracellular structure organization and bioc	P
GO:0043064	14	8.30E-02	1.00E+00	4.27E-02	1.00E+00	9.54E-02	1.00E+00	1.76E-01	1.00E+00	1.49E-01	1.00E+00	2.40E-02	1.00E+00	1.57E-01	1.00E+00	8.92E-02	1.00E+00	flagellum organization and biogenesis	P
GO:0043065	293	1.80E-04	2.50E-02	2.85E-06	8.39E-03	7.05E-04	4.50E-02	5.14E-05	8.00E-03	9.76E-04	4.40E-02	6.04E-05	1.70E-02	1.64E-02	6.63E-01	8.48E-03	4.81E-01	positive regulation of apoptosis	P
GO:0043066	267	7.77E-06	7.00E-03	6.71E-04	6.90E-02	3.86E-04	3.60E-02	6.44E-04	4.70E-02	7.06E-06	2.88E-03	7.20E-03	5.30E-01	1.85E-02	9.11E-01	2.08E-02	1.00E+00	negative regulation of apoptosis	P
GO:0043067	614	8.84E-09	8.06E-04	1.71E-10	0.00E+00	1.02E-06	2.42E-03	2.34E-07	1.96E-03	6.91E-08	1.69E-03	3.12E-08	8.37E-04	1.01E-03	7.07E-02	5.86E-05	9.00E-03	regulation of programmed cell death	P
GO:0043068	296	2.22E-04	2.64E-02	3.05E-06	8.39E-03	7.02E-04	4.50E-02	4.62E-05	8.00E-03	1.14E-03	7.80E-02	7.26E-05	1.70E-02	1.86E-02	9.11E-01	7.37E-03	4.81E-01	positive regulation of programmed cell deat	P
GO:0043069	272	1.03E-05	7.00E-03	1.16E-03	9.10E-02	4.44E-04	3.60E-02	1.12E-03	1.15E-01	1.04E-05	4.00E-03	1.04E-02	7.39E-01	1.55E-02	6.47E-01	2.39E-02	1.00E+00	negative regulation of programmed cell dea	P
GO:0043085	329	1.02E-06	1.95E-03	2.47E-07	8.39E-03	2.16E-03	2.48E-01	5.66E-04	4.70E-02	8.36E-07	2.45E-03	1.09E-06	2.97E-03	5.35E-03	3.57E-01	1.06E-04	2.00E-02	positive regulation of enzyme activity	P
GO:0043086	167	3.90E-04	3.37E-02	2.02E-05	9.58E-03	6.44E-02	1.00E+00	2.00E-02	1.00E+00	2.31E-04	1.70E-02	1.45E-05	7.63E-03	4.92E-02	1.00E+00	2.09E-02	1.00E+00	negative regulation of enzyme activity	P
GO:0043087	118	1.31E-02	6.67E-01	5.09E-02	1.00E+00	7.30E-02	1.00E+00	4.85E-01	1.00E+00	2.55E-02	1.00E+00	7.63E-02	1.00E+00	2.76E-02	1.00E+00	3.04E-02	1.00E+00	regulation of GTPase activity	P
GO:0043112	21	9.68E-02	1.00E+00	8.74E-02	1.00E+00	1.25E-01	1.00E+00	1.82E-01	1.00E+00	1.24E-01	1.00E+00	1.11E-01	1.00E+00	1.83E-01	1.00E+00	2.71E-01	1.00E+00	receptor metabolism	P
GO:0043118	1216	5.52E-11	0.00E+00	9.94E-11	0.00E+00	9.84E-08	2.42E-03	1.72E-05	8.00E-03	1.46E-10	0.00E+00	1.17E-09	0.00E+00	1.84E-02	9.11E-01	2.53E-05	9.00E-03	negative regulation of physiological process	P
GO:0043119	1177	9.57E-05	1.24E-02	1.37E-06	8.39E-03	6.31E-03	4.60E-01	1.37E-04	1.70E-02	9.28E-05	1.70E-02	1.19E-05	4.88E-03	2.44E-02	1.00E+00	3.75E-03	1.85E-01	positive regulation of physiological process	P
GO:0043122	106	5.80E-03	3.50E-01	1.83E-03	9.10E-02	2.84E-02	1.00E+00	8.80E-02	1.00E+00	2.34E-02	1.00E+00	1.91E-03	1.61E-01	7.49E-03	5.44E-01	4.71E-02	1.00E+00	regulation of I-kappaB kinase/NF-kappaB ca	P
GO:0043123	99	7.59E-03	6.34E-01	2.39E-03	1.77E-01	2.43E-02	1.00E+00	6.55E-02	1.00E+00	3.36E-02	1.00E+00	2.99E-03	2.39E-01	6.73E-03	5.44E-01	5.42E-02	1.00E+00	positive regulation of I-kappaB kinase/NF-ka	P
GO:0043130	13	4.94E-03	3.28E-01	1.75E-01	1.00E+00	2.48E-02	1.00E+00	3.15E-01	1.00E+00	1.60E-02	1.00E+00	1.07E-01	1.00E+00	2.39E-02	1.00E+00	3.08E-01	1.00E+00	ubiquitin binding	F
GO:0043149	10	1.85E-01	1.00E+00	2.87E-01	1.00E+00	5.11E-02	1.00E+00	3.52E-01	1.00E+00	3.66E-01	1.00E+00	2.42E-01	1.00E+00	5.16E-01	1.00E+00	4.35E-01	1.00E+00	stress fiber formation	P
GO:0043154	13	2.74E-04	3.37E-02	1.56E-02	1.00E+00	9.00E-03	4.60E-01	2.49E-02	1.00E+00	1.18E-03	7.80E-02	6.29E-02	1.00E+00	3.30E-02	1.00E+00	3.55E-03	1.85E-01	negative regulation of caspase activity	P
GO:0043161	96	2.05E-03	2.02E-01	3.82E-05	9.58E-03	3.00E-01	1.00E+00	7.59E-03	4.55E-01	2.24E-03	2.85E-01	2.30E-04	2.60E-02	6.66E-03	5.44E-01	3.03E-03	1.85E-01	proteasomal ubiquitin-dependent protein ca	P
GO:0043167	4405	4.41E-11	0.00E+00	1.03E-26	0.00E+00	8.08E-06	2.66E-03	7.27E-09	9.71E-04	2.49E-11	0.00E+00	2.75E-28	0.00E+00	1.72E-02	9.11E-01	1.25E-07	1.88E-03	ion binding	F
GO:0043168	67	9.81E-01	1.00E+00	9.99E-01	1.00E+00	9.67E-01	1.00E+00	9.66E-01	1.00E+00	9.77E-01	1.00E+00	9.99E-01	1.00E+00	7.29E-01	1.00E+00	9.57E-01	1.00E+00	anion binding	F
GO:0043169	4011	1.16E-09	8.06E-04	5.13E-23	0.00E+00	2.95E-05	6.00E-03	8.29E-07	2.00E-03	5.01E-10	0.00E+00	2.87E-25	0.00E+00	3.26E-02	1.00E+00	1.88E-06	1.88E-03	cation binding	F
GO:0043170	5162	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.64E-35	0.00E+00	9.81E-45	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.90E-21	0.00E+00	1.82E-32	0.00E+00	macromolecule metabolism	P
GO:0043176	59	4.97E-01	1.00E+00	9.24E-01	1.00E+00	4.78E-01	1.00E+00	7.34E-01	1.00E+00	4.23E-01	1.00E+00	9.64E-01	1.00E+00	6.01E-01	1.00E+00	4.99E-01	1.00E+00	amine binding	F

GO:0043193	18	4.61E-03	3.28E-01	3.61E-02	1.00E+00	7.18E-03	4.60E-01	4.14E-01	1.00E+00	6.81E-03	5.39E-01	8.34E-02	1.00E+00	3.07E-01	1.00E+00	1.00E-02	4.81E-01	positive regulation of gene-specific transcrip	P
GO:0043197	15	6.73E-01	1.00E+00	6.57E-01	1.00E+00	7.12E-01	1.00E+00	8.01E-01	1.00E+00	5.71E-01	1.00E+00	4.87E-01	1.00E+00	6.66E-01	1.00E+00	8.33E-01	1.00E+00	dendritic spine	C
GO:0043226	8642	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.62E-36	0.00E+00	1.48E-41	0.00E+00	organelle	C
GO:0043227	7618	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.33E-37	0.00E+00	1.09E-40	0.00E+00	membrane-bound organelle	C
GO:0043228	2148	5.27E-20	0.00E+00	6.50E-18	0.00E+00	7.48E-09	9.34E-04	5.12E-05	8.00E-03	1.10E-19	0.00E+00	5.35E-18	0.00E+00	4.71E-06	2.00E-03	1.65E-07	1.88E-03	non-membrane-bound organelle	C
GO:0043229	8637	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.59E-36	0.00E+00	9.88E-42	0.00E+00	intracellular organelle	C
GO:0043231	7616	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.20E-37	0.00E+00	1.52E-40	0.00E+00	intracellular membrane-bound organelle	C
GO:0043232	2148	5.27E-20	0.00E+00	6.50E-18	0.00E+00	7.48E-09	9.34E-04	5.12E-05	8.00E-03	1.10E-19	0.00E+00	5.35E-18	0.00E+00	4.71E-06	2.00E-03	1.65E-07	1.88E-03	intracellular non-membrane-bound organell	C
GO:0043233	1245	1.22E-34	0.00E+00	8.57E-29	0.00E+00	2.95E-19	0.00E+00	3.50E-15	0.00E+00	5.58E-31	0.00E+00	4.56E-26	0.00E+00	2.70E-08	8.55E-04	4.48E-06	1.88E-03	organelle lumen	C
GO:0043234	2583	0.00E+00	0.00E+00	1.24E-40	0.00E+00	4.87E-21	0.00E+00	3.57E-15	0.00E+00	3.99E-42	0.00E+00	3.48E-38	0.00E+00	2.79E-18	0.00E+00	2.00E-11	0.00E+00	protein complex	C
GO:0043235	93	3.98E-01	1.00E+00	8.05E-02	1.00E+00	3.24E-01	1.00E+00	2.63E-01	1.00E+00	3.55E-01	1.00E+00	1.19E-01	1.00E+00	6.25E-01	1.00E+00	3.37E-01	1.00E+00	receptor complex	C
GO:0043269	34	5.64E-01	1.00E+00	3.81E-01	1.00E+00	6.31E-01	1.00E+00	5.64E-01	1.00E+00	5.40E-01	1.00E+00	3.93E-01	1.00E+00	4.42E-01	1.00E+00	2.80E-01	1.00E+00	regulation of ion transport	P
GO:0043279	12	8.27E-01	1.00E+00	4.29E-01	1.00E+00	4.56E-01	1.00E+00	2.72E-01	1.00E+00	7.68E-01	1.00E+00	6.10E-01	1.00E+00	9.99E-01	1.00E+00	2.81E-01	1.00E+00	response to alkaloid	P
GO:0043280	50	2.25E-05	8.00E-03	1.21E-04	1.50E-02	2.95E-03	2.48E-01	6.79E-02	1.00E+00	7.92E-05	1.70E-02	6.99E-05	1.70E-02	2.98E-03	1.95E-01	6.75E-03	4.81E-01	positive regulation of caspase activity	P
GO:0043281	66	2.77E-07	1.95E-03	1.99E-05	9.58E-03	1.91E-04	2.40E-02	2.00E-02	1.00E+00	1.56E-06	2.60E-03	8.01E-05	1.70E-02	7.75E-04	6.50E-02	2.58E-04	2.70E-02	regulation of caspase activity	P
GO:0043283	3340	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.20E-26	0.00E+00	3.94E-37	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.23E-15	0.00E+00	7.22E-24	0.00E+00	biopolymer metabolism	P
GO:0043284	47	2.81E-01	1.00E+00	1.75E-01	1.00E+00	7.42E-01	1.00E+00	7.06E-01	1.00E+00	1.74E-01	1.00E+00	1.22E-01	1.00E+00	4.66E-01	1.00E+00	2.17E-01	1.00E+00	biopolymer biosynthesis	P
GO:0043285	379	2.92E-10	0.00E+00	5.70E-16	0.00E+00	8.91E-06	2.66E-03	7.33E-09	9.71E-04	1.24E-07	1.69E-03	5.81E-14	0.00E+00	6.97E-06	2.00E-03	6.00E-06	1.88E-03	biopolymer catabolism	P
GO:0043292	85	7.51E-01	1.00E+00	1.83E-01	1.00E+00	5.24E-01	1.00E+00	2.03E-01	1.00E+00	6.82E-01	1.00E+00	1.03E-01	1.00E+00	9.25E-01	1.00E+00	7.35E-01	1.00E+00	contractile fiber	C
GO:0043296	103	6.56E-03	5.17E-01	4.67E-03	3.60E-01	2.67E-02	1.00E+00	2.71E-03	1.47E-01	1.90E-03	1.76E-01	1.30E-02	7.39E-01	3.82E-01	1.00E+00	1.92E-01	1.00E+00	apical junction complex	C
GO:0043299	12	9.13E-02	1.00E+00	8.17E-02	1.00E+00	7.02E-02	1.00E+00	2.69E-01	1.00E+00	1.18E-01	1.00E+00	9.65E-02	1.00E+00	4.53E-01	1.00E+00	7.62E-02	1.00E+00	leukocyte degranulation	P
GO:0043331	12	1.79E-02	1.00E+00	7.30E-02	1.00E+00	7.71E-02	1.00E+00	1.32E-01	1.00E+00	1.64E-02	1.00E+00	7.54E-02	1.00E+00	1.33E-01	1.00E+00	1.17E-01	1.00E+00	response to dsRNA	P
GO:0043367	18	7.62E-01	1.00E+00	6.37E-01	1.00E+00	4.19E-01	1.00E+00	7.03E-01	1.00E+00	7.82E-01	1.00E+00	4.68E-01	1.00E+00	9.60E-01	1.00E+00	9.89E-01	1.00E+00	CD4-positive, alpha beta T cell differentiatic	P
GO:0043393	15	1.32E-01	1.00E+00	3.10E-01	1.00E+00	1.07E-01	1.00E+00	8.26E-02	1.00E+00	1.05E-01	1.00E+00	5.11E-01	1.00E+00	9.41E-01	1.00E+00	2.12E-01	1.00E+00	regulation of protein binding	P
GO:0043405	117	3.66E-02	1.00E+00	3.32E-03	1.97E-01	5.76E-02	1.00E+00	1.32E-02	8.18E-01	4.39E-02	1.00E+00	4.08E-03	2.70E-01	2.79E-01	1.00E+00	7.75E-02	1.00E+00	regulation of MAPK activity	P
GO:0043406	83	7.07E-02	1.00E+00	1.22E-02	6.77E-01	9.09E-02	1.00E+00	1.49E-02	8.18E-01	8.09E-02	1.00E+00	1.68E-02	8.60E-01	3.48E-01	1.00E+00	1.36E-01	1.00E+00	positive regulation of MAPK activity	P
GO:0043407	31	1.69E-01	1.00E+00	8.25E-02	1.00E+00	1.14E-01	1.00E+00	2.92E-01	1.00E+00	1.92E-01	1.00E+00	7.78E-02	1.00E+00	4.99E-01	1.00E+00	1.36E-01	1.00E+00	negative regulation of MAPK activity	P
GO:0043408	27	4.23E-01	1.00E+00	6.64E-01	1.00E+00	4.91E-01	1.00E+00	2.21E-01	1.00E+00	3.65E-01	1.00E+00	7.70E-01	1.00E+00	6.16E-01	1.00E+00	8.24E-01	1.00E+00	regulation of MAPKKK cascade	P
GO:0043410	17	7.31E-01	1.00E+00	9.09E-01	1.00E+00	7.23E-01	1.00E+00	3.62E-01	1.00E+00	6.11E-01	1.00E+00	9.29E-01	1.00E+00	9.02E-01	1.00E+00	9.62E-01	1.00E+00	positive regulation of MAPKKK cascade	P
GO:0043412	1979	5.88E-22	0.00E+00	2.74E-37	0.00E+00	4.13E-10	9.34E-04	2.50E-21	0.00E+00	1.08E-21	0.00E+00	8.82E-33	0.00E+00	9.38E-05	2.50E-02	9.07E-13	0.00E+00	biopolymer modification	P
GO:0043413	123	1.68E-01	1.00E+00	4.88E-03	3.60E-01	5.47E-01	1.00E+00	3.87E-01	1.00E+00	7.89E-02	1.00E+00	9.35E-04	5.49E-02	4.81E-01	1.00E+00	5.32E-02	1.00E+00	biopolymer glycosylation	P
GO:0043414	50	3.58E-04	3.37E-02	6.41E-05	9.58E-03	6.43E-02	1.00E+00	4.91E-03	3.46E-01	3.15E-04	1.98E-02	6.94E-05	1.70E-02	1.68E-01	1.00E+00	3.92E-02	1.00E+00	biopolymer methylation	P
GO:0043433	21	3.34E-02	1.00E+00	1.40E-03	9.10E-02	2.23E-01	1.00E+00	7.39E-03	4.55E-01	5.01E-02	1.00E+00	4.27E-03	2.70E-01	1.92E-02	9.11E-01	2.10E-01	1.00E+00	negative regulation of transcription factor ac	P
GO:0043434	22	1.50E-01	1.00E+00	7.11E-01	1.00E+00	3.79E-01	1.00E+00	7.58E-01	1.00E+00	1.88E-01	1.00E+00	5.76E-01	1.00E+00	7.65E-02	1.00E+00	9.47E-01	1.00E+00	response to peptide hormone stimulus	P
GO:0043449	30	2.82E-01	1.00E+00	4.97E-01	1.00E+00	3.27E-01	1.00E+00	5.06E-01	1.00E+00	3.33E-01	1.00E+00	5.56E-01	1.00E+00	4.60E-01	1.00E+00	2.26E-01	1.00E+00	alkene metabolism	P
GO:0043450	22	1.76E-01	1.00E+00	2.87E-01	1.00E+00	2.63E-01	1.00E+00	6.78E-01	1.00E+00	2.10E-01	1.00E+00	2.40E-01	1.00E+00	4.76E-01	1.00E+00	1.63E-01	1.00E+00	alkene biosynthesis	P
GO:0043473	40	1.57E-01	1.00E+00	1.33E-01	1.00E+00	2.12E-01	1.00E+00	6.50E-02	1.00E+00	2.95E-01	1.00E+00	3.36E-01	1.00E+00	1.08E-01	1.00E+00	6.22E-02	1.00E+00	pigmentation	P
GO:0043487	15	2.64E-02	1.00E+00	7.15E-02	1.00E+00	1.08E-01	1.00E+00	4.90E-01	1.00E+00	1.16E-02	5.39E-01	1.03E-01	1.00E+00	1.60E-01	1.00E+00	7.01E-02	1.00E+00	regulation of RNA stability	P
GO:0043488	14	4.25E-02	1.00E+00	3.81E-02	1.00E+00	2.02E-01	1.00E+00	4.04E-01	1.00E+00	1.97E-02	1.00E+00	5.94E-02	1.00E+00	1.14E-01	1.00E+00	9.23E-02	1.00E+00	regulation of mRNA stability	P
GO:0043492	130	1.11E-01	1.00E+00	2.71E-01	1.00E+00	5.22E-01	1.00E+00	2.60E-01	1.00E+00	3.68E-02	1.00E+00	3.66E-01	1.00E+00	7.24E-01	1.00E+00	3.45E-01	1.00E+00	ATPase activity, coupled to movement of su	F
GO:0043498	13	3.26E-01	1.00E+00	4.83E-01	1.00E+00	3.73E-01	1.00E+00	2.10E-01	1.00E+00	3.79E-01	1.00E+00	6.42E-01	1.00E+00	2.28E-01	1.00E+00	3.65E-01	1.00E+00	cell surface binding	F
GO:0043506	28	2.56E-01	1.00E+00	6.29E-02	1.00E+00	9.04E-02	1.00E+00	4.78E-02	1.00E+00	2.39E-01	1.00E+00	6.84E-02	1.00E+00	9.89E-01	1.00E+00	3.71E-01	1.00E+00	regulation of JNK activity	P
GO:0043507	26	2.69E-01	1.00E+00	6.98E-02	1.00E+00	1.20E-01	1.00E+00	4.95E-02	1.00E+00	2.50E-01	1.00E+00	8.44E-02	1.00E+00	9.82E-01	1.00E+00	2.99E-01	1.00E+00	positive regulation of JNK activity	P
GO:0043523	53	2.59E-02	1.00E+00	1.91E-02	1.00E+00	3.52E-02	1.00E+00	2.02E-02	1.00E+00	2.70E-02	1.00E+00	3.41E-02	1.00E+00	1.17E-01	1.00E+00	1.51E-01	1.00E+00	regulation of neuron apoptosis	P
GO:0043524	29	2.02E-01	1.00E+00	2.70E-01	1.00E+00	4.73E-02	1.00E+00	6.30E-02	1.00E+00	3.60E-01	1.00E+00	2.86E-01	1.00E+00	3.43E-01	1.00E+00	9.86E-01	1.00E+00	negative regulation of neuron apoptosis	P
GO:0043525	15	9.89E-03	6.67E-01	1.90E-02	1.00E+00	2.08E-02	1.00E+00	7.01E-02	1.00E+00	3.51E-03	2.85E-01	4.77E-02	1.00E+00	3.08E-01	1.00E+00	4.76E-02	1.00E+00	positive regulation of neuron apoptosis	P
GO:0043531	12	5.39E-02	1.00E+00	1.90E-02	1.00E+00	7.46E-02	1.00E+00	1.41E-02	8.18E-01	6.26E-02	1.00E+00	7.25E-02	1.00E+00	5.16E-01	1.00E+00	2.40E-01	1.00E+00	ADP binding	F
GO:0043542	20	6.20E-01	1.00E+00	1.03E-01	1.00E+00	8.66E-01	1.00E+00	1.28E-02	8.18E-01	4.59E-01	1.00E+00	3.22E-01	1.00E+00	4.07E-01	1.00E+00	4.60E-02	1.00E+00	endothelial cell migration	P
GO:0043543	31	9.45E-05	1.24E-02	3.36E-05	9.58E-03	2.48E-03	2.48E-01	2.66E-02	1.00E+00	2.40E-04	1.70E-02	2.46E-04	2.60E-02	1.39E-01	1.00E+00	7.86E-04	9.16E-02	protein amino acid acylation	P
GO:0043549	256	1.02E-03	9.60E-02	1.43E-04	1.50E-02	1.54E-02	6.93E-01	1.92E-02	1.00E+00	4.71E-04	2.20E-02	2.25E-04	2.60E-02	2.83E-01	1.00E+00	5.17E-03	3.60E-01	regulation of kinase activity	P
GO:0043565	593	9.68E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	9.92E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	9.15E-01	1.00E+00	sequence-specific DNA binding	F
GO:0043566	110	1.45E-03	2.02E-01	5.24E-03	3.60E-01	2.17E-02	1.00E+00	6.22E-02	1.00E+00	2.73E-03	2.85E-01	4.86E-03	2.70E-01	4.55E-02	1.00E+00	1.97E-01	1.00E+00	structure-specific DNA binding	F
GO:0043574	14	1.39E-01	1.00E+00	3.11E-01	1.00E+00	4.17E-01	1.00E+00	6.06E-01	1.00E+00	1.07E-01	1.00E+00	2.11E-01	1.00E+00	2.71E-01	1.00E+00	3.55E-01	1.00E+00	peroxisomal transport	P
GO:0043583	66	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ear development	P
GO:0043588	14	1.00E+00	1.00E+00	9.62E-01	1.00E+00	9.98E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	9.93E-01	1.00E+00	3.24E-01	1.00E+00	skin development	P
GO:0043596	16	2.61E-03	2.39E-01	2.07E-04	2.80E-02	7.78E-02	1.00E+00	1.50E-02	8.18E-01	2.77E-03	2.85E-01	4.94E-04	4.10E-02	2.32E-01	1.00E+00	7.49E-02	1.00E+00	replication fork (sensu Eukaryota)	C
GO:0043601	14	2.92E-03	2.39E-01	2.49E-03	1.77E-01	1.54E-01	1.00E+00	4.56E-02	1.00E+00	1.64E-03	1.76E-01	2.81E-03	2.39E-01	1.41E-01	1.00E+00	5.79E-02	1.00E+00	replisome (sensu Eukaryota)	C
GO:0043616	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	8.96E-01	1.00E+00	7.12E-01	1.00E+00	keratinocyte proliferation	P
GO:0043621	10	5.05E-02	1.00E+00	2.21E-01	1.00E+00	9.17E-02	1.00E+00	1.63E-01	1.00E+00	4.34E-02	1.00E+00	2.39E-01	1.00E+00	1.00E+00	1.00E+00	5.43E-01	1.00E+00	protein self-association	F
GO:0043627	31	9.98E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.24E-01	1.00E+00	9.90E-01	1.00E+00	9.95E-01	1.00E+00	7.47E-01	1.00E+00	4.77E-01	1.00E+00	response to estrogen stimulus	P
GO:0043631	12	8.51E-02	1.00E+00	1.50E-05	9.58E-03	6.67E-02	1.00E+00	6.75E-03	4.53E-01	8.04E-02	1.00E+00	2.12E-05	7.63E-03	9.58E-01	1.00E+00	5.62E-02	1.00E+00	RNA polyadenylation	P
GO:0043632	233	2.64E-06	1.95E-03	2.02E-10	0.00E+00	6.69E-03	4.60E-01	3.75E-06	8.00E-03	1.70E-05	4.19E-03	5.19E-09	8.37E-04	9.21E-04	7.07E-02	1.43E-04	2.00E-02	modification-dependent macromolecule cata	P
GO:0043648	11	3.66E-01	1.00E+00	2.22E-01	1.00E+00	6.79E-01	1.00E+00	2.67E-02	1.00E+00	2.40E-01	1.00E+00	4.65E-01	1.00E+00	9.56E-01	1.00E+00	3.91E-01	1.00E+00	dicarboxylic acid metabolism	P
GO:0043681	13	5.86E-03	3.50E-01	1.47E-01	1.00E+00	4.11E-02	1.00E+00	2.27E-01	1.00E+00	1.98E-02	1.00E+00	8.68E-02	1.00E+00	2.79E-01	1.00E+00	9.98E-01	1.00E+00	protein import into mitochondrion	P
GO:0044237	8229	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.26E-44	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.23E-27	0.00E+00	1.82E-44	0.00E+00	cellular metabolism	P
GO:0044238	8208	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.06E-40	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.78E-30	0.00E+00	2.80E-44	0.00E+00	primary metabolism	P
GO:0044242	52	1.44E-01	1.00E+00	5.00E-01	1.00E+00	2.05E-01	1.00E+00	5.53E-01	1.00E+00	1.46E-01	1.00E+00	6.13E-01	1.00E+00	4.25E-01	1.00E+00	1.40E-01	1.00E+00	cellular lipid catabolism	P
GO:0044247	15	9.97E-01	1.00E+00	7.71E-01	1.00E+00	7.06E-01	1.00E+00	8.06E-01	1.00E+00	1.00E+00	1.00E+00	6.91E-01	1.00E+00	7.42E-01	1.00E+00	8.53E-01	1.00E+00	cellular polysaccharide catabolism	P
GO:0044248	676	3.71E-12	0.00E+00	2.00E-16	0.00E+00	9.89E-07	2.42E-03	5.24E-10	0.00E+00	5.24E-10	0.00E+00	1.42E-13	0.00E+00	4.19E-05	6.00E-03	4.32E-07	1.88E-03	cellular catabolism	P
GO:0044249	1403	1.35E-20	0.00E+00	1.17E-18	0.00E+00	6.00E-10	9.34E-04	3.29E-09	0.00E+00	4.18E-18	0.00E+00	1.39E-16	0.00E+00	3.06E-08	8.55E-04	4.27E-07	1.88E-03	cellular biosynthesis	P
GO:0044255	676	6.47E-04	3.44E-02	1.33E-04	1.50E-02	3.34E-02	1.00E+00	3.21E-03	1.47E-01	1.74E-03	1.76E-01	6.09E-04	5.49E-02	5.48E-03	3.57E-01	1.91E-03	1.40E-01	cellular lipid metabolism	P
GO:0044257	258	2.52E-05	8.00E-03	1.19E-09	0.00E+00	5.27E-03	4.19E-01	8.75E-06	8.00E-03	1.83E-04	1.70E-02	1.78E-08	8.37E-04	4.17E-03	3.57E-01	3.34E-04	2.70E-02	cellular protein catabolism	P
GO:0044260	3429	1.61E-36	0.00E+00	0.00E+00	0.00E+00	2.12E-19	0.00E+00	1.30E-23	0.00E+00	3.56E-33	0.00E+00	2.80E-44	0.00E+00	6.08E-10	0.00E+00	2.27E-16	0.00E+00	cellular macromolecule metabolism	P
GO:0044262	400	6.30E-03	5.17E-01	1.14E-02	6.77E-01	2.10E-02	1.00E+00	1.89E-02	1.00E+00	7.16E-03	5.39E-01	3.16E-02	1.00E+00	3.65E-01	1.00E+00	1.04E-01	1.00E+00	cellular carbohydrate metabolism	P
GO:0044264	86	7.05E-01	1.00E+00	4.62E-01	1.00E+00	8.59E-01	1.00E+00	8.27E-01	1.00E+00	5.77E-01	1.00E+00	2.03E-01	1.00E+00	5.90E-01	1.00E+00	8.10E-01	1.00E+00	cellular polysaccharide metabolism	P

GO:0044265	426	3.90E-11	0.00E+00	1.53E-14	0.00E+00	1.93E-06	2.42E-03	9.49E-08	9.71E-04	5.55E-09	9.64E-04	1.17E-12	0.00E+00	7.57E-05	2.50E-02	2.67E-06	1.88E-03	cellular macromolecule catabolism	P
GO:0044267	3371	4.86E-37	0.00E+00	0.00E+00	0.00E+00	1.02E-19	0.00E+00	1.29E-24	0.00E+00	1.02E-33	0.00E+00	1.40E-44	0.00E+00	1.25E-09	0.00E+00	1.10E-16	0.00E+00	cellular protein metabolism	P
GO:0044270	72	1.45E-02	6.67E-01	1.19E-02	6.77E-01	9.40E-02	1.00E+00	4.28E-02	1.00E+00	2.05E-02	1.00E+00	6.62E-03	5.30E-01	8.15E-02	1.00E+00	6.68E-01	1.00E+00	nitrogen compound catabolism	P
GO:0044271	127	3.83E-01	1.00E+00	9.49E-02	1.00E+00	4.16E-01	1.00E+00	2.49E-02	1.00E+00	4.20E-01	1.00E+00	1.59E-01	1.00E+00	3.27E-01	1.00E+00	2.62E-01	1.00E+00	nitrogen compound biosynthesis	P
GO:0044272	45	6.73E-01	1.00E+00	6.08E-01	1.00E+00	2.39E-01	1.00E+00	5.22E-01	1.00E+00	6.39E-01	1.00E+00	5.40E-01	1.00E+00	9.81E-01	1.00E+00	9.47E-01	1.00E+00	sulfur compound biosynthesis	P
GO:0044275	120	6.08E-04	3.37E-02	3.63E-03	1.97E-01	6.20E-04	3.60E-02	3.53E-02	1.00E+00	3.17E-03	2.85E-01	5.91E-03	3.51E-01	1.24E-01	1.00E+00	5.29E-02	1.00E+00	cellular carbohydrate catabolism	P
GO:0044403	60	3.13E-03	2.39E-01	3.18E-02	1.00E+00	6.58E-02	1.00E+00	4.29E-01	1.00E+00	4.87E-03	4.18E-01	2.88E-02	1.00E+00	9.73E-02	1.00E+00	4.43E-02	1.00E+00	symbiosis, encompassing mutualism throug	P
GO:0044409	11	6.16E-01	1.00E+00	2.35E-01	1.00E+00	9.19E-01	1.00E+00	3.58E-01	1.00E+00	5.71E-01	1.00E+00	2.09E-01	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	entry into host	P
GO:0044419	260	1.22E-09	8.06E-04	9.22E-12	0.00E+00	1.31E-05	3.72E-03	2.57E-04	2.70E-02	5.03E-09	9.64E-04	4.47E-12	0.00E+00	7.69E-04	6.50E-02	6.87E-04	9.16E-02	interspecies interaction between organisms	P
GO:0044420	114	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	9.99E-01	1.00E+00	9.34E-01	1.00E+00	extracellular matrix part	C
GO:0044421	820	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.53E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.29E-01	1.00E+00	1.00E+00	1.00E+00	extracellular region part	C
GO:0044422	3898	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.24E-28	0.00E+00	1.60E-21	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.67E-17	0.00E+00	7.41E-14	0.00E+00	organelle part	C
GO:0044423	18	4.81E-01	1.00E+00	5.70E-01	1.00E+00	9.45E-01	1.00E+00	5.97E-01	1.00E+00	2.59E-01	1.00E+00	7.17E-01	1.00E+00	8.41E-01	1.00E+00	1.73E-01	1.00E+00	virion part	C
GO:0044424	10357	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.99E-38	0.00E+00	0.00E+00	0.00E+00	intracellular part	C
GO:0044425	6255	3.45E-01	1.00E+00	1.61E-02	1.00E+00	4.35E-01	1.00E+00	6.19E-01	1.00E+00	1.94E-01	1.00E+00	1.36E-03	6.40E-02	7.53E-01	1.00E+00	2.64E-01	1.00E+00	membrane part	C
GO:0044427	455	6.16E-10	8.06E-04	4.35E-10	0.00E+00	3.44E-03	3.27E-01	5.83E-03	3.46E-01	3.40E-10	0.00E+00	1.89E-09	0.00E+00	5.72E-04	6.50E-02	4.38E-06	1.88E-03	chromosomal part	C
GO:0044428	1266	0.00E+00	0.00E+00	1.01E-43	0.00E+00	8.93E-22	0.00E+00	2.50E-18	0.00E+00	2.83E-43	0.00E+00	7.01E-40	0.00E+00	2.06E-11	0.00E+00	3.13E-12	0.00E+00	nuclear part	C
GO:0044429	548	9.60E-18	0.00E+00	3.77E-11	0.00E+00	6.23E-11	9.34E-04	1.03E-06	2.00E-03	5.14E-15	0.00E+00	3.90E-10	0.00E+00	9.83E-05	2.50E-02	6.87E-03	4.81E-01	mitochondrial part	C
GO:0044430	753	5.73E-04	3.37E-02	4.01E-03	1.97E-01	4.71E-03	3.27E-01	2.00E-01	1.00E+00	7.16E-04	4.00E-02	7.13E-04	5.49E-02	2.32E-01	1.00E+00	2.34E-01	1.00E+00	cytoskeletal part	C
GO:0044431	410	1.04E-02	6.67E-01	4.30E-05	9.58E-03	5.35E-02	1.00E+00	9.11E-03	7.13E-01	1.55E-02	1.00E+00	3.67E-05	1.20E-02	4.71E-02	1.00E+00	2.39E-01	1.00E+00	Golgi apparatus part	C
GO:0044432	566	3.18E-04	3.37E-02	2.14E-05	9.58E-03	1.41E-02	6.93E-01	2.97E-02	1.00E+00	1.22E-03	7.80E-02	1.89E-05	7.63E-03	1.16E-02	6.30E-01	5.20E-03	3.60E-01	endoplasmic reticulum part	C
GO:0044433	153	2.72E-03	2.39E-01	2.40E-02	1.00E+00	7.67E-03	4.60E-01	5.29E-02	1.00E+00	3.86E-03	2.85E-01	3.11E-02	1.00E+00	1.18E-01	1.00E+00	4.40E-01	1.00E+00	cytoplasmic vesicle part	C
GO:0044437	73	3.12E-03	2.39E-01	2.78E-02	1.00E+00	1.16E-01	1.00E+00	1.19E-01	1.00E+00	5.83E-03	5.39E-01	7.91E-02	1.00E+00	1.84E-01	1.00E+00	3.38E-02	1.00E+00	vacuolar part	C
GO:0044438	47	4.49E-03	3.28E-01	3.22E-01	1.00E+00	5.48E-02	1.00E+00	1.88E-01	1.00E+00	1.01E-02	5.39E-01	3.27E-01	1.00E+00	1.29E-03	1.68E-01	5.61E-01	1.00E+00	microbody part	C
GO:0044439	47	4.49E-03	3.28E-01	3.22E-01	1.00E+00	5.48E-02	1.00E+00	1.88E-01	1.00E+00	1.01E-02	5.39E-01	3.27E-01	1.00E+00	1.29E-03	1.68E-01	5.61E-01	1.00E+00	peroxisomal part	C
GO:0044440	111	9.84E-05	1.24E-02	1.72E-04	1.50E-02	9.11E-02	1.00E+00	8.35E-03	7.13E-01	1.43E-04	1.70E-02	1.12E-03	5.49E-02	2.11E-03	1.95E-01	8.87E-03	4.81E-01	endosomal part	C
GO:0044441	10	6.09E-02	1.00E+00	6.82E-01	1.00E+00	9.72E-02	1.00E+00	3.55E-01	1.00E+00	6.08E-02	1.00E+00	5.66E-01	1.00E+00	2.70E-01	1.00E+00	9.97E-01	1.00E+00	cilium part	C
GO:0044444	4172	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.44E-32	0.00E+00	1.05E-29	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.07E-21	0.00E+00	6.46E-17	0.00E+00	cytoplasmic part	C
GO:0044445	75	5.22E-04	3.37E-02	7.85E-02	1.00E+00	1.54E-02	6.93E-01	2.46E-02	1.00E+00	5.10E-04	2.20E-02	1.98E-01	1.00E+00	2.29E-02	1.00E+00	2.11E-01	1.00E+00	cytosolic part	C
GO:0044446	3898	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.24E-28	0.00E+00	1.60E-21	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.67E-17	0.00E+00	7.41E-14	0.00E+00	intracellular organelle part	C
GO:0044447	16	3.26E-01	1.00E+00	7.96E-01	1.00E+00	1.72E-01	1.00E+00	6.79E-01	1.00E+00	5.03E-01	1.00E+00	5.30E-01	1.00E+00	3.31E-01	1.00E+00	9.86E-01	1.00E+00	axoneme part	C
GO:0044448	57	6.32E-04	3.44E-02	1.46E-04	1.50E-02	1.11E-03	9.80E-02	5.51E-02	1.00E+00	5.42E-03	4.18E-01	2.41E-04	2.60E-02	3.02E-03	1.95E-01	3.01E-02	1.00E+00	cell cortex part	C
GO:0044449	81	7.15E-01	1.00E+00	1.95E-01	1.00E+00	4.71E-01	1.00E+00	2.66E-01	1.00E+00	6.91E-01	1.00E+00	1.12E-01	1.00E+00	8.84E-01	1.00E+00	6.09E-01	1.00E+00	contractile fiber part	C
GO:0044450	28	6.44E-03	5.17E-01	1.81E-01	1.00E+00	3.85E-03	3.27E-01	8.92E-02	1.00E+00	1.58E-02	1.00E+00	4.08E-01	1.00E+00	1.44E-01	1.00E+00	1.60E-01	1.00E+00	microtubule organizing center part	C
GO:0044451	460	8.67E-15	0.00E+00	1.20E-13	0.00E+00	9.82E-08	2.42E-03	1.96E-08	9.71E-04	2.80E-14	0.00E+00	2.07E-12	0.00E+00	6.32E-04	6.50E-02	7.61E-04	9.16E-02	nucleoplasm part	C
GO:0044452	43	1.94E-02	1.00E+00	6.37E-03	3.60E-01	2.39E-01	1.00E+00	7.59E-02	1.00E+00	2.20E-02	1.00E+00	6.28E-02	1.00E+00	7.82E-02	1.00E+00	1.10E-02	5.11E-01	nucleolar part	C
GO:0044453	104	3.38E-07	1.95E-03	8.31E-12	0.00E+00	2.80E-03	2.48E-01	3.44E-05	8.00E-03	3.23E-07	1.69E-03	9.61E-11	0.00E+00	3.02E-02	1.00E+00	1.15E-04	2.00E-02	nuclear membrane part	C
GO:0044454	86	2.96E-04	3.37E-02	1.12E-04	1.50E-02	6.47E-03	4.60E-01	2.24E-02	1.00E+00	6.65E-04	4.00E-02	1.93E-04	2.60E-02	9.09E-02	1.00E+00	2.35E-02	1.00E+00	nuclear chromosome part	C
GO:0044455	109	1.04E-08	8.06E-04	9.52E-06	9.58E-03	1.37E-04	1.50E-02	1.26E-03	1.15E-01	6.02E-09	9.64E-04	3.59E-05	1.20E-02	5.91E-02	1.00E+00	5.57E-02	1.00E+00	mitochondrial membrane part	C
GO:0044456	144	9.82E-01	1.00E+00	9.95E-01	1.00E+00	9.86E-01	1.00E+00	9.88E-01	1.00E+00	9.26E-01	1.00E+00	9.84E-01	1.00E+00	9.88E-01	1.00E+00	9.36E-01	1.00E+00	synapse part	C
GO:0044459	1905	8.73E-01	1.00E+00	4.18E-01	1.00E+00	6.07E-01	1.00E+00	9.04E-01	1.00E+00	7.28E-01	1.00E+00	1.21E-01	1.00E+00	9.87E-01	1.00E+00	8.21E-01	1.00E+00	plasma membrane part	C
GO:0044460	15	7.09E-01	1.00E+00	5.65E-01	1.00E+00	3.64E-01	1.00E+00	8.01E-01	1.00E+00	8.03E-01	1.00E+00	5.88E-01	1.00E+00	6.30E-01	1.00E+00	1.49E-01	1.00E+00	flagellar part	C
GO:0044461	12	5.59E-01	1.00E+00	4.53E-01	1.00E+00	3.68E-01	1.00E+00	7.08E-01	1.00E+00	6.44E-01	1.00E+00	4.47E-01	1.00E+00	4.59E-01	1.00E+00	1.36E-01	1.00E+00	flagellar part (sensu Bacteria)	C
GO:0044462	29	8.00E-01	1.00E+00	9.16E-01	1.00E+00	6.34E-01	1.00E+00	9.96E-01	1.00E+00	8.75E-01	1.00E+00	7.79E-01	1.00E+00	4.18E-01	1.00E+00	7.16E-01	1.00E+00	external encapsulating structure part	C
GO:0044463	94	7.95E-01	1.00E+00	7.46E-01	1.00E+00	5.32E-01	1.00E+00	7.89E-01	1.00E+00	8.57E-01	1.00E+00	5.17E-01	1.00E+00	6.09E-01	1.00E+00	8.66E-01	1.00E+00	cell projection part	C
GO:0044464	14956	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.85E-36	0.00E+00	1.62E-36	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.29E-22	0.00E+00	2.39E-32	0.00E+00	cell part	C
GO:0045005	30	1.06E-03	9.60E-02	9.21E-05	1.50E-02	1.11E-01	1.00E+00	3.14E-03	1.47E-01	5.06E-04	2.20E-02	3.27E-05	1.20E-02	9.97E-02	1.00E+00	9.04E-01	1.00E+00	maintenance of fidelity during DNA-depend	P
GO:0045026	13	7.93E-01	1.00E+00	4.55E-01	1.00E+00	9.66E-01	1.00E+00	5.14E-01	1.00E+00	7.44E-01	1.00E+00	8.30E-01	1.00E+00	5.04E-01	1.00E+00	1.85E-02	1.00E+00	plasma membrane fusion	P
GO:0045028	129	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.24E-01	1.00E+00	9.97E-01	1.00E+00	purinergic nucleotide receptor activity, G-pr	F
GO:0045045	238	5.16E-03	3.28E-01	2.37E-02	1.00E+00	6.48E-03	4.60E-01	1.47E-01	1.00E+00	1.17E-02	5.39E-01	1.52E-02	7.39E-01	2.52E-01	1.00E+00	3.45E-01	1.00E+00	secretory pathway	P
GO:0045047	18	2.31E-01	1.00E+00	4.96E-01	1.00E+00	1.34E-01	1.00E+00	9.75E-01	1.00E+00	3.61E-01	1.00E+00	4.82E-01	1.00E+00	1.80E-01	1.00E+00	1.28E-01	1.00E+00	protein targeting to ER	P
GO:0045055	73	8.71E-01	1.00E+00	7.79E-01	1.00E+00	7.22E-01	1.00E+00	7.57E-01	1.00E+00	8.47E-01	1.00E+00	7.54E-01	1.00E+00	8.73E-01	1.00E+00	6.70E-01	1.00E+00	regulated secretory pathway	P
GO:0045058	16	2.90E-01	1.00E+00	2.36E-01	1.00E+00	7.99E-02	1.00E+00	1.80E-01	1.00E+00	4.22E-01	1.00E+00	8.51E-01	1.00E+00	6.76E-01	1.00E+00	1.27E-02	6.47E-01	T cell selection	P
GO:0045061	10	2.60E-01	1.00E+00	1.10E-01	1.00E+00	9.93E-02	1.00E+00	1.56E-01	1.00E+00	3.81E-01	1.00E+00	5.45E-01	1.00E+00	5.72E-01	1.00E+00	1.27E-02	6.47E-01	thymic T cell selection	P
GO:0045069	13	5.23E-02	1.00E+00	5.76E-01	1.00E+00	2.07E-01	1.00E+00	7.71E-01	1.00E+00	4.51E-02	1.00E+00	6.38E-01	1.00E+00	3.08E-01	1.00E+00	7.41E-02	1.00E+00	regulation of viral genome replication	P
GO:0045072	13	8.63E-01	1.00E+00	4.00E-01	1.00E+00	5.74E-01	1.00E+00	6.15E-01	1.00E+00	9.65E-01	1.00E+00	3.29E-01	1.00E+00	4.36E-01	1.00E+00	4.19E-01	1.00E+00	regulation of interferon-gamma biosynthesis	P
GO:0045073	11	6.19E-02	1.00E+00	1.03E-01	1.00E+00	3.64E-02	1.00E+00	2.16E-01	1.00E+00	1.57E-01	1.00E+00	1.81E-01	1.00E+00	1.03E-01	1.00E+00	1.01E-02	4.81E-01	regulation of chemokine biosynthesis	P
GO:0045076	16	9.79E-01	1.00E+00	8.69E-01	1.00E+00	9.27E-01	1.00E+00	6.53E-01	1.00E+00	9.08E-01	1.00E+00	9.38E-01	1.00E+00	9.63E-01	1.00E+00	5.23E-01	1.00E+00	regulation of interleukin-2 biosynthesis	P
GO:0045078	10	6.29E-01	1.00E+00	2.19E-01	1.00E+00	3.42E-01	1.00E+00	2.52E-01	1.00E+00	8.81E-01	1.00E+00	2.16E-01	1.00E+00	1.34E-01	1.00E+00	2.24E-01	1.00E+00	positive regulation of interferon-gamma bios	P
GO:0045086	10	9.09E-01	1.00E+00	6.31E-01	1.00E+00	6.74E-01	1.00E+00	6.42E-01	1.00E+00	8.67E-01	1.00E+00	6.86E-01	1.00E+00	8.78E-01	1.00E+00	4.23E-01	1.00E+00	positive regulation of interleukin-2 biosynthe	P
GO:0045087	122	9.59E-01	1.00E+00	9.19E-01	1.00E+00	9.76E-01	1.00E+00	9.41E-01	1.00E+00	9.01E-01	1.00E+00	8.78E-01	1.00E+00	8.66E-01	1.00E+00	5.76E-01	1.00E+00	innate immune response	P
GO:0045088	15	8.03E-01	1.00E+00	6.30E-01	1.00E+00	6.84E-01	1.00E+00	4.19E-01	1.00E+00	7.40E-01	1.00E+00	8.47E-01	1.00E+00	9.44E-01	1.00E+00	1.74E-01	1.00E+00	regulation of innate immune response	P
GO:0045089	13	8.61E-01	1.00E+00	7.38E-01	1.00E+00	7.35E-01	1.00E+00	6.70E-01	1.00E+00	8.48E-01	1.00E+00	8.44E-01	1.00E+00	8.44E-01	1.00E+00	2.70E-01	1.00E+00	positive regulation of innate immune respor	P
GO:0045095	66	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	9.12E-01	1.00E+00	keratin filament	C
GO:0045103	15	3.43E-01	1.00E+00	1.74E-01	1.00E+00	1.13E-01	1.00E+00	9.46E-02	1.00E+00	3.67E-01	1.00E+00	2.43E-01	1.00E+00	5.36E-01	1.00E+00	2.73E-01	1.00E+00	intermediate filament-based process	P
GO:0045104	13	5.74E-01	1.00E+00	2.31E-01	1.00E+00	3.12E-01	1.00E+00	1.25E-01	1.00E+00	5.57E-01	1.00E+00	2.90E-01	1.00E+00	6.53E-01	1.00E+00	3.60E-01	1.00E+00	intermediate filament cytoskeleton organiza	P
GO:0045111	183	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	intermediate filament cytoskeleton	C
GO:0045120	12	5.45E-03	3.28E-01	7.63E-03	3.60E-01	5.90E-02	1.00E+00	8.84E-02	1.00E+00	9.41E-03	5.39E-01	1.16E-02	7.39E-01	2.48E-01	1.00E+00	1.82E-01	1.00E+00	pronucleus	C
GO:0045121	54	3.07E-01	1.00E+00	6.10E-01	1.00E+00	2.53E-01	1.00E+00	3.44E-01	1.00E+00	4.18E-01	1.00E+00	6.39E-01	1.00E+00	1.14E-01	1.00E+00	9.14E-01	1.00E+00	lipid raft	C
GO:0045125	21	2.26E-01	1.00E+00	2.73E-01	1.00E+00	4.79E-01	1.00E+00	4.00E-01	1.00E+00	1.85E-01	1.00E+00	2.50E-01	1.00E+00	4.02E-01	1.00E+00	4.03E-01	1.00E+00	bioactive lipid receptor activity	F
GO:0045137	74	6.99E-01	1.00E+00	7.13E-01	1.00E+00	4.83E-01	1.00E+00	7.94E-01	1.00E+00	6.37E-01	1.00E+00	5.79E-01	1.00E+00	9.22E-01	1.00E+00	6.43E-01	1.00E+00	development of primary sexual characteristi	P
GO:0045165	125	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.95E-01	1.00E+00	cell fate commitment	P
GO:0045168	14	8.33E-01	1.00E+00	9.96E-01	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	6.16E-01	1.00E+00	9.75E-01	1.00E+00	9.49E-01	1.00E+00	9.83E-01	1.00E+00	cell-cell signaling during cell fate commitme	P
GO:0045177	127	6.65E-01	1.00E+00	4.30E-02	1.00E+00	1.40E-01	1.00E+00	8.38E-02	1.00E+00	7.64E-01	1.00E+00	9.69E-02	1.00E+00	8.81E-01	1.00E+00	2.01E-01	1.00E+00	apical part of cell	C
GO:0045178	26	5.50E-01	1.00E+00	5.78E-01	1.00E+00	6.46E-01	1.00E+00	9.89E-01	1.00E+00	7.49E-01	1.00E+00	5.04E-01	1.00E+00	3.71E-02	1.00E+00	1.69E-01	1.00E+00	basal part of cell	C

GO:0045182	121	6.07E-07	1.95E-03	4.59E-09	4.97E-03	9.69E-04	9.80E-02	2.15E-04	2.70E-02	4.53E-06	2.60E-03	1.32E-07	9.20E-04	5.24E-04	6.50E-02	3.63E-05	9.00E-03	translation regulator activity	F
GO:0045184	897	1.24E-23	0.00E+00	1.25E-24	0.00E+00	3.74E-13	0.00E+00	1.22E-10	0.00E+00	5.07E-21	0.00E+00	1.63E-23	0.00E+00	6.57E-06	2.00E-03	1.54E-06	1.88E-03	establishment of protein localization	P
GO:0045185	32	3.40E-01	1.00E+00	3.56E-01	1.00E+00	5.47E-01	1.00E+00	4.63E-01	1.00E+00	3.02E-01	1.00E+00	3.71E-01	1.00E+00	3.42E-01	1.00E+00	3.47E-01	1.00E+00	maintenance of protein localization	P
GO:0045190	24	3.70E-01	1.00E+00	8.52E-02	1.00E+00	5.33E-01	1.00E+00	2.44E-01	1.00E+00	2.26E-01	1.00E+00	6.59E-02	1.00E+00	9.92E-01	1.00E+00	5.55E-01	1.00E+00	isotype switching	P
GO:0045191	14	7.26E-01	1.00E+00	2.46E-01	1.00E+00	7.54E-01	1.00E+00	4.00E-01	1.00E+00	6.95E-01	1.00E+00	2.10E-01	1.00E+00	8.89E-01	1.00E+00	5.39E-01	1.00E+00	regulation of isotype switching	P
GO:0045202	263	9.34E-01	1.00E+00	9.17E-01	1.00E+00	9.19E-01	1.00E+00	9.76E-01	1.00E+00	8.41E-01	1.00E+00	7.72E-01	1.00E+00	9.52E-01	1.00E+00	9.03E-01	1.00E+00	synapse	C
GO:0045211	124	9.61E-01	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	9.93E-01	1.00E+00	8.70E-01	1.00E+00	9.87E-01	1.00E+00	9.68E-01	1.00E+00	9.01E-01	1.00E+00	postsynaptic membrane	C
GO:0045216	22	3.25E-02	1.00E+00	5.50E-02	1.00E+00	2.64E-02	1.00E+00	4.87E-02	1.00E+00	7.75E-02	1.00E+00	1.71E-01	1.00E+00	1.41E-01	1.00E+00	5.41E-02	1.00E+00	intercellular junction assembly and mainten	P
GO:0045255	16	4.52E-03	3.28E-01	1.44E-01	1.00E+00	7.76E-03	4.60E-01	1.41E-01	1.00E+00	3.88E-03	2.85E-01	1.85E-01	1.00E+00	1.75E-01	1.00E+00	2.49E-01	1.00E+00	hydrogen-translocating F-type ATPase com	C
GO:0045259	18	2.61E-03	2.39E-01	1.07E-01	1.00E+00	2.50E-03	2.48E-01	1.09E-01	1.00E+00	2.55E-03	2.85E-01	1.29E-01	1.00E+00	1.82E-01	1.00E+00	2.62E-01	1.00E+00	proton-transporting ATP synthase complex	C
GO:0045263	11	2.21E-02	1.00E+00	2.35E-01	1.00E+00	7.13E-03	4.60E-01	1.85E-01	1.00E+00	2.70E-02	1.00E+00	3.01E-01	1.00E+00	1.77E-01	1.00E+00	3.47E-01	1.00E+00	proton-transporting ATP synthase complex,	C
GO:0045271	36	2.28E-04	2.64E-02	6.99E-03	3.60E-01	3.80E-02	1.00E+00	3.32E-02	1.00E+00	6.72E-04	4.00E-02	2.96E-02	1.00E+00	3.27E-02	1.00E+00	5.08E-02	1.00E+00	respiratory chain complex I	C
GO:0045296	12	9.81E-01	1.00E+00	9.53E-02	1.00E+00	8.60E-01	1.00E+00	7.82E-02	1.00E+00	9.81E-01	1.00E+00	9.04E-02	1.00E+00	8.67E-01	1.00E+00	5.63E-01	1.00E+00	cadherin binding	F
GO:0045321	249	1.22E-01	1.00E+00	3.17E-02	1.00E+00	1.35E-01	1.00E+00	4.92E-02	1.00E+00	1.15E-01	1.00E+00	5.84E-02	1.00E+00	5.25E-01	1.00E+00	8.81E-02	1.00E+00	leukocyte activation	P
GO:0045333	48	4.16E-02	1.00E+00	4.44E-02	1.00E+00	9.69E-03	4.60E-01	9.10E-02	1.00E+00	6.93E-02	1.00E+00	5.34E-02	1.00E+00	4.06E-01	1.00E+00	2.12E-01	1.00E+00	cellular respiration	P
GO:0045334	10	9.28E-03	6.67E-01	6.36E-02	1.00E+00	5.14E-02	1.00E+00	1.85E-01	1.00E+00	8.96E-03	5.39E-01	4.10E-02	1.00E+00	8.49E-02	1.00E+00	3.38E-01	1.00E+00	clathrin-coated endocytic vesicle	C
GO:0045351	11	2.58E-01	1.00E+00	5.93E-01	1.00E+00	6.91E-01	1.00E+00	6.30E-01	1.00E+00	2.21E-01	1.00E+00	6.51E-01	1.00E+00	2.08E-02	9.11E-01	2.65E-01	1.00E+00	interferon type I biosynthesis	P
GO:0045408	13	7.39E-01	1.00E+00	6.01E-01	1.00E+00	7.54E-01	1.00E+00	4.32E-01	1.00E+00	8.51E-01	1.00E+00	5.18E-01	1.00E+00	1.46E-01	1.00E+00	9.96E-01	1.00E+00	regulation of interleukin-6 biosynthesis	P
GO:0045428	16	3.50E-01	1.00E+00	2.28E-01	1.00E+00	1.40E-01	1.00E+00	1.05E-01	1.00E+00	4.69E-01	1.00E+00	2.35E-01	1.00E+00	4.02E-01	1.00E+00	6.02E-01	1.00E+00	regulation of nitric oxide biosynthesis	P
GO:0045429	13	3.15E-01	1.00E+00	2.32E-01	1.00E+00	2.92E-01	1.00E+00	6.94E-02	1.00E+00	3.43E-01	1.00E+00	2.91E-01	1.00E+00	2.89E-01	1.00E+00	4.35E-01	1.00E+00	positive regulation of nitric oxide biosynthes	P
GO:0045444	32	2.04E-01	1.00E+00	1.43E-01	1.00E+00	1.55E-01	1.00E+00	1.73E-01	1.00E+00	2.56E-01	1.00E+00	2.22E-01	1.00E+00	3.24E-01	1.00E+00	1.10E-01	1.00E+00	fat cell differentiation	P
GO:0045445	47	9.82E-01	1.00E+00	4.97E-01	1.00E+00	8.79E-01	1.00E+00	6.21E-01	1.00E+00	9.64E-01	1.00E+00	4.57E-01	1.00E+00	9.48E-01	1.00E+00	4.19E-01	1.00E+00	myoblast differentiation	P
GO:0045446	12	3.56E-01	1.00E+00	2.98E-01	1.00E+00	4.85E-01	1.00E+00	4.94E-01	1.00E+00	3.58E-01	1.00E+00	3.68E-01	1.00E+00	1.32E-01	1.00E+00	8.91E-02	1.00E+00	endothelial cell differentiation	P
GO:0045449	2682	1.52E-28	0.00E+00	8.35E-38	0.00E+00	9.40E-12	0.00E+00	2.58E-15	0.00E+00	7.87E-28	0.00E+00	3.71E-34	0.00E+00	8.50E-10	0.00E+00	1.49E-14	0.00E+00	regulation of transcription	P
GO:0045453	21	7.40E-01	1.00E+00	6.43E-01	1.00E+00	5.25E-01	1.00E+00	5.71E-01	1.00E+00	7.20E-01	1.00E+00	6.56E-01	1.00E+00	7.94E-01	1.00E+00	5.58E-01	1.00E+00	bone resorption	P
GO:0045454	56	2.06E-02	1.00E+00	3.60E-03	1.97E-01	3.08E-01	1.00E+00	3.62E-02	1.00E+00	3.85E-02	1.00E+00	3.95E-03	2.70E-01	3.60E-02	1.00E+00	5.34E-02	1.00E+00	cell redox homeostasis	P
GO:0045471	18	3.56E-01	1.00E+00	5.30E-01	1.00E+00	1.63E-01	1.00E+00	1.40E-01	1.00E+00	6.29E-01	1.00E+00	6.85E-01	1.00E+00	2.06E-01	1.00E+00	5.58E-01	1.00E+00	response to ethanol	P
GO:0045494	20	6.61E-01	1.00E+00	7.80E-01	1.00E+00	4.58E-01	1.00E+00	6.66E-01	1.00E+00	5.47E-01	1.00E+00	6.61E-01	1.00E+00	1.00E+00	1.00E+00	5.75E-01	1.00E+00	photoreceptor maintenance	P
GO:0045577	13	3.61E-01	1.00E+00	7.44E-01	1.00E+00	4.34E-01	1.00E+00	8.05E-01	1.00E+00	2.72E-01	1.00E+00	5.57E-01	1.00E+00	6.51E-01	1.00E+00	8.28E-01	1.00E+00	regulation of B cell differentiation	P
GO:0045580	18	9.73E-01	1.00E+00	6.39E-01	1.00E+00	8.82E-01	1.00E+00	6.02E-01	1.00E+00	9.83E-01	1.00E+00	7.95E-01	1.00E+00	9.75E-01	1.00E+00	2.30E-01	1.00E+00	regulation of T cell differentiation	P
GO:0045582	11	7.63E-01	1.00E+00	2.98E-01	1.00E+00	6.40E-01	1.00E+00	4.48E-01	1.00E+00	7.86E-01	1.00E+00	3.35E-01	1.00E+00	8.88E-01	1.00E+00	1.68E-01	1.00E+00	positive regulation of T cell differentiation	P
GO:0045595	207	6.27E-01	1.00E+00	6.23E-01	1.00E+00	9.94E-01	1.00E+00	7.67E-01	1.00E+00	2.63E-01	1.00E+00	7.12E-01	1.00E+00	9.17E-01	1.00E+00	8.49E-02	1.00E+00	regulation of cell differentiation	P
GO:0045596	100	9.11E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	5.87E-01	1.00E+00	9.40E-01	1.00E+00	9.76E-01	1.00E+00	5.20E-01	1.00E+00	negative regulation of cell differentiation	P
GO:0045597	85	9.89E-01	1.00E+00	9.89E-01	1.00E+00	9.92E-01	1.00E+00	9.34E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	8.93E-01	1.00E+00	3.37E-01	1.00E+00	positive regulation of cell differentiation	P
GO:0045619	27	8.01E-01	1.00E+00	6.31E-01	1.00E+00	8.41E-01	1.00E+00	8.04E-01	1.00E+00	6.83E-01	1.00E+00	6.35E-01	1.00E+00	9.14E-01	1.00E+00	3.21E-01	1.00E+00	regulation of lymphocyte differentiation	P
GO:0045621	15	5.53E-01	1.00E+00	1.85E-01	1.00E+00	4.95E-01	1.00E+00	3.92E-01	1.00E+00	4.95E-01	1.00E+00	2.36E-01	1.00E+00	8.37E-01	1.00E+00	8.42E-02	1.00E+00	positive regulation of lymphocyte differentia	P
GO:0045637	44	5.99E-01	1.00E+00	7.23E-01	1.00E+00	9.18E-01	1.00E+00	8.77E-01	1.00E+00	4.00E-01	1.00E+00	6.06E-01	1.00E+00	7.38E-01	1.00E+00	6.00E-01	1.00E+00	regulation of myeloid cell differentiation	P
GO:0045638	22	4.90E-01	1.00E+00	5.51E-01	1.00E+00	9.71E-01	1.00E+00	6.66E-01	1.00E+00	2.88E-01	1.00E+00	3.59E-01	1.00E+00	5.06E-01	1.00E+00	9.77E-01	1.00E+00	negative regulation of myeloid cell differenti	P
GO:0045639	20	9.92E-01	1.00E+00	9.90E-01	1.00E+00	9.31E-01	1.00E+00	9.12E-01	1.00E+00	9.87E-01	1.00E+00	9.76E-01	1.00E+00	9.44E-01	1.00E+00	8.40E-01	1.00E+00	positive regulation of myeloid cell differentia	P
GO:0045646	14	5.26E-01	1.00E+00	6.71E-01	1.00E+00	7.47E-01	1.00E+00	9.25E-01	1.00E+00	3.82E-01	1.00E+00	5.65E-01	1.00E+00	8.13E-01	1.00E+00	3.55E-01	1.00E+00	regulation of erythrocyte differentiation	P
GO:0045664	45	9.60E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	7.23E-01	1.00E+00	9.06E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of neuron differentiation	P
GO:0045665	27	9.60E-01	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.00E-01	1.00E+00	8.34E-01	1.00E+00	9.74E-01	1.00E+00	9.62E-01	1.00E+00	9.74E-01	1.00E+00	negative regulation of neuron differentiation	P
GO:0045666	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of neuron differentiation	P
GO:0045667	25	8.85E-01	1.00E+00	5.51E-01	1.00E+00	9.96E-01	1.00E+00	6.14E-01	1.00E+00	7.04E-01	1.00E+00	7.64E-01	1.00E+00	7.42E-01	1.00E+00	5.78E-02	1.00E+00	regulation of osteoblast differentiation	P
GO:0045669	19	8.35E-01	1.00E+00	5.43E-01	1.00E+00	9.99E-01	1.00E+00	5.88E-01	1.00E+00	6.66E-01	1.00E+00	7.93E-01	1.00E+00	5.33E-01	1.00E+00	5.48E-02	1.00E+00	positive regulation of osteoblast differentiati	P
GO:0045670	14	8.60E-01	1.00E+00	6.83E-01	1.00E+00	9.44E-01	1.00E+00	7.58E-01	1.00E+00	7.38E-01	1.00E+00	6.84E-01	1.00E+00	7.90E-01	1.00E+00	2.90E-01	1.00E+00	regulation of osteoclast differentiation	P
GO:0045682	10	1.23E-01	1.00E+00	4.89E-01	1.00E+00	5.18E-02	1.00E+00	1.76E-01	1.00E+00	2.06E-01	1.00E+00	8.57E-01	1.00E+00	1.45E-01	1.00E+00	1.63E-01	1.00E+00	regulation of epidermis development	P
GO:0045685	11	9.51E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	8.49E-01	1.00E+00	8.92E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	7.17E-01	1.00E+00	regulation of glial cell differentiation	P
GO:0045727	61	2.74E-01	1.00E+00	1.34E-01	1.00E+00	6.15E-02	1.00E+00	2.20E-01	1.00E+00	5.37E-01	1.00E+00	1.80E-01	1.00E+00	3.83E-01	1.00E+00	7.89E-02	1.00E+00	positive regulation of protein biosynthesis	P
GO:0045735	82	6.83E-02	1.00E+00	3.61E-01	1.00E+00	8.12E-01	1.00E+00	5.08E-01	1.00E+00	4.52E-02	1.00E+00	2.83E-01	1.00E+00	1.25E-02	6.30E-01	7.01E-01	1.00E+00	nutrient reservoir activity	F
GO:0045736	11	1.91E-02	1.00E+00	3.71E-03	1.97E-01	4.28E-01	1.00E+00	2.59E-02	1.00E+00	6.25E-03	5.39E-01	6.97E-03	5.30E-01	6.01E-01	1.00E+00	5.51E-01	1.00E+00	negative regulation of cyclin-dependent pro	P
GO:0045740	15	4.80E-01	1.00E+00	6.20E-01	1.00E+00	1.71E-01	1.00E+00	1.54E-01	1.00E+00	5.97E-01	1.00E+00	8.58E-01	1.00E+00	7.70E-01	1.00E+00	8.65E-01	1.00E+00	positive regulation of DNA replication	P
GO:0045761	44	9.68E-01	1.00E+00	8.71E-01	1.00E+00	9.43E-01	1.00E+00	5.78E-01	1.00E+00	9.62E-01	1.00E+00	9.31E-01	1.00E+00	7.98E-01	1.00E+00	4.37E-01	1.00E+00	regulation of adenylate cyclase activity	P
GO:0045762	28	6.55E-01	1.00E+00	5.67E-01	1.00E+00	5.56E-01	1.00E+00	1.90E-01	1.00E+00	7.19E-01	1.00E+00	8.38E-01	1.00E+00	3.89E-01	1.00E+00	1.54E-01	1.00E+00	positive regulation of adenylate cyclase acti	P
GO:0045763	13	2.06E-02	1.00E+00	2.81E-02	1.00E+00	2.26E-03	2.48E-01	5.28E-02	1.00E+00	2.95E-02	1.00E+00	6.95E-02	1.00E+00	3.51E-01	1.00E+00	2.37E-01	1.00E+00	negative regulation of amino acid metabolis	P
GO:0045764	43	8.80E-01	1.00E+00	8.70E-01	1.00E+00	3.47E-01	1.00E+00	3.46E-01	1.00E+00	8.86E-01	1.00E+00	9.56E-01	1.00E+00	9.66E-01	1.00E+00	7.15E-01	1.00E+00	positive regulation of amino acid metabolisr	P
GO:0045765	48	1.81E-01	1.00E+00	1.11E-01	1.00E+00	6.54E-02	1.00E+00	1.64E-01	1.00E+00	2.73E-01	1.00E+00	1.95E-01	1.00E+00	4.51E-01	1.00E+00	3.87E-02	1.00E+00	regulation of angiogenesis	P
GO:0045766	16	6.22E-01	1.00E+00	3.61E-01	1.00E+00	4.05E-01	1.00E+00	2.08E-01	1.00E+00	7.87E-01	1.00E+00	4.90E-01	1.00E+00	5.03E-01	1.00E+00	3.02E-01	1.00E+00	positive regulation of angiogenesis	P
GO:0045767	15	8.33E-03	6.34E-01	7.02E-03	3.60E-01	8.02E-03	4.60E-01	9.47E-03	7.13E-01	7.53E-03	5.39E-01	3.09E-02	1.00E+00	6.08E-01	1.00E+00	3.72E-03	1.85E-01	regulation of anti-apoptosis	P
GO:0045768	11	5.46E-03	3.28E-01	2.99E-02	1.00E+00	1.92E-02	1.00E+00	3.17E-02	1.00E+00	4.73E-03	4.18E-01	9.84E-02	1.00E+00	1.95E-01	1.00E+00	4.98E-03	3.60E-01	positive regulation of anti-apoptosis	P
GO:0045778	18	9.65E-01	1.00E+00	4.54E-01	1.00E+00	9.90E-01	1.00E+00	5.70E-01	1.00E+00	9.30E-01	1.00E+00	5.06E-01	1.00E+00	6.38E-01	1.00E+00	1.83E-01	1.00E+00	positive regulation of ossification	P
GO:0045785	13	3.40E-01	1.00E+00	1.15E-01	1.00E+00	4.35E-01	1.00E+00	3.82E-02	1.00E+00	3.53E-01	1.00E+00	2.35E-01	1.00E+00	2.55E-01	1.00E+00	3.43E-01	1.00E+00	positive regulation of cell adhesion	P
GO:0045786	227	5.88E-03	3.50E-01	2.39E-03	1.77E-01	3.60E-02	1.00E+00	2.38E-02	1.00E+00	8.18E-03	5.39E-01	3.45E-03	2.70E-01	1.43E-01	1.00E+00	4.42E-02	1.00E+00	negative regulation of progression through	P
GO:0045787	38	5.18E-02	1.00E+00	2.51E-02	1.00E+00	1.72E-01	1.00E+00	1.01E-01	1.00E+00	4.19E-02	1.00E+00	6.37E-02	1.00E+00	3.18E-01	1.00E+00	8.54E-03	4.81E-01	positive regulation of progression through c	P
GO:0045792	67	8.88E-02	1.00E+00	1.38E-02	7.47E-01	4.77E-02	1.00E+00	4.84E-02	1.00E+00	8.38E-02	1.00E+00	2.25E-02	1.00E+00	7.40E-01	1.00E+00	9.82E-02	1.00E+00	negative regulation of cell size	P
GO:0045793	11	8.62E-01	1.00E+00	4.51E-01	1.00E+00	4.60E-01	1.00E+00	3.24E-01	1.00E+00	9.39E-01	1.00E+00	4.03E-01	1.00E+00	8.58E-01	1.00E+00	8.81E-01	1.00E+00	positive regulation of cell size	P
GO:0045807	19	2.27E-01	1.00E+00	3.70E-02	1.00E+00	4.90E-01	1.00E+00	4.01E-02	1.00E+00	1.02E-01	1.00E+00	1.41E-02	7.39E-01	6.88E-01	1.00E+00	7.44E-01	1.00E+00	positive regulation of endocytosis	P
GO:0045814	16	2.92E-03	2.39E-01	1.79E-02	1.00E+00	9.35E-02	1.00E+00	1.19E-01	1.00E+00	9.37E-04	4.40E-02	2.74E-02	1.00E+00	6.52E-02	1.00E+00	1.64E-02	8.49E-01	negative regulation of gene expression, epi	P
GO:0045830	10	8.69E-01	1.00E+00	2.43E-01	1.00E+00	6.77E-01	1.00E+00	5.57E-01	1.00E+00	8.41E-01	1.00E+00	1.58E-01	1.00E+00	9.16E-01	1.00E+00	5.93E-01	1.00E+00	positive regulation of isotype switching	P
GO:0045834	14	1.56E-01	1.00E+00	4.84E-01	1.00E+00	5.15E-02	1.00E+00	3.57E-01	1.00E+00	5.15E-01	1.00E+00	4.84E-01	1.00E+00	2.66E-02	1.00E+00	6.17E-01	1.00E+00	positive regulation of lipid metabolism	P
GO:0045840	20	1.24E-01	1.00E+00	6.05E-02	1.00E+00	6.23E-02	1.00E+00	8.79E-02	1.00E+00	1.80E-01	1.00E+00	1.41E-01	1.00E+00	3.70E-01	1.00E+00	3.94E-02	1.00E+00	positive regulation of mitosis	P
GO:0045843	10	2.37E-01	1.00E+00	3.47E-01	1.00E+00	4.64E-01	1.00E+00	9.19E-01	1.00E+00	2.30E-01	1.00E+00	3.40E-01	1.00E+00	1.64E-01	1.00E+00	7.20E-02	1.00E+00	negative regulation of striated muscle devel	P
GO:0045859	249	2.67E-03	2.39E-01	4.49E-04	6.90E-02	2.13E-02	1.00E+00	2.87E-02	1.00E+00	1.61E-03	1.76E-01	6.78E-04	5.49E-02	3.23E-01	1.00E+00	7.29E-03	4.81E-01	regulation of protein kinase activity	P
GO:0045860	151	5.24E-02	1.00E+00	3.40E-02	1.00E+00	1.17E-01	1.00E+00	1.41E-01	1.00E+00	3.70E-02	1.00E+00	3.24E-02	1.00E+00	3.76E-01	1.00E+00	4.24E-02	1.00E+00	positive regulation of protein kinase activity	P
GO:0045884	15	5.11E-01	1.00E+00	5.78E-01	1.00E+00	3.34E-01	1.00E+00	5.70E-01	1.00E+00	5.35E-01	1.00E+00	5.60E-01	1.00E+00	8.11E-01	1.00E+00	4.98E-01	1.00E+00	regulation of survival gene product activity	P

GO:0045892	262	3.17E-05	1.00E-02	1.83E-04	1.50E-02	8.02E-02	1.00E+00	5.55E-03	3.46E-01	2.94E-06	2.60E-03	6.14E-04	5.49E-02	5.53E-02	1.00E+00	1.40E-02	8.49E-01	negative regulation of transcription, DNA-de	P
GO:0045893	352	4.30E-02	1.00E+00	9.06E-02	1.00E+00	5.01E-02	1.00E+00	1.18E-01	1.00E+00	5.94E-02	1.00E+00	1.00E-01	1.00E+00	2.21E-01	1.00E+00	4.15E-01	1.00E+00	positive regulation of transcription, DNA-dep	P
GO:0045913	14	1.85E-01	1.00E+00	4.12E-01	1.00E+00	2.48E-01	1.00E+00	3.37E-01	1.00E+00	1.37E-01	1.00E+00	3.61E-01	1.00E+00	3.67E-01	1.00E+00	9.31E-01	1.00E+00	positive regulation of carbohydrate metabol	P
GO:0045926	79	3.24E-02	1.00E+00	6.62E-03	3.60E-01	5.64E-02	1.00E+00	1.30E-02	8.18E-01	1.54E-02	1.00E+00	3.48E-02	1.00E+00	5.12E-01	1.00E+00	3.27E-02	1.00E+00	negative regulation of growth	P
GO:0045927	38	9.20E-01	1.00E+00	9.99E-01	1.00E+00	7.25E-01	1.00E+00	9.81E-01	1.00E+00	9.05E-01	1.00E+00	9.88E-01	1.00E+00	9.56E-01	1.00E+00	9.98E-01	1.00E+00	positive regulation of growth	P
GO:0045930	16	7.31E-01	1.00E+00	5.45E-01	1.00E+00	3.54E-01	1.00E+00	6.97E-01	1.00E+00	7.79E-01	1.00E+00	4.21E-01	1.00E+00	8.22E-01	1.00E+00	8.72E-01	1.00E+00	negative regulation of progression through	P
GO:0045934	381	3.93E-09	8.06E-04	6.32E-08	4.97E-03	8.29E-05	1.20E-02	4.98E-05	8.00E-03	4.98E-09	9.64E-04	5.66E-07	2.97E-03	3.65E-02	1.00E+00	1.49E-03	9.16E-02	negative regulation of nucleobase, nucleosi	P
GO:0045935	438	1.25E-02	6.67E-01	6.18E-03	3.60E-01	1.37E-02	6.93E-01	1.65E-02	8.18E-01	2.08E-02	1.00E+00	8.50E-03	7.39E-01	2.63E-01	1.00E+00	3.74E-01	1.00E+00	positive regulation of nucleobase, nucleosid	P
GO:0045936	19	3.71E-02	1.00E+00	9.38E-03	5.18E-01	4.25E-02	1.00E+00	4.05E-02	1.00E+00	4.30E-02	1.00E+00	3.46E-02	1.00E+00	1.57E-01	1.00E+00	6.35E-02	1.00E+00	negative regulation of phosphate metabolisı	P
GO:0045937	41	9.90E-01	1.00E+00	9.50E-01	1.00E+00	5.17E-01	1.00E+00	6.36E-01	1.00E+00	9.94E-01	1.00E+00	9.75E-01	1.00E+00	9.84E-01	1.00E+00	8.92E-01	1.00E+00	positive regulation of phosphate metabolisn	P
GO:0045941	417	1.82E-02	1.00E+00	8.58E-03	5.03E-01	3.04E-02	1.00E+00	3.20E-02	1.00E+00	2.39E-02	1.00E+00	9.60E-03	7.39E-01	2.79E-01	1.00E+00	3.29E-01	1.00E+00	positive regulation of transcription	P
GO:0045944	253	5.39E-01	1.00E+00	8.41E-01	1.00E+00	3.98E-01	1.00E+00	6.12E-01	1.00E+00	5.81E-01	1.00E+00	8.19E-01	1.00E+00	5.36E-01	1.00E+00	9.05E-01	1.00E+00	positive regulation of transcription from RNA	P
GO:0046006	11	9.90E-01	1.00E+00	9.97E-01	1.00E+00	9.75E-01	1.00E+00	9.99E-01	1.00E+00	8.58E-01	1.00E+00	9.72E-01	1.00E+00	9.14E-01	1.00E+00	9.91E-01	1.00E+00	regulation of activated T cell proliferation	P
GO:0046034	40	1.66E-02	6.67E-01	9.09E-02	1.00E+00	9.46E-02	1.00E+00	2.32E-01	1.00E+00	8.51E-03	5.39E-01	1.14E-01	1.00E+00	3.58E-01	1.00E+00	1.12E-01	1.00E+00	ATP metabolism	P
GO:0046036	12	2.15E-02	1.00E+00	1.03E-01	1.00E+00	5.38E-02	1.00E+00	8.83E-02	1.00E+00	2.46E-02	1.00E+00	1.88E-01	1.00E+00	1.70E-01	1.00E+00	1.59E-01	1.00E+00	CTP metabolism	P
GO:0046039	11	2.48E-02	1.00E+00	1.66E-01	1.00E+00	2.36E-02	1.00E+00	1.63E-01	1.00E+00	3.63E-02	1.00E+00	2.35E-01	1.00E+00	1.88E-01	1.00E+00	2.38E-01	1.00E+00	GTP metabolism	P
GO:0046051	11	2.48E-02	1.00E+00	1.66E-01	1.00E+00	2.36E-02	1.00E+00	1.63E-01	1.00E+00	3.63E-02	1.00E+00	2.35E-01	1.00E+00	1.88E-01	1.00E+00	2.38E-01	1.00E+00	UTP metabolism	P
GO:0046058	26	7.13E-01	1.00E+00	4.49E-01	1.00E+00	6.14E-01	1.00E+00	3.46E-01	1.00E+00	5.39E-01	1.00E+00	4.16E-01	1.00E+00	9.55E-01	1.00E+00	6.94E-01	1.00E+00	cAMP metabolism	P
GO:0046068	15	9.87E-01	1.00E+00	7.46E-01	1.00E+00	9.88E-01	1.00E+00	5.81E-01	1.00E+00	9.83E-01	1.00E+00	7.06E-01	1.00E+00	5.58E-01	1.00E+00	9.69E-01	1.00E+00	cGMP metabolism	P
GO:0046112	10	2.30E-01	1.00E+00	2.13E-01	1.00E+00	9.95E-01	1.00E+00	5.64E-01	1.00E+00	1.96E-01	1.00E+00	6.47E-02	1.00E+00	3.18E-02	1.00E+00	6.14E-01	1.00E+00	nucleobase biosynthesis	P
GO:0046128	10	1.08E-01	1.00E+00	5.79E-02	1.00E+00	4.58E-01	1.00E+00	4.81E-02	1.00E+00	8.86E-02	1.00E+00	6.94E-02	1.00E+00	1.34E-01	1.00E+00	2.93E-01	1.00E+00	purine ribonucleoside metabolism	P
GO:0046148	39	1.25E-02	6.67E-01	1.42E-02	7.47E-01	4.75E-02	1.00E+00	6.87E-02	1.00E+00	1.42E-02	1.00E+00	3.81E-02	1.00E+00	4.51E-01	1.00E+00	1.02E-01	1.00E+00	pigment biosynthesis	P
GO:0046164	96	4.59E-05	1.00E-02	1.71E-04	1.50E-02	2.90E-04	3.60E-02	1.60E-03	1.24E-01	3.33E-04	1.98E-02	2.55E-03	2.39E-01	5.22E-02	1.00E+00	7.87E-03	4.81E-01	alcohol catabolism	P
GO:0046165	35	8.00E-02	1.00E+00	1.41E-01	1.00E+00	2.00E-01	1.00E+00	4.68E-01	1.00E+00	7.53E-02	1.00E+00	2.83E-01	1.00E+00	2.77E-01	1.00E+00	2.54E-02	1.00E+00	alcohol biosynthesis	P
GO:0046209	26	2.22E-01	1.00E+00	1.10E-01	1.00E+00	5.19E-02	1.00E+00	2.82E-02	1.00E+00	3.43E-01	1.00E+00	1.44E-01	1.00E+00	3.89E-01	1.00E+00	6.26E-01	1.00E+00	nitric oxide metabolism	P
GO:0046320	12	5.58E-01	1.00E+00	1.99E-01	1.00E+00	9.84E-01	1.00E+00	1.76E-01	1.00E+00	3.05E-01	1.00E+00	3.19E-01	1.00E+00	6.75E-01	1.00E+00	1.15E-01	1.00E+00	regulation of fatty acid oxidation	P
GO:0046323	17	5.42E-02	1.00E+00	8.23E-02	1.00E+00	1.77E-01	1.00E+00	2.10E-01	1.00E+00	5.57E-02	1.00E+00	1.01E-01	1.00E+00	2.59E-01	1.00E+00	1.86E-01	1.00E+00	glucose import	P
GO:0046324	16	6.57E-02	1.00E+00	7.91E-02	1.00E+00	1.30E-01	1.00E+00	2.97E-01	1.00E+00	7.46E-02	1.00E+00	7.28E-02	1.00E+00	2.88E-01	1.00E+00	1.53E-01	1.00E+00	regulation of glucose import	P
GO:0046328	25	6.60E-02	1.00E+00	8.69E-01	1.00E+00	1.17E-01	1.00E+00	7.50E-01	1.00E+00	6.55E-02	1.00E+00	9.19E-01	1.00E+00	2.09E-01	1.00E+00	2.98E-01	1.00E+00	regulation of JNK cascade	P
GO:0046330	15	3.13E-01	1.00E+00	1.00E+00	1.00E+00	3.96E-01	1.00E+00	1.00E+00	1.00E+00	2.76E-01	1.00E+00	1.00E+00	1.00E+00	3.68E-01	1.00E+00	2.54E-01	1.00E+00	positive regulation of JNK cascade	P
GO:0046332	19	6.83E-02	1.00E+00	2.90E-01	1.00E+00	4.11E-01	1.00E+00	1.18E-01	1.00E+00	2.45E-02	1.00E+00	4.03E-01	1.00E+00	3.00E-01	1.00E+00	6.85E-01	1.00E+00	SMAD binding	F
GO:0046356	24	6.17E-02	1.00E+00	1.65E-01	1.00E+00	1.33E-02	5.53E-01	8.30E-02	1.00E+00	1.08E-01	1.00E+00	2.70E-01	1.00E+00	4.90E-01	1.00E+00	2.67E-01	1.00E+00	acetyl-CoA catabolism	P
GO:0046364	34	7.94E-02	1.00E+00	9.77E-02	1.00E+00	1.64E-01	1.00E+00	3.96E-01	1.00E+00	7.63E-02	1.00E+00	2.37E-01	1.00E+00	3.03E-01	1.00E+00	1.93E-02	1.00E+00	monosaccharide biosynthesis	P
GO:0046365	89	9.67E-05	1.24E-02	4.12E-04	6.90E-02	1.49E-04	1.50E-02	3.02E-03	1.47E-01	5.96E-04	4.00E-02	3.36E-03	2.70E-01	1.28E-01	1.00E+00	1.80E-02	1.00E+00	monosaccharide catabolism	P
GO:0046394	90	1.83E-01	1.00E+00	1.23E-02	6.77E-01	2.20E-01	1.00E+00	9.63E-02	1.00E+00	3.64E-01	1.00E+00	1.45E-02	7.39E-01	1.28E-01	1.00E+00	2.91E-01	1.00E+00	carboxylic acid biosynthesis	P
GO:0046395	10	1.41E-01	1.00E+00	1.09E-01	1.00E+00	2.12E-01	1.00E+00	2.92E-01	1.00E+00	1.86E-01	1.00E+00	1.64E-01	1.00E+00	3.01E-01	1.00E+00	8.40E-02	1.00E+00	carboxylic acid catabolism	P
GO:0046425	24	1.76E-01	1.00E+00	1.62E-01	1.00E+00	3.40E-02	1.00E+00	6.10E-02	1.00E+00	2.36E-01	1.00E+00	3.11E-01	1.00E+00	7.94E-01	1.00E+00	4.97E-01	1.00E+00	regulation of JAK-STAT cascade	P
GO:0046427	14	7.77E-01	1.00E+00	7.59E-01	1.00E+00	4.16E-01	1.00E+00	3.00E-01	1.00E+00	8.35E-01	1.00E+00	8.77E-01	1.00E+00	7.16E-01	1.00E+00	9.38E-01	1.00E+00	positive regulation of JAK-STAT cascade	P
GO:0046456	29	2.87E-01	1.00E+00	6.43E-02	1.00E+00	1.01E-01	1.00E+00	2.92E-01	1.00E+00	5.31E-01	1.00E+00	8.78E-02	1.00E+00	2.30E-01	1.00E+00	5.34E-02	1.00E+00	icosanoid biosynthesis	P
GO:0046466	26	3.03E-01	1.00E+00	6.86E-01	1.00E+00	5.86E-01	1.00E+00	7.35E-01	1.00E+00	3.23E-01	1.00E+00	6.85E-01	1.00E+00	2.88E-01	1.00E+00	4.32E-01	1.00E+00	membrane lipid catabolism	P
GO:0046467	107	8.04E-03	6.34E-01	7.75E-04	6.90E-02	1.42E-01	1.00E+00	1.81E-02	1.00E+00	1.32E-02	1.00E+00	8.03E-04	5.49E-02	5.32E-02	1.00E+00	1.05E-01	1.00E+00	membrane lipid biosynthesis	P
GO:0046470	13	1.71E-01	1.00E+00	5.65E-03	3.60E-01	1.93E-01	1.00E+00	7.92E-02	1.00E+00	1.64E-01	1.00E+00	5.47E-03	2.70E-01	5.68E-01	1.00E+00	6.59E-02	1.00E+00	phosphatidylcholine metabolism	P
GO:0046474	51	2.89E-02	1.00E+00	5.81E-03	3.60E-01	2.06E-01	1.00E+00	7.20E-02	1.00E+00	1.76E-02	1.00E+00	5.14E-03	2.70E-01	4.29E-01	1.00E+00	5.14E-02	1.00E+00	glycerophospholipid biosynthesis	P
GO:0046483	91	3.50E-05	1.00E-02	2.90E-06	8.39E-03	1.43E-04	1.50E-02	1.75E-03	1.24E-01	3.78E-04	2.20E-02	5.13E-06	4.00E-03	1.33E-01	1.00E+00	2.62E-02	1.00E+00	heterocycle metabolism	P
GO:0046486	36	3.19E-01	1.00E+00	7.97E-02	1.00E+00	2.56E-01	1.00E+00	3.07E-01	1.00E+00	4.28E-01	1.00E+00	6.36E-02	1.00E+00	1.90E-01	1.00E+00	7.85E-02	1.00E+00	glycerolipid metabolism	P
GO:0046488	16	5.33E-02	1.00E+00	8.00E-03	3.60E-01	2.85E-01	1.00E+00	1.77E-02	1.00E+00	9.65E-02	1.00E+00	3.88E-02	1.00E+00	2.64E-01	1.00E+00	8.75E-03	4.81E-01	phosphatidylinositol metabolism	P
GO:0046489	37	6.63E-03	5.17E-01	3.40E-02	1.00E+00	6.75E-02	1.00E+00	9.33E-02	1.00E+00	5.88E-03	5.39E-01	5.49E-02	1.00E+00	3.56E-01	1.00E+00	9.85E-02	1.00E+00	phosphoinositide biosynthesis	P
GO:0046519	36	3.27E-03	2.73E-01	9.81E-04	9.10E-02	3.36E-02	1.00E+00	1.95E-01	1.00E+00	2.98E-03	2.85E-01	6.31E-03	3.51E-01	1.51E-01	1.00E+00	6.78E-04	9.16E-02	sphingoid metabolism	P
GO:0046520	10	1.48E-02	6.67E-01	6.43E-04	6.90E-02	9.84E-03	4.60E-01	8.05E-02	1.00E+00	1.64E-02	1.00E+00	1.33E-03	6.40E-02	1.76E-01	1.00E+00	1.35E-02	6.47E-01	sphingoid biosynthesis	P
GO:0046530	14	6.35E-01	1.00E+00	5.84E-01	1.00E+00	2.08E-01	1.00E+00	9.63E-01	1.00E+00	7.72E-01	1.00E+00	4.97E-01	1.00E+00	7.79E-01	1.00E+00	2.94E-01	1.00E+00	photoreceptor cell differentiation	P
GO:0046545	43	5.72E-01	1.00E+00	7.67E-01	1.00E+00	2.95E-01	1.00E+00	7.83E-01	1.00E+00	6.16E-01	1.00E+00	7.20E-01	1.00E+00	8.35E-01	1.00E+00	5.00E-01	1.00E+00	development of primary female sexual char	P
GO:0046546	31	4.05E-01	1.00E+00	1.88E-01	1.00E+00	5.13E-01	1.00E+00	6.09E-01	1.00E+00	3.16E-01	1.00E+00	1.35E-01	1.00E+00	7.32E-01	1.00E+00	2.33E-01	1.00E+00	development of primary male sexual charac	P
GO:0046620	13	3.51E-01	1.00E+00	9.94E-01	1.00E+00	1.57E-01	1.00E+00	4.32E-01	1.00E+00	5.21E-01	1.00E+00	1.00E+00	1.00E+00	1.89E-01	1.00E+00	9.78E-01	1.00E+00	regulation of organ size	P
GO:0046631	34	7.80E-01	1.00E+00	5.24E-01	1.00E+00	4.84E-01	1.00E+00	9.15E-01	1.00E+00	7.92E-01	1.00E+00	3.16E-01	1.00E+00	9.06E-01	1.00E+00	7.31E-01	1.00E+00	alpha-beta T cell activation	P
GO:0046632	26	6.02E-01	1.00E+00	5.26E-01	1.00E+00	4.61E-01	1.00E+00	7.75E-01	1.00E+00	6.03E-01	1.00E+00	3.42E-01	1.00E+00	8.22E-01	1.00E+00	8.83E-01	1.00E+00	alpha-beta T cell differentiation	P
GO:0046649	218	7.80E-02	1.00E+00	2.66E-02	1.00E+00	1.10E-01	1.00E+00	5.08E-02	1.00E+00	8.24E-02	1.00E+00	5.33E-02	1.00E+00	3.51E-01	1.00E+00	8.21E-02	1.00E+00	lymphocyte activation	P
GO:0046651	79	5.47E-01	1.00E+00	1.90E-01	1.00E+00	3.61E-01	1.00E+00	2.96E-01	1.00E+00	7.15E-01	1.00E+00	2.06E-01	1.00E+00	2.58E-01	1.00E+00	2.58E-01	1.00E+00	lymphocyte proliferation	P
GO:0046658	16	8.40E-01	1.00E+00	7.47E-01	1.00E+00	5.06E-01	1.00E+00	3.37E-01	1.00E+00	7.56E-01	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	5.24E-01	1.00E+00	anchored to plasma membrane	C
GO:0046660	45	6.17E-01	1.00E+00	8.25E-01	1.00E+00	3.39E-01	1.00E+00	7.80E-01	1.00E+00	6.62E-01	1.00E+00	7.99E-01	1.00E+00	8.33E-01	1.00E+00	5.82E-01	1.00E+00	female sex differentiation	P
GO:0046661	47	4.91E-01	1.00E+00	2.52E-01	1.00E+00	5.79E-01	1.00E+00	7.27E-01	1.00E+00	4.09E-01	1.00E+00	1.63E-01	1.00E+00	5.73E-01	1.00E+00	3.22E-01	1.00E+00	male sex differentiation	P
GO:0046677	32	4.33E-01	1.00E+00	9.35E-02	1.00E+00	3.80E-02	1.00E+00	3.53E-01	1.00E+00	6.10E-01	1.00E+00	8.63E-02	1.00E+00	9.77E-01	1.00E+00	1.17E-01	1.00E+00	response to antibiotic	P
GO:0046716	10	4.08E-01	1.00E+00	3.75E-01	1.00E+00	2.91E-01	1.00E+00	3.25E-01	1.00E+00	6.59E-01	1.00E+00	3.76E-01	1.00E+00	1.11E-01	1.00E+00	5.01E-01	1.00E+00	muscle maintenance	P
GO:0046718	11	6.16E-01	1.00E+00	2.35E-01	1.00E+00	9.19E-01	1.00E+00	3.58E-01	1.00E+00	5.71E-01	1.00E+00	2.09E-01	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	entry of virus into host cell	P
GO:0046777	60	5.68E-03	3.50E-01	8.48E-03	5.03E-01	9.02E-02	1.00E+00	1.12E-02	8.18E-01	9.58E-03	5.39E-01	6.83E-03	5.30E-01	3.87E-03	3.57E-01	5.78E-01	1.00E+00	protein amino acid autophosphorylation	P
GO:0046785	16	4.95E-01	1.00E+00	8.65E-01	1.00E+00	4.69E-01	1.00E+00	7.91E-01	1.00E+00	7.21E-01	1.00E+00	8.86E-01	1.00E+00	1.26E-01	1.00E+00	6.00E-01	1.00E+00	microtubule polymerization	P
GO:0046822	40	4.35E-03	3.28E-01	1.77E-03	9.10E-02	1.07E-01	1.00E+00	1.03E-01	1.00E+00	1.27E-03	7.80E-02	6.81E-03	5.30E-01	4.37E-01	1.00E+00	4.95E-03	3.60E-01	regulation of nucleocytoplasmic transport	P
GO:0046823	15	5.17E-01	1.00E+00	2.60E-01	1.00E+00	7.04E-01	1.00E+00	4.91E-01	1.00E+00	3.61E-01	1.00E+00	2.86E-01	1.00E+00	7.19E-01	1.00E+00	2.09E-01	1.00E+00	negative regulation of nucleocytoplasmic tra	P
GO:0046824	17	4.20E-02	1.00E+00	8.32E-02	1.00E+00	1.51E-01	1.00E+00	7.04E-01	1.00E+00	2.17E-02	1.00E+00	1.37E-01	1.00E+00	3.78E-01	1.00E+00	3.30E-02	1.00E+00	positive regulation of nucleocytoplasmic tra	P
GO:0046834	17	1.10E-02	6.67E-01	1.22E-02	6.77E-01	9.64E-02	1.00E+00	8.58E-03	7.13E-01	2.34E-02	1.00E+00	9.55E-02	1.00E+00	5.64E-03	3.57E-01	3.14E-03	1.85E-01	lipid phosphorylation	P
GO:0046839	16	9.95E-01	1.00E+00	2.56E-01	1.00E+00	9.84E-01	1.00E+00	4.62E-01	1.00E+00	9.90E-01	1.00E+00	1.86E-01	1.00E+00	1.89E-01	1.00E+00	4.29E-01	1.00E+00	phospholipid dephosphorylation	P
GO:0046847	17	1.68E-01	1.00E+00	1.27E-01	1.00E+00	1.07E-01	1.00E+00	1.46E-01	1.00E+00	2.18E-01	1.00E+00	1.24E-01	1.00E+00	1.23E-01	1.00E+00	3.25E-01	1.00E+00	filopodium formation	P
GO:0046849	159	5.58E-01	1.00E+00	6.92E-01	1.00E+00	5.31E-01	1.00E+00	4.90E-01	1.00E+00	4.03E-01	1.00E+00	6.78E-01	1.00E+00	9.55E-01	1.00E+00	7.96E-01	1.00E+00	bone remodeling	P
GO:0046850	40	9.88E-01	1.00E+00	4.45E-01	1.00E+00	9.80E-01	1.00E+00	5.26E-01	1.00E+00	9.50E-01	1.00E+00	5.10E-01	1.00E+00	9.64E-01	1.00E+00	2.19E-01	1.00E+00	regulation of bone remodeling	P
GO:0046851	15	9.53E-01	1.00E+00	3.51E-01	1.00E+00	5.41E-01	1.00E+00	2.86E-01	1.00E+00	9.45E-01	1.00E+00	3.70E-01	1.00E+00	1.00E+00	1.00E+00	7.69E-01	1.00E+00	negative regulation of bone remodeling	P
GO:0046852	20	9.83E-01	1.00E+00	5.79E-01	1.00E+00	9.95E-01	1.00E+00	5.99E-01	1.00E+00	9.62E-01	1.00E+00	6.27E-01	1.00E+00	5.74E-01	1.00E+00	2.53E-01	1.00E+00	positive regulation of bone remodeling	P

GO:0046854	16	1.25E-02	6.67E-01	8.83E-03	5.03E-01	9.51E-02	1.00E+00	3.91E-03	2.41E-01	3.33E-02	1.00E+00	1.00E-01	1.00E+00	1.94E-03	1.95E-01	1.44E-03	9.16E-02	phosphoinositide phosphorylation	P
GO:0046872	4323	1.40E-11	0.00E+00	6.99E-28	0.00E+00	3.73E-06	2.66E-03	1.36E-09	0.00E+00	9.57E-12	0.00E+00	2.78E-29	0.00E+00	1.40E-02	6.47E-01	9.25E-08	1.88E-03	metal ion binding	F
GO:0046873	66	6.62E-02	1.00E+00	3.26E-02	1.00E+00	8.64E-01	1.00E+00	1.88E-01	1.00E+00	1.95E-02	1.00E+00	3.95E-03	2.70E-01	5.66E-01	1.00E+00	9.00E-01	1.00E+00	metal ion transporter activity	F
GO:0046879	64	9.97E-01	1.00E+00	9.87E-01	1.00E+00	9.33E-01	1.00E+00	9.84E-01	1.00E+00	9.87E-01	1.00E+00	9.55E-01	1.00E+00	9.95E-01	1.00E+00	9.74E-01	1.00E+00	hormone secretion	P
GO:0046883	33	8.89E-01	1.00E+00	6.86E-01	1.00E+00	6.19E-01	1.00E+00	8.10E-01	1.00E+00	8.84E-01	1.00E+00	5.72E-01	1.00E+00	9.57E-01	1.00E+00	8.19E-01	1.00E+00	regulation of hormone secretion	P
GO:0046888	16	8.39E-01	1.00E+00	7.77E-01	1.00E+00	7.66E-01	1.00E+00	6.68E-01	1.00E+00	9.15E-01	1.00E+00	7.57E-01	1.00E+00	5.07E-01	1.00E+00	9.19E-01	1.00E+00	negative regulation of hormone secretion	P
GO:0046890	17	5.29E-03	3.28E-01	3.69E-02	1.00E+00	6.34E-04	3.60E-02	2.68E-02	1.00E+00	3.43E-02	1.00E+00	9.90E-02	1.00E+00	6.58E-02	1.00E+00	1.63E-01	1.00E+00	regulation of lipid biosynthesis	P
GO:0046903	380	8.55E-03	6.34E-01	3.97E-02	1.00E+00	1.70E-02	6.93E-01	2.31E-01	1.00E+00	1.16E-02	5.39E-01	1.74E-02	8.81E-01	4.53E-01	1.00E+00	5.04E-01	1.00E+00	secretion	P
GO:0046906	165	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.04E-01	1.00E+00	9.85E-01	1.00E+00	7.43E-01	1.00E+00	7.36E-01	1.00E+00	tetrapyrrole binding	F
GO:0046907	830	6.16E-25	0.00E+00	5.93E-23	0.00E+00	1.30E-14	0.00E+00	5.30E-09	0.00E+00	2.17E-22	0.00E+00	9.27E-23	0.00E+00	2.81E-05	5.44E-03	3.54E-06	1.88E-03	intracellular transport	P
GO:0046914	2860	1.56E-21	0.00E+00	4.24E-34	0.00E+00	2.11E-09	9.34E-04	5.78E-11	0.00E+00	1.64E-21	0.00E+00	9.68E-35	0.00E+00	1.47E-05	5.44E-03	6.73E-10	7.71E-04	transition metal ion binding	F
GO:0046915	35	3.12E-02	1.00E+00	4.59E-03	3.60E-01	9.09E-01	1.00E+00	1.50E-01	1.00E+00	1.31E-02	1.00E+00	7.25E-04	5.49E-02	2.69E-01	1.00E+00	4.42E-01	1.00E+00	transition metal ion transporter activity	F
GO:0046916	49	2.27E-01	1.00E+00	1.61E-01	1.00E+00	3.16E-01	1.00E+00	9.86E-03	7.13E-01	3.92E-01	1.00E+00	2.78E-01	1.00E+00	6.30E-02	1.00E+00	8.35E-01	1.00E+00	transition metal ion homeostasis	P
GO:0046928	22	9.86E-01	1.00E+00	9.62E-01	1.00E+00	9.78E-01	1.00E+00	7.24E-01	1.00E+00	9.56E-01	1.00E+00	9.98E-01	1.00E+00	9.60E-01	1.00E+00	4.54E-01	1.00E+00	regulation of neurotransmitter secretion	P
GO:0046930	71	2.17E-08	9.77E-04	3.65E-15	0.00E+00	3.68E-03	3.27E-01	1.19E-07	1.96E-03	1.18E-08	9.64E-04	4.64E-13	0.00E+00	2.67E-03	1.95E-01	1.79E-04	2.00E-02	pore complex	C
GO:0046933	22	5.46E-02	1.00E+00	5.99E-01	1.00E+00	1.17E-01	1.00E+00	4.83E-01	1.00E+00	7.07E-02	1.00E+00	7.71E-01	1.00E+00	1.41E-01	1.00E+00	3.31E-01	1.00E+00	hydrogen-transporting ATP synthase activity	F
GO:0046942	148	2.99E-01	1.00E+00	3.06E-01	1.00E+00	7.20E-01	1.00E+00	8.46E-01	1.00E+00	1.59E-01	1.00E+00	9.56E-02	1.00E+00	6.62E-01	1.00E+00	8.47E-01	1.00E+00	carboxylic acid transport	P
GO:0046943	129	7.31E-01	1.00E+00	7.46E-01	1.00E+00	9.63E-01	1.00E+00	8.89E-01	1.00E+00	6.19E-01	1.00E+00	5.49E-01	1.00E+00	4.92E-01	1.00E+00	9.15E-01	1.00E+00	carboxylic acid transporter activity	F
GO:0046961	36	3.87E-02	1.00E+00	6.69E-01	1.00E+00	3.16E-01	1.00E+00	1.32E-01	1.00E+00	3.63E-02	1.00E+00	8.96E-01	1.00E+00	9.31E-02	1.00E+00	7.40E-01	1.00E+00	hydrogen-transporting ATPase activity, rotat	F
GO:0046966	29	2.21E-02	1.00E+00	1.08E-03	9.10E-02	5.04E-02	1.00E+00	2.16E-03	1.24E-01	9.99E-03	5.39E-01	1.89E-03	1.61E-01	8.22E-01	1.00E+00	1.10E-01	1.00E+00	thyroid hormone receptor binding	F
GO:0046982	156	3.04E-02	1.00E+00	5.91E-03	3.60E-01	4.58E-02	1.00E+00	1.35E-03	1.15E-01	2.01E-02	1.00E+00	2.82E-02	1.00E+00	7.08E-01	1.00E+00	1.67E-01	1.00E+00	protein heterodimerization activity	F
GO:0046983	427	2.16E-05	8.00E-03	2.05E-06	8.39E-03	5.25E-03	4.19E-01	8.12E-08	9.71E-04	6.40E-06	2.88E-03	1.30E-04	1.70E-02	1.33E-01	1.00E+00	3.59E-02	1.00E+00	protein dimerization activity	F
GO:0047485	48	1.52E-03	2.02E-01	5.42E-04	6.90E-02	1.06E-03	9.80E-02	3.13E-02	1.00E+00	2.09E-02	1.00E+00	9.56E-04	5.49E-02	7.03E-03	5.44E-01	3.00E-03	1.85E-01	protein N-terminus binding	F
GO:0048002	24	8.91E-01	1.00E+00	9.11E-01	1.00E+00	9.81E-01	1.00E+00	7.61E-01	1.00E+00	8.25E-01	1.00E+00	8.38E-01	1.00E+00	5.96E-01	1.00E+00	9.64E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0048008	11	7.50E-01	1.00E+00	2.10E-01	1.00E+00	3.86E-01	1.00E+00	7.39E-02	1.00E+00	8.16E-01	1.00E+00	4.66E-01	1.00E+00	9.80E-01	1.00E+00	7.10E-01	1.00E+00	platelet-derived growth factor receptor signa	P
GO:0048009	15	8.53E-01	1.00E+00	9.99E-01	1.00E+00	8.22E-01	1.00E+00	9.51E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	2.91E-01	1.00E+00	9.77E-01	1.00E+00	insulin-like growth factor receptor signaling	P
GO:0048010	17	6.47E-01	1.00E+00	7.72E-01	1.00E+00	9.99E-01	1.00E+00	9.74E-01	1.00E+00	2.95E-01	1.00E+00	8.17E-01	1.00E+00	7.26E-01	1.00E+00	2.17E-01	1.00E+00	vascular endothelial growth factor receptor	P
GO:0048011	11	2.25E-01	1.00E+00	3.96E-02	1.00E+00	3.30E-01	1.00E+00	2.26E-02	1.00E+00	4.72E-01	1.00E+00	1.24E-01	1.00E+00	1.02E-01	1.00E+00	3.86E-02	1.00E+00	nerve growth factor receptor signaling pathv	P
GO:0048015	123	4.87E-01	1.00E+00	8.01E-01	1.00E+00	4.57E-01	1.00E+00	9.52E-01	1.00E+00	5.49E-01	1.00E+00	6.67E-01	1.00E+00	1.81E-01	1.00E+00	4.45E-01	1.00E+00	phosphoinositide-mediated signaling	P
GO:0048019	12	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	7.73E-01	1.00E+00	9.72E-01	1.00E+00	receptor antagonist activity	F
GO:0048029	20	7.11E-01	1.00E+00	1.99E-01	1.00E+00	6.78E-01	1.00E+00	1.99E-01	1.00E+00	7.56E-01	1.00E+00	1.73E-01	1.00E+00	3.17E-01	1.00E+00	5.09E-01	1.00E+00	monosaccharide binding	F
GO:0048037	255	1.48E-04	2.50E-02	1.62E-02	1.00E+00	2.02E-03	2.48E-01	1.14E-02	8.18E-01	8.84E-04	4.40E-02	5.27E-02	1.00E+00	1.42E-02	6.47E-01	9.21E-02	1.00E+00	cofactor binding	F
GO:0048041	15	1.31E-01	1.00E+00	5.51E-02	1.00E+00	5.50E-02	1.00E+00	1.55E-02	8.18E-01	1.65E-01	1.00E+00	8.34E-02	1.00E+00	8.40E-01	1.00E+00	7.08E-01	1.00E+00	focal adhesion formation	P
GO:0048066	19	1.78E-01	1.00E+00	1.39E-01	1.00E+00	1.74E-01	1.00E+00	8.43E-02	1.00E+00	3.00E-01	1.00E+00	3.13E-01	1.00E+00	1.58E-01	1.00E+00	4.61E-02	1.00E+00	pigmentation during development	P
GO:0048144	23	4.66E-01	1.00E+00	3.89E-01	1.00E+00	6.23E-01	1.00E+00	3.45E-01	1.00E+00	3.55E-01	1.00E+00	3.23E-01	1.00E+00	6.23E-01	1.00E+00	8.49E-01	1.00E+00	fibroblast proliferation	P
GO:0048145	23	4.66E-01	1.00E+00	3.89E-01	1.00E+00	6.23E-01	1.00E+00	3.45E-01	1.00E+00	3.55E-01	1.00E+00	3.23E-01	1.00E+00	6.23E-01	1.00E+00	8.49E-01	1.00E+00	regulation of fibroblast proliferation	P
GO:0048146	18	8.64E-01	1.00E+00	9.26E-01	1.00E+00	7.81E-01	1.00E+00	9.64E-01	1.00E+00	7.90E-01	1.00E+00	7.11E-01	1.00E+00	9.64E-01	1.00E+00	9.70E-01	1.00E+00	positive regulation of fibroblast proliferation	P
GO:0048167	38	1.46E-01	1.00E+00	5.75E-01	1.00E+00	1.24E-01	1.00E+00	4.20E-01	1.00E+00	1.41E-01	1.00E+00	4.11E-01	1.00E+00	3.91E-01	1.00E+00	1.00E+00	1.00E+00	regulation of synaptic plasticity	P
GO:0048168	19	6.30E-01	1.00E+00	9.57E-01	1.00E+00	6.55E-01	1.00E+00	6.95E-01	1.00E+00	6.30E-01	1.00E+00	9.35E-01	1.00E+00	4.07E-01	1.00E+00	9.94E-01	1.00E+00	regulation of neuronal synaptic plasticity	P
GO:0048169	11	7.11E-01	1.00E+00	9.88E-01	1.00E+00	6.32E-01	1.00E+00	9.38E-01	1.00E+00	8.11E-01	1.00E+00	9.80E-01	1.00E+00	3.13E-01	1.00E+00	8.66E-01	1.00E+00	regulation of long-term neuronal synaptic pl	P
GO:0048193	89	3.78E-04	3.37E-02	5.71E-04	6.90E-02	5.89E-03	4.60E-01	8.15E-02	1.00E+00	3.27E-04	1.98E-02	8.34E-05	1.70E-02	6.27E-01	1.00E+00	4.48E-01	1.00E+00	Golgi vesicle transport	P
GO:0048194	11	3.83E-02	1.00E+00	1.70E-01	1.00E+00	3.12E-01	1.00E+00	3.03E-01	1.00E+00	2.34E-02	1.00E+00	1.98E-01	1.00E+00	1.09E-01	1.00E+00	1.36E-01	1.00E+00	Golgi vesicle budding	P
GO:0048199	12	5.08E-02	1.00E+00	1.70E-01	1.00E+00	3.80E-01	1.00E+00	4.37E-01	1.00E+00	1.80E-02	1.00E+00	1.28E-01	1.00E+00	2.81E-01	1.00E+00	3.59E-01	1.00E+00	vesicle targeting, to, from or within Golgi	P
GO:0048200	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	Golgi transport vesicle coating	P
GO:0048204	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	vesicle targeting, inter-Golgi cisterna	P
GO:0048205	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	COPI coating of Golgi vesicle	P
GO:0048206	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	vesicle targeting, cis-Golgi to rough ER	P
GO:0048219	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	inter-Golgi cisterna vesicle-mediated transp	P
GO:0048220	10	8.17E-02	1.00E+00	2.74E-01	1.00E+00	3.58E-01	1.00E+00	3.84E-01	1.00E+00	4.71E-02	1.00E+00	2.78E-01	1.00E+00	2.57E-01	1.00E+00	2.77E-01	1.00E+00	cis-Golgi to rough ER vesicle-mediated tran	P
GO:0048232	265	2.17E-02	1.00E+00	2.14E-02	1.00E+00	2.15E-01	1.00E+00	2.72E-02	1.00E+00	4.38E-02	1.00E+00	1.43E-02	7.39E-01	5.04E-03	3.57E-01	7.41E-01	1.00E+00	male gamete generation	P
GO:0048265	15	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.23E-01	1.00E+00	6.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.39E-01	1.00E+00	9.95E-01	1.00E+00	response to pain	P
GO:0048278	22	5.29E-02	1.00E+00	2.77E-01	1.00E+00	1.73E-01	1.00E+00	6.97E-02	1.00E+00	1.46E-01	1.00E+00	3.34E-01	1.00E+00	2.07E-02	9.11E-01	7.52E-01	1.00E+00	vesicle docking	P
GO:0048286	11	9.94E-01	1.00E+00	3.78E-01	1.00E+00	1.00E+00	1.00E+00	7.24E-01	1.00E+00	7.75E-01	1.00E+00	3.92E-01	1.00E+00	1.00E+00	1.00E+00	2.69E-01	1.00E+00	alveolus development	P
GO:0048306	21	5.48E-01	1.00E+00	3.95E-01	1.00E+00	4.79E-01	1.00E+00	4.02E-01	1.00E+00	4.01E-01	1.00E+00	6.64E-01	1.00E+00	9.72E-01	1.00E+00	5.89E-02	1.00E+00	calcium-dependent protein binding	F
GO:0048332	35	2.61E-01	1.00E+00	1.67E-01	1.00E+00	5.07E-01	1.00E+00	6.26E-01	1.00E+00	1.80E-01	1.00E+00	2.51E-01	1.00E+00	5.08E-01	1.00E+00	3.80E-02	1.00E+00	mesoderm morphogenesis	P
GO:0048468	603	8.90E-01	1.00E+00	8.70E-01	1.00E+00	6.68E-01	1.00E+00	4.73E-01	1.00E+00	7.44E-01	1.00E+00	8.63E-01	1.00E+00	9.96E-01	1.00E+00	9.01E-01	1.00E+00	cell development	P
GO:0048469	83	9.51E-01	1.00E+00	7.61E-01	1.00E+00	6.47E-01	1.00E+00	2.15E-01	1.00E+00	8.09E-01	1.00E+00	8.04E-01	1.00E+00	9.98E-01	1.00E+00	9.79E-01	1.00E+00	cell maturation	P
GO:0048471	90	5.70E-03	3.50E-01	1.59E-03	9.10E-02	1.05E-01	1.00E+00	2.86E-02	1.00E+00	5.10E-03	4.18E-01	6.02E-03	3.51E-01	1.97E-02	9.11E-01	2.76E-03	1.85E-01	perinuclear region	C
GO:0048475	65	1.44E-06	1.95E-03	1.82E-05	9.58E-03	1.43E-04	1.50E-02	1.42E-01	1.00E+00	1.01E-05	4.00E-03	1.67E-06	2.97E-03	6.87E-04	6.50E-02	8.89E-02	1.00E+00	coated membrane	C
GO:0048477	24	9.60E-02	1.00E+00	2.77E-01	1.00E+00	2.17E-01	1.00E+00	2.13E-01	1.00E+00	7.19E-02	1.00E+00	3.10E-01	1.00E+00	1.39E-01	1.00E+00	6.49E-01	1.00E+00	oogenesis	P
GO:0048483	12	6.09E-01	1.00E+00	9.38E-01	1.00E+00	2.69E-01	1.00E+00	8.27E-01	1.00E+00	7.00E-01	1.00E+00	9.96E-01	1.00E+00	7.09E-01	1.00E+00	2.37E-01	1.00E+00	autonomic nervous system development	P
GO:0048487	11	4.35E-05	1.00E-02	1.53E-03	9.10E-02	1.12E-02	5.32E-01	1.49E-01	1.00E+00	1.99E-05	5.00E-03	9.88E-04	5.49E-02	3.75E-01	1.00E+00	2.25E-01	1.00E+00	beta-tubulin binding	F
GO:0048488	11	3.75E-01	1.00E+00	4.09E-01	1.00E+00	4.60E-01	1.00E+00	7.25E-01	1.00E+00	2.95E-01	1.00E+00	4.02E-01	1.00E+00	5.73E-01	1.00E+00	1.50E-01	1.00E+00	synaptic vesicle endocytosis	P
GO:0048489	27	5.21E-01	1.00E+00	2.14E-01	1.00E+00	7.36E-01	1.00E+00	6.01E-01	1.00E+00	4.61E-01	1.00E+00	1.85E-01	1.00E+00	4.34E-01	1.00E+00	1.84E-01	1.00E+00	synaptic vesicle transport	P
GO:0048500	11	2.75E-01	1.00E+00	4.76E-01	1.00E+00	1.62E-01	1.00E+00	9.75E-01	1.00E+00	3.30E-01	1.00E+00	4.41E-01	1.00E+00	4.03E-01	1.00E+00	1.07E-01	1.00E+00	signal recognition particle	C
GO:0048511	82	3.63E-01	1.00E+00	5.24E-01	1.00E+00	2.47E-01	1.00E+00	4.19E-01	1.00E+00	4.19E-01	1.00E+00	4.75E-01	1.00E+00	5.13E-01	1.00E+00	5.75E-01	1.00E+00	rhythmic process	P
GO:0048513	1400	9.68E-01	1.00E+00	9.69E-01	1.00E+00	8.05E-01	1.00E+00	8.40E-01	1.00E+00	9.53E-01	1.00E+00	9.74E-01	1.00E+00	9.72E-01	1.00E+00	8.43E-01	1.00E+00	organ development	P
GO:0048514	199	9.36E-01	1.00E+00	5.37E-01	1.00E+00	9.27E-01	1.00E+00	5.14E-01	1.00E+00	9.51E-01	1.00E+00	7.40E-01	1.00E+00	3.06E-01	1.00E+00	6.42E-02	1.00E+00	blood vessel morphogenesis	P
GO:0048515	42	1.04E-01	1.00E+00	2.85E-02	1.00E+00	2.16E-01	1.00E+00	2.60E-02	1.00E+00	9.20E-02	1.00E+00	8.11E-02	1.00E+00	4.81E-01	1.00E+00	1.38E-01	1.00E+00	spermatid differentiation	P
GO:0048518	1524	5.28E-07	1.95E-03	2.98E-09	4.97E-03	3.17E-03	2.48E-01	2.33E-06	3.00E-03	2.46E-07	1.69E-03	6.64E-08	8.37E-04	5.89E-03	3.57E-01	3.95E-04	2.70E-02	positive regulation of biological process	P
GO:0048519	1484	2.11E-11	0.00E+00	8.32E-11	0.00E+00	3.73E-07	2.42E-03	2.01E-05	8.00E-03	2.18E-11	0.00E+00	9.35E-10	0.00E+00	3.62E-02	1.00E+00	2.07E-05	9.00E-03	negative regulation of biological process	P
GO:0048522	1194	5.98E-05	1.10E-02	6.27E-07	8.39E-03	1.22E-03	9.80E-02	7.61E-05	1.20E-02	1.27E-04	1.70E-02	7.00E-06	4.88E-03	2.57E-02	1.00E+00	4.79E-03	3.60E-01	positive regulation of cellular process	P
GO:0048523	1285	4.84E-10	8.06E-04	2.46E-09	4.97E-03	1.37E-06	2.42E-03	4.33E-05	8.00E-03	4.98E-10	0.00E+00	3.40E-08	8.37E-04	6.29E-02	1.00E+00	4.68E-05	9.00E-03	negative regulation of cellular process	P
GO:0048534	249	2.92E-02	1.00E+00	9.80E-02	1.00E+00	7.51E-02	1.00E+00	4.16E-02	1.00E+00	1.61E-02	1.00E+00	2.62E-01	1.00E+00	5.76E-01	1.00E+00	1.15E-01	1.00E+00	hemopoietic or lymphoid organ developmer	P
GO:0048536	11	8.92E-01	1.00E+00	8.88E-01	1.00E+00	6.38E-01	1.00E+00	2.35E-01	1.00E+00	8.61E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	spleen development	P

GO:0048538	12	1.58E-01	1.00E+00	3.83E-01	1.00E+00	7.55E-02	1.00E+00	9.09E-02	1.00E+00	3.23E-01	1.00E+00	6.65E-01	1.00E+00	2.22E-01	1.00E+00	4.78E-01	1.00E+00	thymus development	P
GO:0048545	58	9.94E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	9.57E-01	1.00E+00	9.51E-01	1.00E+00	7.66E-01	1.00E+00	2.47E-01	1.00E+00	response to steroid hormone stimulus	P
GO:0048546	14	8.99E-01	1.00E+00	9.98E-01	1.00E+00	8.92E-01	1.00E+00	9.84E-01	1.00E+00	7.60E-01	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	6.03E-01	1.00E+00	digestive tract morphogenesis	P
GO:0048547	13	9.10E-01	1.00E+00	9.93E-01	1.00E+00	9.86E-01	1.00E+00	9.67E-01	1.00E+00	7.27E-01	1.00E+00	9.97E-01	1.00E+00	9.72E-01	1.00E+00	5.29E-01	1.00E+00	gut morphogenesis	P
GO:0048562	22	5.41E-01	1.00E+00	9.92E-01	1.00E+00	7.57E-01	1.00E+00	9.90E-01	1.00E+00	3.41E-01	1.00E+00	9.77E-01	1.00E+00	7.98E-01	1.00E+00	7.41E-01	1.00E+00	embryonic organ morphogenesis	P
GO:0048565	24	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.05E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.50E-01	1.00E+00	gut development	P
GO:0048566	14	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	8.39E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	embryonic gut development	P
GO:0048568	41	8.59E-01	1.00E+00	9.86E-01	1.00E+00	9.56E-01	1.00E+00	9.96E-01	1.00E+00	6.20E-01	1.00E+00	9.25E-01	1.00E+00	9.74E-01	1.00E+00	9.30E-01	1.00E+00	embryonic organ development	P
GO:0048583	12	9.89E-01	1.00E+00	1.00E+00	1.00E+00	4.66E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	6.02E-01	1.00E+00	9.94E-01	1.00E+00	regulation of response to stimulus	P
GO:0048589	53	4.54E-02	1.00E+00	2.25E-02	1.00E+00	9.38E-02	1.00E+00	3.85E-01	1.00E+00	5.07E-02	1.00E+00	1.25E-02	7.39E-01	2.64E-01	1.00E+00	1.10E-01	1.00E+00	developmental growth	P
GO:0048592	35	2.61E-01	1.00E+00	7.61E-01	1.00E+00	6.52E-02	1.00E+00	8.56E-01	1.00E+00	2.50E-01	1.00E+00	7.56E-01	1.00E+00	6.92E-01	1.00E+00	1.94E-01	1.00E+00	eye morphogenesis	P
GO:0048593	16	1.94E-01	1.00E+00	3.81E-01	1.00E+00	3.11E-01	1.00E+00	5.12E-01	1.00E+00	1.23E-01	1.00E+00	3.83E-01	1.00E+00	4.96E-01	1.00E+00	1.66E-01	1.00E+00	eye morphogenesis (sensu Vertebrata)	P
GO:0048598	208	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.88E-01	1.00E+00	embryonic morphogenesis	P
GO:0048599	13	4.43E-01	1.00E+00	7.23E-01	1.00E+00	8.91E-01	1.00E+00	2.90E-01	1.00E+00	3.23E-01	1.00E+00	6.52E-01	1.00E+00	1.57E-01	1.00E+00	8.00E-01	1.00E+00	oocyte development	P
GO:0048609	128	9.28E-01	1.00E+00	9.95E-01	1.00E+00	7.88E-01	1.00E+00	9.18E-01	1.00E+00	9.69E-01	1.00E+00	9.97E-01	1.00E+00	3.25E-01	1.00E+00	7.67E-01	1.00E+00	reproductive organismal physiological proce	P
GO:0048627	25	6.65E-01	1.00E+00	1.73E-02	1.00E+00	2.67E-01	1.00E+00	1.25E-02	8.18E-01	6.11E-01	1.00E+00	4.24E-02	1.00E+00	9.57E-01	1.00E+00	3.72E-01	1.00E+00	myoblast development	P
GO:0048628	24	7.15E-01	1.00E+00	3.75E-02	1.00E+00	2.63E-01	1.00E+00	1.55E-02	8.18E-01	6.90E-01	1.00E+00	8.98E-02	1.00E+00	9.38E-01	1.00E+00	4.19E-01	1.00E+00	myoblast maturation	P
GO:0048637	82	8.18E-01	1.00E+00	9.52E-02	1.00E+00	6.26E-01	1.00E+00	1.50E-01	1.00E+00	8.35E-01	1.00E+00	9.54E-02	1.00E+00	6.55E-01	1.00E+00	2.43E-01	1.00E+00	skeletal muscle development	P
GO:0048644	20	9.64E-01	1.00E+00	8.88E-01	1.00E+00	9.82E-01	1.00E+00	4.07E-01	1.00E+00	9.40E-01	1.00E+00	7.38E-01	1.00E+00	6.67E-01	1.00E+00	1.00E+00	1.00E+00	muscle morphogenesis	P
GO:0048646	72	2.46E-01	1.00E+00	2.10E-01	1.00E+00	4.52E-01	1.00E+00	4.72E-01	1.00E+00	2.25E-01	1.00E+00	3.77E-01	1.00E+00	2.45E-01	1.00E+00	2.09E-02	1.00E+00	anatomical structure formation	P
GO:0048659	32	5.38E-01	1.00E+00	3.13E-01	1.00E+00	4.70E-01	1.00E+00	8.65E-01	1.00E+00	6.42E-01	1.00E+00	2.82E-01	1.00E+00	2.23E-01	1.00E+00	9.38E-02	1.00E+00	smooth muscle cell proliferation	P
GO:0048660	30	6.01E-01	1.00E+00	3.03E-01	1.00E+00	5.15E-01	1.00E+00	9.16E-01	1.00E+00	6.18E-01	1.00E+00	2.50E-01	1.00E+00	4.78E-01	1.00E+00	8.79E-02	1.00E+00	regulation of smooth muscle cell proliferatio	P
GO:0048661	20	4.25E-01	1.00E+00	3.39E-01	1.00E+00	3.86E-01	1.00E+00	9.71E-01	1.00E+00	4.88E-01	1.00E+00	3.19E-01	1.00E+00	4.95E-01	1.00E+00	1.44E-02	8.49E-01	positive regulation of smooth muscle cell pr	P
GO:0048662	10	8.54E-01	1.00E+00	3.79E-01	1.00E+00	7.60E-01	1.00E+00	4.70E-01	1.00E+00	7.45E-01	1.00E+00	3.08E-01	1.00E+00	4.64E-01	1.00E+00	9.52E-01	1.00E+00	negative regulation of smooth muscle cell p	P
GO:0048663	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	neuron fate commitment	P
GO:0048665	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	neuron fate specification	P
GO:0048666	258	9.62E-01	1.00E+00	9.66E-01	1.00E+00	6.78E-01	1.00E+00	9.54E-01	1.00E+00	9.15E-01	1.00E+00	9.51E-01	1.00E+00	9.97E-01	1.00E+00	7.19E-01	1.00E+00	neuron development	P
GO:0048667	188	9.74E-01	1.00E+00	9.09E-01	1.00E+00	7.87E-01	1.00E+00	9.62E-01	1.00E+00	9.64E-01	1.00E+00	8.84E-01	1.00E+00	9.45E-01	1.00E+00	4.05E-01	1.00E+00	neuron morphogenesis during differentiatior	P
GO:0048675	24	6.22E-01	1.00E+00	2.60E-01	1.00E+00	6.57E-01	1.00E+00	5.89E-01	1.00E+00	6.12E-01	1.00E+00	2.46E-01	1.00E+00	4.25E-01	1.00E+00	1.97E-01	1.00E+00	axon extension	P
GO:0048699	390	9.65E-01	1.00E+00	9.86E-01	1.00E+00	8.70E-01	1.00E+00	9.24E-01	1.00E+00	8.46E-01	1.00E+00	9.76E-01	1.00E+00	9.99E-01	1.00E+00	9.33E-01	1.00E+00	generation of neurons	P
GO:0048701	10	8.70E-01	1.00E+00	9.98E-01	1.00E+00	9.78E-01	1.00E+00	9.91E-01	1.00E+00	8.63E-01	1.00E+00	9.97E-01	1.00E+00	5.10E-01	1.00E+00	6.16E-01	1.00E+00	embryonic cranial skeleton morphogenesis	P
GO:0048704	44	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.96E-01	1.00E+00	embryonic skeletal morphogenesis	P
GO:0048705	54	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	skeletal morphogenesis	P
GO:0048706	58	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	9.94E-01	1.00E+00	embryonic skeletal development	P
GO:0048709	18	2.57E-01	1.00E+00	9.37E-01	1.00E+00	4.00E-01	1.00E+00	6.82E-01	1.00E+00	2.05E-01	1.00E+00	9.77E-01	1.00E+00	4.34E-01	1.00E+00	8.56E-01	1.00E+00	oligodendrocyte differentiation	P
GO:0048729	123	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.88E-01	1.00E+00	9.87E-01	1.00E+00	4.32E-01	1.00E+00	tissue morphogenesis	P
GO:0048730	89	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.64E-01	1.00E+00	epidermis morphogenesis	P
GO:0048731	950	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	system development	P
GO:0048732	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gland development	P
GO:0048736	77	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	5.68E-01	1.00E+00	9.86E-01	1.00E+00	appendage development	P
GO:0048738	11	3.85E-01	1.00E+00	9.07E-02	1.00E+00	7.01E-01	1.00E+00	5.08E-02	1.00E+00	1.65E-01	1.00E+00	1.19E-01	1.00E+00	7.89E-01	1.00E+00	3.28E-01	1.00E+00	cardiac muscle development	P
GO:0048741	79	7.86E-01	1.00E+00	8.03E-02	1.00E+00	6.25E-01	1.00E+00	1.28E-01	1.00E+00	7.85E-01	1.00E+00	7.95E-02	1.00E+00	6.72E-01	1.00E+00	2.50E-01	1.00E+00	skeletal muscle fiber development	P
GO:0048747	80	8.07E-01	1.00E+00	8.87E-02	1.00E+00	6.59E-01	1.00E+00	1.51E-01	1.00E+00	7.94E-01	1.00E+00	8.11E-02	1.00E+00	7.03E-01	1.00E+00	2.70E-01	1.00E+00	muscle fiber development	P
GO:0048754	54	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	branching morphogenesis of a tube	P
GO:0048762	43	9.93E-01	1.00E+00	9.87E-01	1.00E+00	9.63E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.52E-01	1.00E+00	9.44E-01	1.00E+00	9.01E-01	1.00E+00	mesenchymal cell differentiation	P
GO:0048770	80	4.87E-09	8.06E-04	4.66E-07	8.39E-03	3.33E-02	1.00E+00	2.78E-03	1.47E-01	2.59E-09	9.64E-04	6.61E-08	8.37E-04	3.57E-03	3.57E-01	5.90E-02	1.00E+00	pigment granule	C
GO:0048771	174	7.64E-01	1.00E+00	7.93E-01	1.00E+00	7.00E-01	1.00E+00	5.49E-01	1.00E+00	6.15E-01	1.00E+00	8.10E-01	1.00E+00	9.70E-01	1.00E+00	7.45E-01	1.00E+00	tissue remodeling	P
GO:0048806	16	1.00E+00	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	8.61E-01	1.00E+00	9.98E-01	1.00E+00	8.33E-01	1.00E+00	9.43E-01	1.00E+00	8.66E-01	1.00E+00	genitalia development	P
GO:0048812	188	9.74E-01	1.00E+00	9.09E-01	1.00E+00	7.87E-01	1.00E+00	9.62E-01	1.00E+00	9.64E-01	1.00E+00	8.84E-01	1.00E+00	9.45E-01	1.00E+00	4.05E-01	1.00E+00	neurite morphogenesis	P
GO:0048813	14	5.19E-01	1.00E+00	5.52E-01	1.00E+00	5.57E-01	1.00E+00	4.36E-01	1.00E+00	4.31E-01	1.00E+00	6.55E-01	1.00E+00	7.87E-01	1.00E+00	2.74E-01	1.00E+00	dendrite morphogenesis	P
GO:0048820	11	9.94E-01	1.00E+00	9.90E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.84E-01	1.00E+00	3.85E-01	1.00E+00	1.28E-01	1.00E+00	hair follicle maturation	P
GO:0048821	10	7.12E-01	1.00E+00	3.88E-01	1.00E+00	7.79E-01	1.00E+00	3.04E-01	1.00E+00	6.54E-01	1.00E+00	5.22E-01	1.00E+00	3.86E-01	1.00E+00	7.36E-01	1.00E+00	erythrocyte development	P
GO:0048839	54	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	inner ear development	P
GO:0048856	2382	9.82E-01	1.00E+00	9.51E-01	1.00E+00	7.28E-01	1.00E+00	6.03E-01	1.00E+00	9.68E-01	1.00E+00	9.69E-01	1.00E+00	9.92E-01	1.00E+00	7.55E-01	1.00E+00	anatomical structure development	P
GO:0048858	188	9.74E-01	1.00E+00	9.09E-01	1.00E+00	7.87E-01	1.00E+00	9.62E-01	1.00E+00	9.64E-01	1.00E+00	8.84E-01	1.00E+00	9.45E-01	1.00E+00	4.05E-01	1.00E+00	cell projection morphogenesis	P
GO:0050136	45	3.52E-03	2.73E-01	3.45E-02	1.00E+00	6.59E-02	1.00E+00	1.29E-01	1.00E+00	6.96E-03	5.39E-01	8.39E-02	1.00E+00	4.53E-02	1.00E+00	7.89E-02	1.00E+00	NADH dehydrogenase (quinone) activity	F
GO:0050381	25	7.70E-01	1.00E+00	9.91E-01	1.00E+00	8.62E-01	1.00E+00	9.99E-01	1.00E+00	6.53E-01	1.00E+00	9.34E-01	1.00E+00	5.82E-01	1.00E+00	7.91E-01	1.00E+00	unspecific monooxygenase activity	F
GO:0050435	14	7.23E-02	1.00E+00	2.24E-01	1.00E+00	2.13E-01	1.00E+00	4.06E-01	1.00E+00	4.02E-02	1.00E+00	2.32E-01	1.00E+00	9.75E-01	1.00E+00	3.40E-01	1.00E+00	beta-amyloid metabolism	P
GO:0050650	11	9.99E-01	1.00E+00	9.13E-01	1.00E+00	4.27E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	9.24E-01	1.00E+00	5.30E-01	1.00E+00	6.51E-01	1.00E+00	chondroitin sulfate proteoglycan biosynthes	P
GO:0050654	12	9.98E-01	1.00E+00	9.54E-01	1.00E+00	3.09E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	4.55E-01	1.00E+00	5.83E-01	1.00E+00	chondroitin sulfate proteoglycan metabolism	P
GO:0050657	87	5.85E-07	1.95E-03	5.42E-10	0.00E+00	3.85E-04	3.60E-02	1.81E-05	8.00E-03	1.63E-06	2.60E-03	2.17E-09	0.00E+00	3.61E-02	1.00E+00	6.99E-04	9.16E-02	nucleic acid transport	P
GO:0050658	87	5.85E-07	1.95E-03	5.42E-10	0.00E+00	3.85E-04	3.60E-02	1.81E-05	8.00E-03	1.63E-06	2.60E-03	2.17E-09	0.00E+00	3.61E-02	1.00E+00	6.99E-04	9.16E-02	RNA transport	P
GO:0050660	84	5.47E-01	1.00E+00	5.94E-01	1.00E+00	7.82E-01	1.00E+00	3.32E-01	1.00E+00	4.87E-01	1.00E+00	7.28E-01	1.00E+00	2.97E-01	1.00E+00	5.69E-01	1.00E+00	FAD binding	F
GO:0050661	34	9.11E-01	1.00E+00	8.46E-01	1.00E+00	8.03E-01	1.00E+00	6.13E-01	1.00E+00	9.19E-01	1.00E+00	9.68E-01	1.00E+00	8.17E-01	1.00E+00	3.95E-01	1.00E+00	NADP binding	F
GO:0050662	186	8.56E-04	8.30E-02	4.12E-02	1.00E+00	1.19E-02	5.32E-01	2.24E-02	1.00E+00	2.21E-03	2.85E-01	9.52E-02	1.00E+00	3.10E-02	1.00E+00	2.01E-01	1.00E+00	coenzyme binding	F
GO:0050663	29	2.37E-01	1.00E+00	1.64E-01	1.00E+00	2.39E-01	1.00E+00	2.55E-01	1.00E+00	2.98E-01	1.00E+00	2.43E-01	1.00E+00	3.21E-01	1.00E+00	3.31E-01	1.00E+00	cytokine secretion	P
GO:0050670	57	7.70E-01	1.00E+00	3.67E-01	1.00E+00	3.00E-01	1.00E+00	7.14E-01	1.00E+00	8.73E-01	1.00E+00	3.25E-01	1.00E+00	7.78E-01	1.00E+00	3.21E-01	1.00E+00	regulation of lymphocyte proliferation	P
GO:0050671	41	5.73E-01	1.00E+00	3.77E-01	1.00E+00	1.69E-01	1.00E+00	6.22E-01	1.00E+00	6.98E-01	1.00E+00	4.21E-01	1.00E+00	6.97E-01	1.00E+00	2.50E-01	1.00E+00	positive regulation of lymphocyte proliferatic	P
GO:0050672	21	9.49E-01	1.00E+00	6.07E-01	1.00E+00	7.20E-01	1.00E+00	9.30E-01	1.00E+00	9.78E-01	1.00E+00	5.19E-01	1.00E+00	8.22E-01	1.00E+00	4.94E-01	1.00E+00	negative regulation of lymphocyte proliferati	P
GO:0050673	50	9.97E-01	1.00E+00	9.79E-01	1.00E+00	9.29E-01	1.00E+00	8.21E-01	1.00E+00	9.91E-01	1.00E+00	9.73E-01	1.00E+00	9.98E-01	1.00E+00	8.35E-01	1.00E+00	epithelial cell proliferation	P
GO:0050678	44	9.99E-01	1.00E+00	9.88E-01	1.00E+00	9.08E-01	1.00E+00	8.08E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	7.13E-01	1.00E+00	regulation of epithelial cell proliferation	P
GO:0050679	23	7.57E-01	1.00E+00	5.77E-01	1.00E+00	6.13E-01	1.00E+00	6.18E-01	1.00E+00	6.87E-01	1.00E+00	6.18E-01	1.00E+00	9.61E-01	1.00E+00	1.51E-01	1.00E+00	positive regulation of epithelial cell proliferat	P
GO:0050680	19	1.00E+00	1.00E+00	9.58E-01	1.00E+00	9.00E-01	1.00E+00	4.28E-01	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	9.91E-01	1.00E+00	9.97E-01	1.00E+00	negative regulation of epithelial cell prolifera	P
GO:0050681	24	1.38E-01	1.00E+00	6.42E-02	1.00E+00	2.68E-01	1.00E+00	5.33E-01	1.00E+00	1.22E-01	1.00E+00	6.81E-02	1.00E+00	8.89E-01	1.00E+00	8.20E-02	1.00E+00	androgen receptor binding	F
GO:0050688	16	5.68E-04	3.37E-02	8.87E-02	1.00E+00	1.16E-02	5.32E-01	7.74E-01	1.00E+00	6.71E-04	4.00E-02	4.81E-02	1.00E+00	5.02E-02	1.00E+00	1.84E-01	1.00E+00	regulation of antiviral response	P

GO:0050701	15	4.70E-02	1.00E+00	1.62E-02	1.00E+00	1.32E-01	1.00E+00	1.46E-01	1.00E+00	6.43E-02	1.00E+00	4.99E-02	1.00E+00	8.28E-02	1.00E+00	2.16E-01	1.00E+00	interleukin-1 secretion	P
GO:0050702	14	5.18E-02	1.00E+00	2.10E-02	1.00E+00	1.56E-01	1.00E+00	2.62E-01	1.00E+00	5.57E-02	1.00E+00	3.79E-02	1.00E+00	1.55E-01	1.00E+00	1.77E-01	1.00E+00	interleukin-1 beta secretion	P
GO:0050704	13	1.18E-01	1.00E+00	4.60E-02	1.00E+00	2.55E-01	1.00E+00	9.87E-02	1.00E+00	1.44E-01	1.00E+00	1.58E-01	1.00E+00	1.10E-01	1.00E+00	2.73E-01	1.00E+00	regulation of interleukin-1 secretion	P
GO:0050706	12	1.28E-01	1.00E+00	5.76E-02	1.00E+00	2.91E-01	1.00E+00	1.91E-01	1.00E+00	1.29E-01	1.00E+00	1.30E-01	1.00E+00	2.09E-01	1.00E+00	2.29E-01	1.00E+00	regulation of interleukin-1 beta secretion	P
GO:0050707	25	3.15E-01	1.00E+00	1.95E-01	1.00E+00	2.93E-01	1.00E+00	1.64E-01	1.00E+00	4.13E-01	1.00E+00	3.76E-01	1.00E+00	2.87E-01	1.00E+00	3.39E-01	1.00E+00	regulation of cytokine secretion	P
GO:0050708	42	1.80E-01	1.00E+00	2.22E-01	1.00E+00	1.70E-01	1.00E+00	1.19E-01	1.00E+00	1.82E-01	1.00E+00	4.24E-01	1.00E+00	6.12E-01	1.00E+00	4.09E-01	1.00E+00	regulation of protein secretion	P
GO:0050709	13	4.75E-01	1.00E+00	6.55E-01	1.00E+00	2.78E-01	1.00E+00	6.70E-01	1.00E+00	5.88E-01	1.00E+00	7.03E-01	1.00E+00	7.07E-01	1.00E+00	3.28E-01	1.00E+00	negative regulation of protein secretion	P
GO:0050710	10	2.76E-01	1.00E+00	4.08E-01	1.00E+00	1.59E-01	1.00E+00	4.88E-01	1.00E+00	3.99E-01	1.00E+00	4.96E-01	1.00E+00	5.81E-01	1.00E+00	2.28E-01	1.00E+00	negative regulation of cytokine secretion	P
GO:0050714	24	1.05E-01	1.00E+00	1.70E-01	1.00E+00	1.81E-01	1.00E+00	2.20E-01	1.00E+00	1.21E-01	1.00E+00	3.42E-01	1.00E+00	2.17E-01	1.00E+00	2.36E-01	1.00E+00	positive regulation of protein secretion	P
GO:0050715	18	2.70E-01	1.00E+00	1.28E-01	1.00E+00	4.94E-01	1.00E+00	2.01E-01	1.00E+00	2.89E-01	1.00E+00	2.61E-01	1.00E+00	1.89E-01	1.00E+00	2.42E-01	1.00E+00	positive regulation of cytokine secretion	P
GO:0050716	12	9.76E-02	1.00E+00	3.06E-02	1.00E+00	2.40E-01	1.00E+00	6.52E-02	1.00E+00	1.11E-01	1.00E+00	1.29E-01	1.00E+00	1.40E-01	1.00E+00	3.16E-01	1.00E+00	positive regulation of interleukin-1 secretion	P
GO:0050718	11	1.07E-01	1.00E+00	3.92E-02	1.00E+00	2.75E-01	1.00E+00	1.37E-01	1.00E+00	9.80E-02	1.00E+00	1.03E-01	1.00E+00	2.58E-01	1.00E+00	2.69E-01	1.00E+00	positive regulation of interleukin-1 beta secr	P
GO:0050727	43	3.20E-01	1.00E+00	2.43E-01	1.00E+00	2.32E-01	1.00E+00	8.94E-01	1.00E+00	5.38E-01	1.00E+00	2.06E-01	1.00E+00	8.31E-02	1.00E+00	6.74E-02	1.00E+00	regulation of inflammatory response	P
GO:0050728	19	3.60E-01	1.00E+00	2.96E-01	1.00E+00	2.35E-01	1.00E+00	4.64E-01	1.00E+00	6.11E-01	1.00E+00	3.85E-01	1.00E+00	1.18E-01	1.00E+00	1.05E-01	1.00E+00	negative regulation of inflammatory respons	P
GO:0050729	15	2.97E-01	1.00E+00	2.87E-01	1.00E+00	2.68E-01	1.00E+00	9.85E-01	1.00E+00	3.72E-01	1.00E+00	1.80E-01	1.00E+00	3.69E-01	1.00E+00	2.23E-01	1.00E+00	positive regulation of inflammatory respons	P
GO:0050730	47	7.20E-01	1.00E+00	8.93E-01	1.00E+00	3.17E-01	1.00E+00	3.90E-01	1.00E+00	6.74E-01	1.00E+00	9.58E-01	1.00E+00	9.82E-01	1.00E+00	8.64E-01	1.00E+00	regulation of peptidyl-tyrosine phosphorylati	P
GO:0050731	30	9.48E-01	1.00E+00	9.82E-01	1.00E+00	6.07E-01	1.00E+00	6.33E-01	1.00E+00	9.32E-01	1.00E+00	9.93E-01	1.00E+00	9.67E-01	1.00E+00	9.63E-01	1.00E+00	positive regulation of peptidyl-tyrosine phos	P
GO:0050750	11	5.65E-01	1.00E+00	4.36E-01	1.00E+00	1.55E-01	1.00E+00	3.02E-01	1.00E+00	6.48E-01	1.00E+00	5.41E-01	1.00E+00	9.52E-01	1.00E+00	5.39E-01	1.00E+00	low-density lipoprotein receptor binding	F
GO:0050755	12	8.25E-02	1.00E+00	1.31E-01	1.00E+00	7.66E-02	1.00E+00	2.23E-01	1.00E+00	1.50E-01	1.00E+00	2.31E-01	1.00E+00	1.66E-01	1.00E+00	1.88E-02	1.00E+00	chemokine metabolism	P
GO:0050764	11	4.74E-01	1.00E+00	9.82E-03	5.18E-01	2.37E-01	1.00E+00	9.10E-04	5.90E-02	3.07E-01	1.00E+00	1.12E-02	7.39E-01	1.00E+00	1.00E+00	4.18E-01	1.00E+00	regulation of phagocytosis	P
GO:0050767	59	3.99E-01	1.00E+00	3.43E-01	1.00E+00	6.73E-01	1.00E+00	1.70E-01	1.00E+00	3.22E-01	1.00E+00	2.23E-01	1.00E+00	2.45E-01	1.00E+00	9.80E-01	1.00E+00	regulation of neurogenesis	P
GO:0050768	20	8.02E-02	1.00E+00	6.40E-02	1.00E+00	1.73E-01	1.00E+00	9.52E-02	1.00E+00	5.43E-02	1.00E+00	7.44E-02	1.00E+00	4.65E-01	1.00E+00	4.70E-01	1.00E+00	negative regulation of neurogenesis	P
GO:0050769	24	4.71E-01	1.00E+00	4.04E-01	1.00E+00	8.21E-01	1.00E+00	2.58E-01	1.00E+00	2.89E-01	1.00E+00	2.02E-01	1.00E+00	5.85E-01	1.00E+00	9.83E-01	1.00E+00	positive regulation of neurogenesis	P
GO:0050770	35	9.10E-01	1.00E+00	7.46E-01	1.00E+00	8.15E-01	1.00E+00	2.83E-01	1.00E+00	8.98E-01	1.00E+00	6.60E-01	1.00E+00	7.00E-01	1.00E+00	9.99E-01	1.00E+00	regulation of axonogenesis	P
GO:0050772	16	8.79E-01	1.00E+00	5.25E-01	1.00E+00	8.71E-01	1.00E+00	1.32E-01	1.00E+00	7.12E-01	1.00E+00	5.09E-01	1.00E+00	1.00E+00	1.00E+00	8.50E-01	1.00E+00	positive regulation of axonogenesis	P
GO:0050776	116	4.76E-01	1.00E+00	3.42E-01	1.00E+00	7.08E-01	1.00E+00	4.39E-01	1.00E+00	3.56E-01	1.00E+00	4.84E-01	1.00E+00	5.86E-01	1.00E+00	9.38E-02	1.00E+00	regulation of immune response	P
GO:0050777	14	2.63E-01	1.00E+00	1.24E-01	1.00E+00	1.75E-01	1.00E+00	2.22E-01	1.00E+00	3.74E-01	1.00E+00	1.37E-01	1.00E+00	1.70E-01	1.00E+00	1.60E-01	1.00E+00	negative regulation of immune response	P
GO:0050778	98	4.67E-01	1.00E+00	5.86E-01	1.00E+00	7.83E-01	1.00E+00	5.63E-01	1.00E+00	2.95E-01	1.00E+00	6.75E-01	1.00E+00	7.29E-01	1.00E+00	2.12E-01	1.00E+00	positive regulation of immune response	P
GO:0050789	5039	5.82E-43	0.00E+00	0.00E+00	0.00E+00	5.09E-20	0.00E+00	8.85E-24	0.00E+00	3.55E-41	0.00E+00	0.00E+00	0.00E+00	1.30E-11	0.00E+00	1.25E-22	0.00E+00	regulation of biological process	P
GO:0050790	598	3.94E-10	0.00E+00	9.34E-12	0.00E+00	2.54E-05	6.00E-03	9.68E-05	1.20E-02	7.09E-10	0.00E+00	6.45E-11	0.00E+00	9.41E-04	7.07E-02	1.83E-06	1.88E-03	regulation of catalytic activity	P
GO:0050791	4397	1.05E-38	0.00E+00	0.00E+00	0.00E+00	1.82E-17	0.00E+00	1.05E-21	0.00E+00	1.83E-37	0.00E+00	0.00E+00	0.00E+00	1.49E-11	0.00E+00	4.26E-21	0.00E+00	regulation of physiological process	P
GO:0050792	17	1.37E-01	1.00E+00	6.40E-01	1.00E+00	5.80E-01	1.00E+00	8.31E-01	1.00E+00	8.17E-02	1.00E+00	6.85E-01	1.00E+00	2.76E-01	1.00E+00	1.27E-01	1.00E+00	regulation of viral life cycle	P
GO:0050793	277	4.24E-01	1.00E+00	4.48E-01	1.00E+00	9.61E-01	1.00E+00	4.31E-01	1.00E+00	1.93E-01	1.00E+00	5.43E-01	1.00E+00	6.07E-01	1.00E+00	1.82E-01	1.00E+00	regulation of development	P
GO:0050794	4463	2.39E-39	0.00E+00	0.00E+00	0.00E+00	3.79E-19	0.00E+00	8.83E-24	0.00E+00	7.29E-38	0.00E+00	0.00E+00	0.00E+00	1.22E-09	0.00E+00	4.34E-20	0.00E+00	regulation of cellular process	P
GO:0050796	18	5.41E-01	1.00E+00	3.26E-01	1.00E+00	3.77E-01	1.00E+00	4.33E-01	1.00E+00	5.46E-01	1.00E+00	3.20E-01	1.00E+00	8.78E-01	1.00E+00	3.49E-01	1.00E+00	regulation of insulin secretion	P
GO:0050798	14	8.62E-01	1.00E+00	8.03E-01	1.00E+00	9.19E-01	1.00E+00	9.45E-01	1.00E+00	7.17E-01	1.00E+00	6.63E-01	1.00E+00	6.38E-01	1.00E+00	9.99E-01	1.00E+00	activated T cell proliferation	P
GO:0050801	234	7.63E-01	1.00E+00	7.51E-01	1.00E+00	6.46E-01	1.00E+00	3.79E-01	1.00E+00	8.09E-01	1.00E+00	5.58E-01	1.00E+00	3.80E-01	1.00E+00	1.00E+00	1.00E+00	ion homeostasis	P
GO:0050803	67	9.44E-02	1.00E+00	3.32E-01	1.00E+00	2.21E-01	1.00E+00	1.47E-01	1.00E+00	4.14E-02	1.00E+00	3.33E-01	1.00E+00	5.73E-01	1.00E+00	8.31E-01	1.00E+00	regulation of synapse structure and functior	P
GO:0050804	64	8.96E-02	1.00E+00	5.01E-01	1.00E+00	1.92E-01	1.00E+00	2.36E-01	1.00E+00	4.63E-02	1.00E+00	5.30E-01	1.00E+00	4.71E-01	1.00E+00	8.26E-01	1.00E+00	regulation of synaptic transmission	P
GO:0050806	19	3.53E-02	1.00E+00	1.71E-01	1.00E+00	7.61E-02	1.00E+00	2.43E-01	1.00E+00	3.07E-02	1.00E+00	2.34E-01	1.00E+00	1.88E-01	1.00E+00	1.86E-01	1.00E+00	positive regulation of synaptic transmission	P
GO:0050808	45	7.63E-01	1.00E+00	4.09E-01	1.00E+00	3.05E-01	1.00E+00	1.16E-01	1.00E+00	8.08E-01	1.00E+00	4.02E-01	1.00E+00	8.39E-01	1.00E+00	9.47E-01	1.00E+00	synapse organization and biogenesis	P
GO:0050810	11	1.08E-02	6.67E-01	1.45E-01	1.00E+00	1.08E-03	9.80E-02	9.82E-02	1.00E+00	3.38E-02	1.00E+00	1.92E-01	1.00E+00	1.56E-01	1.00E+00	2.16E-01	1.00E+00	regulation of steroid biosynthesis	P
GO:0050817	161	8.86E-01	1.00E+00	5.92E-01	1.00E+00	7.86E-01	1.00E+00	3.86E-01	1.00E+00	7.84E-01	1.00E+00	5.72E-01	1.00E+00	9.58E-01	1.00E+00	8.29E-01	1.00E+00	coagulation	P
GO:0050818	34	6.81E-02	1.00E+00	2.06E-01	1.00E+00	7.70E-02	1.00E+00	4.48E-01	1.00E+00	1.47E-01	1.00E+00	1.14E-01	1.00E+00	9.08E-02	1.00E+00	6.67E-01	1.00E+00	regulation of coagulation	P
GO:0050819	29	1.32E-01	1.00E+00	1.72E-01	1.00E+00	1.59E-01	1.00E+00	4.14E-01	1.00E+00	1.70E-01	1.00E+00	1.07E-01	1.00E+00	2.30E-01	1.00E+00	4.49E-01	1.00E+00	negative regulation of coagulation	P
GO:0050821	19	1.51E-01	1.00E+00	1.70E-01	1.00E+00	2.26E-01	1.00E+00	1.62E-01	1.00E+00	1.49E-01	1.00E+00	1.35E-01	1.00E+00	5.06E-01	1.00E+00	5.92E-01	1.00E+00	protein stabilization	P
GO:0050824	214	7.99E-02	1.00E+00	2.21E-01	1.00E+00	8.40E-03	4.60E-01	1.33E-01	1.00E+00	2.71E-01	1.00E+00	2.32E-01	1.00E+00	1.94E-01	1.00E+00	7.55E-01	1.00E+00	water binding	F
GO:0050825	214	7.99E-02	1.00E+00	2.21E-01	1.00E+00	8.40E-03	4.60E-01	1.33E-01	1.00E+00	2.71E-01	1.00E+00	2.32E-01	1.00E+00	1.94E-01	1.00E+00	7.55E-01	1.00E+00	ice binding	F
GO:0050826	214	7.99E-02	1.00E+00	2.21E-01	1.00E+00	8.40E-03	4.60E-01	1.33E-01	1.00E+00	2.71E-01	1.00E+00	2.32E-01	1.00E+00	1.94E-01	1.00E+00	7.55E-01	1.00E+00	response to freezing	P
GO:0050830	12	3.00E-01	1.00E+00	6.02E-01	1.00E+00	5.04E-01	1.00E+00	2.58E-01	1.00E+00	2.03E-01	1.00E+00	8.16E-01	1.00E+00	9.44E-01	1.00E+00	7.16E-01	1.00E+00	defense response to Gram-positive bacteriu	P
GO:0050832	14	9.85E-01	1.00E+00	9.61E-01	1.00E+00	8.39E-01	1.00E+00	8.62E-01	1.00E+00	9.53E-01	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	defense response to fungus	P
GO:0050839	17	5.15E-01	1.00E+00	3.29E-02	1.00E+00	3.97E-01	1.00E+00	3.04E-02	1.00E+00	5.51E-01	1.00E+00	5.16E-02	1.00E+00	4.59E-01	1.00E+00	3.18E-01	1.00E+00	cell adhesion molecule binding	F
GO:0050848	17	1.33E-01	1.00E+00	2.87E-01	1.00E+00	7.63E-02	1.00E+00	3.88E-01	1.00E+00	1.50E-01	1.00E+00	2.62E-01	1.00E+00	6.48E-01	1.00E+00	7.75E-01	1.00E+00	regulation of calcium-mediated signaling	P
GO:0050850	15	3.61E-01	1.00E+00	3.97E-01	1.00E+00	1.96E-01	1.00E+00	6.79E-01	1.00E+00	2.94E-01	1.00E+00	3.20E-01	1.00E+00	9.69E-01	1.00E+00	7.68E-01	1.00E+00	positive regulation of calcium-mediated sigr	P
GO:0050851	33	2.66E-03	2.39E-01	2.40E-01	1.00E+00	2.96E-02	1.00E+00	3.11E-01	1.00E+00	4.71E-03	4.18E-01	2.50E-01	1.00E+00	2.84E-01	1.00E+00	3.28E-01	1.00E+00	antigen receptor-mediated signaling pathwa	P
GO:0050852	21	6.68E-02	1.00E+00	4.57E-01	1.00E+00	7.85E-02	1.00E+00	3.87E-01	1.00E+00	9.40E-02	1.00E+00	5.11E-01	1.00E+00	4.75E-01	1.00E+00	5.08E-01	1.00E+00	T cell receptor signaling pathway	P
GO:0050853	13	1.38E-02	6.67E-01	7.52E-02	1.00E+00	9.10E-03	4.60E-01	1.56E-01	1.00E+00	2.27E-02	1.00E+00	6.56E-02	1.00E+00	2.29E-01	1.00E+00	1.02E-01	1.00E+00	B cell receptor signaling pathway	P
GO:0050854	10	2.12E-01	1.00E+00	7.27E-01	1.00E+00	1.21E-01	1.00E+00	5.46E-01	1.00E+00	2.65E-01	1.00E+00	8.43E-01	1.00E+00	6.11E-01	1.00E+00	6.53E-01	1.00E+00	regulation of antigen receptor-mediated sig	P
GO:0050863	72	5.15E-01	1.00E+00	4.65E-01	1.00E+00	2.49E-01	1.00E+00	7.06E-01	1.00E+00	5.93E-01	1.00E+00	4.82E-01	1.00E+00	4.95E-01	1.00E+00	3.17E-01	1.00E+00	regulation of T cell activation	P
GO:0050864	40	4.83E-01	1.00E+00	2.87E-01	1.00E+00	6.42E-01	1.00E+00	4.56E-01	1.00E+00	3.89E-01	1.00E+00	2.45E-01	1.00E+00	5.18E-01	1.00E+00	4.00E-01	1.00E+00	regulation of B cell activation	P
GO:0050868	20	5.04E-01	1.00E+00	5.98E-01	1.00E+00	5.95E-01	1.00E+00	9.61E-01	1.00E+00	4.67E-01	1.00E+00	4.63E-01	1.00E+00	4.44E-01	1.00E+00	6.10E-01	1.00E+00	negative regulation of T cell activation	P
GO:0050869	11	6.27E-01	1.00E+00	9.78E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.69E-01	1.00E+00	6.81E-01	1.00E+00	3.24E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of B cell activation	P
GO:0050870	51	5.14E-01	1.00E+00	4.18E-01	1.00E+00	1.36E-01	1.00E+00	6.54E-01	1.00E+00	7.03E-01	1.00E+00	4.78E-01	1.00E+00	5.03E-01	1.00E+00	1.70E-01	1.00E+00	positive regulation of T cell activation	P
GO:0050871	27	6.74E-01	1.00E+00	1.90E-01	1.00E+00	4.54E-01	1.00E+00	2.42E-01	1.00E+00	5.93E-01	1.00E+00	2.48E-01	1.00E+00	9.23E-01	1.00E+00	2.21E-01	1.00E+00	positive regulation of B cell activation	P
GO:0050874	3024	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organismal physiological process	P
GO:0050875	11563	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.20E-29	0.00E+00	1.63E-40	0.00E+00	cellular physiological process	P
GO:0050876	129	9.18E-01	1.00E+00	9.96E-01	1.00E+00	7.34E-01	1.00E+00	9.23E-01	1.00E+00	9.66E-01	1.00E+00	9.98E-01	1.00E+00	3.49E-01	1.00E+00	7.36E-01	1.00E+00	reproductive physiological process	P
GO:0050877	1113	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurophysiological process	P
GO:0050878	174	8.02E-01	1.00E+00	5.30E-01	1.00E+00	5.55E-01	1.00E+00	2.35E-01	1.00E+00	7.45E-01	1.00E+00	5.71E-01	1.00E+00	9.30E-01	1.00E+00	7.41E-01	1.00E+00	regulation of body fluids	P
GO:0050879	54	9.62E-01	1.00E+00	9.99E-01	1.00E+00	7.44E-01	1.00E+00	8.94E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	8.92E-01	1.00E+00	9.89E-01	1.00E+00	organismal movement	P
GO:0050880	60	9.97E-01	1.00E+00	9.64E-01	1.00E+00	9.44E-01	1.00E+00	8.20E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	3.30E-01	1.00E+00	7.22E-01	1.00E+00	regulation of blood vessel size	P
GO:0050881	38	9.67E-01	1.00E+00	9.89E-01	1.00E+00	8.05E-01	1.00E+00	7.41E-01	1.00E+00	9.37E-01	1.00E+00	9.96E-01	1.00E+00	9.35E-01	1.00E+00	9.68E-01	1.00E+00	musculoskeletal movement	P
GO:0050885	33	9.72E-01	1.00E+00	9.79E-01	1.00E+00	7.82E-01	1.00E+00	7.97E-01	1.00E+00	9.56E-01	1.00E+00	9.85E-01	1.00E+00	9.20E-01	1.00E+00	9.66E-01	1.00E+00	regulation of balance	P
GO:0050886	19	9.14E-01	1.00E+00	1.00E+00	1.00E+00	8.05E-01	1.00E+00	9.03E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	2.57E-01	1.00E+00	4.93E-01	1.00E+00	endocrine physiological process	P
GO:0050892	14	7.66E-02	1.00E+00	1.40E-01	1.00E+00	1.53E-02	6.93E-01	7.98E-02	1.00E+00	2.78E-01	1.00E+00	2.58E-01	1.00E+00	2.60E-01	1.00E+00	3.83E-01	1.00E+00	intestinal absorption	P

GO:0050896	2879	7.54E-01	1.00E+00	6.47E-01	1.00E+00	8.46E-01	1.00E+00	4.70E-01	1.00E+00	5.75E-01	1.00E+00	4.73E-01	1.00E+00	7.96E-01	1.00E+00	9.47E-01	1.00E+00	response to stimulus	P
GO:0050897	15	1.08E-01	1.00E+00	3.16E-02	1.00E+00	1.42E-01	1.00E+00	4.15E-02	1.00E+00	9.15E-02	1.00E+00	6.57E-02	1.00E+00	1.00E+00	1.00E+00	3.14E-01	1.00E+00	cobalt ion binding	F
GO:0050900	49	1.88E-01	1.00E+00	1.16E-01	1.00E+00	1.39E-01	1.00E+00	7.39E-02	1.00E+00	2.97E-01	1.00E+00	2.07E-01	1.00E+00	1.45E-01	1.00E+00	1.18E-01	1.00E+00	leukocyte migration	P
GO:0050905	16	7.03E-01	1.00E+00	9.43E-01	1.00E+00	7.64E-01	1.00E+00	6.77E-01	1.00E+00	6.98E-01	1.00E+00	9.48E-01	1.00E+00	3.37E-01	1.00E+00	9.52E-01	1.00E+00	neuromuscular physiological process	P
GO:0050906	21	1.86E-01	1.00E+00	7.78E-01	1.00E+00	7.39E-02	1.00E+00	4.92E-01	1.00E+00	1.73E-01	1.00E+00	7.81E-01	1.00E+00	9.86E-01	1.00E+00	8.93E-01	1.00E+00	detection of stimulus during sensory percep	P
GO:0050909	35	9.21E-01	1.00E+00	9.98E-01	1.00E+00	1.90E-01	1.00E+00	9.17E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	6.42E-01	1.00E+00	5.21E-01	1.00E+00	sensory perception of taste	P
GO:0050918	14	7.28E-01	1.00E+00	4.96E-01	1.00E+00	6.88E-01	1.00E+00	6.30E-01	1.00E+00	7.78E-01	1.00E+00	6.06E-01	1.00E+00	5.00E-01	1.00E+00	9.15E-02	1.00E+00	positive chemotaxis	P
GO:0050920	15	9.57E-01	1.00E+00	5.56E-01	1.00E+00	9.10E-01	1.00E+00	4.84E-01	1.00E+00	9.37E-01	1.00E+00	6.77E-01	1.00E+00	9.53E-01	1.00E+00	1.63E-01	1.00E+00	regulation of chemotaxis	P
GO:0050921	14	9.91E-01	1.00E+00	7.87E-01	1.00E+00	9.97E-01	1.00E+00	5.54E-01	1.00E+00	9.78E-01	1.00E+00	8.98E-01	1.00E+00	9.33E-01	1.00E+00	2.77E-01	1.00E+00	positive regulation of chemotaxis	P
GO:0050926	12	9.65E-01	1.00E+00	6.79E-01	1.00E+00	9.83E-01	1.00E+00	6.28E-01	1.00E+00	9.44E-01	1.00E+00	7.68E-01	1.00E+00	8.36E-01	1.00E+00	2.39E-01	1.00E+00	regulation of positive chemotaxis	P
GO:0050927	12	9.65E-01	1.00E+00	6.79E-01	1.00E+00	9.83E-01	1.00E+00	6.28E-01	1.00E+00	9.44E-01	1.00E+00	7.68E-01	1.00E+00	8.36E-01	1.00E+00	2.39E-01	1.00E+00	positive regulation of positive chemotaxis	P
GO:0050930	10	9.58E-01	1.00E+00	4.52E-01	1.00E+00	9.63E-01	1.00E+00	4.10E-01	1.00E+00	9.33E-01	1.00E+00	5.67E-01	1.00E+00	9.33E-01	1.00E+00	2.23E-01	1.00E+00	induction of positive chemotaxis	P
GO:0050931	17	4.13E-01	1.00E+00	3.88E-01	1.00E+00	7.97E-01	1.00E+00	6.58E-01	1.00E+00	4.16E-01	1.00E+00	4.35E-01	1.00E+00	1.58E-01	1.00E+00	1.50E-01	1.00E+00	pigment cell differentiation	P
GO:0050953	218	6.80E-01	1.00E+00	3.60E-01	1.00E+00	3.17E-01	1.00E+00	1.68E-01	1.00E+00	7.73E-01	1.00E+00	3.81E-01	1.00E+00	7.99E-01	1.00E+00	3.90E-01	1.00E+00	sensory perception of light stimulus	P
GO:0050954	150	9.67E-01	1.00E+00	9.69E-01	1.00E+00	8.26E-01	1.00E+00	9.60E-01	1.00E+00	9.58E-01	1.00E+00	9.28E-01	1.00E+00	9.12E-01	1.00E+00	9.55E-01	1.00E+00	sensory perception of mechanical stimulus	P
GO:0050982	10	6.73E-01	1.00E+00	6.24E-01	1.00E+00	4.78E-01	1.00E+00	2.85E-01	1.00E+00	7.69E-01	1.00E+00	5.95E-01	1.00E+00	6.35E-01	1.00E+00	9.62E-01	1.00E+00	detection of mechanical stimulus	P
GO:0050999	10	9.54E-01	1.00E+00	6.85E-01	1.00E+00	1.95E-01	1.00E+00	4.87E-01	1.00E+00	9.99E-01	1.00E+00	6.67E-01	1.00E+00	7.95E-01	1.00E+00	9.81E-01	1.00E+00	regulation of nitric-oxide synthase activity	P
GO:0051015	39	7.97E-03	6.34E-01	5.85E-03	3.60E-01	2.78E-03	2.48E-01	2.79E-01	1.00E+00	2.39E-02	1.00E+00	4.36E-03	2.70E-01	1.53E-01	1.00E+00	9.32E-02	1.00E+00	actin filament binding	F
GO:0051016	21	1.96E-01	1.00E+00	5.36E-01	1.00E+00	1.58E-01	1.00E+00	3.93E-01	1.00E+00	2.23E-01	1.00E+00	6.58E-01	1.00E+00	8.35E-01	1.00E+00	4.73E-01	1.00E+00	barbed-end actin filament capping	P
GO:0051017	23	5.97E-02	1.00E+00	1.45E-01	1.00E+00	2.06E-02	1.00E+00	2.44E-01	1.00E+00	9.67E-02	1.00E+00	8.73E-02	1.00E+00	2.80E-01	1.00E+00	7.39E-01	1.00E+00	actin filament bundle formation	P
GO:0051020	79	9.00E-02	1.00E+00	2.53E-02	1.00E+00	2.57E-01	1.00E+00	3.39E-01	1.00E+00	9.44E-02	1.00E+00	5.93E-02	1.00E+00	1.94E-01	1.00E+00	3.85E-03	1.85E-01	GTPase binding	F
GO:0051028	77	5.88E-06	7.00E-03	8.24E-09	4.97E-03	2.69E-03	2.48E-01	6.02E-05	1.20E-02	8.87E-06	2.88E-03	3.10E-08	8.37E-04	2.83E-02	1.00E+00	1.33E-03	9.16E-02	mRNA transport	P
GO:0051046	100	7.18E-01	1.00E+00	5.52E-01	1.00E+00	5.30E-01	1.00E+00	3.59E-01	1.00E+00	6.91E-01	1.00E+00	6.66E-01	1.00E+00	9.25E-01	1.00E+00	6.07E-01	1.00E+00	regulation of secretion	P
GO:0051047	36	2.71E-01	1.00E+00	3.07E-01	1.00E+00	4.78E-01	1.00E+00	3.10E-01	1.00E+00	2.59E-01	1.00E+00	4.66E-01	1.00E+00	2.79E-01	1.00E+00	3.16E-01	1.00E+00	positive regulation of secretion	P
GO:0051048	32	6.39E-01	1.00E+00	7.07E-01	1.00E+00	3.94E-01	1.00E+00	7.61E-01	1.00E+00	7.84E-01	1.00E+00	6.71E-01	1.00E+00	6.44E-01	1.00E+00	6.68E-01	1.00E+00	negative regulation of secretion	P
GO:0051049	155	1.98E-04	2.50E-02	2.71E-06	8.39E-03	1.47E-02	6.93E-01	7.76E-03	4.55E-01	9.49E-05	1.70E-02	5.98E-06	4.00E-03	1.40E-01	1.00E+00	6.34E-04	9.16E-02	regulation of transport	P
GO:0051050	61	1.39E-02	6.67E-01	7.56E-03	3.60E-01	8.78E-02	1.00E+00	1.89E-01	1.00E+00	3.50E-03	2.85E-01	8.21E-03	7.39E-01	6.43E-01	1.00E+00	3.13E-02	1.00E+00	positive regulation of transport	P
GO:0051051	43	1.35E-02	6.67E-01	1.54E-02	1.00E+00	1.70E-02	6.93E-01	2.39E-01	1.00E+00	1.63E-02	1.00E+00	2.93E-02	1.00E+00	3.18E-01	1.00E+00	6.21E-03	3.60E-01	negative regulation of transport	P
GO:0051052	72	2.28E-06	1.95E-03	6.18E-05	9.58E-03	4.91E-05	1.20E-02	6.04E-04	4.70E-02	2.92E-05	5.00E-03	2.86E-04	2.60E-02	1.73E-02	9.11E-01	3.74E-02	1.00E+00	regulation of DNA metabolism	P
GO:0051053	23	2.50E-06	1.95E-03	1.01E-03	9.10E-02	3.78E-04	3.60E-02	4.24E-02	1.00E+00	1.34E-04	1.70E-02	7.36E-04	5.49E-02	1.52E-02	6.47E-01	1.90E-02	1.00E+00	negative regulation of DNA metabolism	P
GO:0051054	22	4.69E-01	1.00E+00	5.08E-01	1.00E+00	1.87E-01	1.00E+00	1.53E-01	1.00E+00	6.44E-01	1.00E+00	7.41E-01	1.00E+00	6.81E-01	1.00E+00	8.40E-01	1.00E+00	positive regulation of DNA metabolism	P
GO:0051056	156	1.84E-01	1.00E+00	1.03E-02	5.18E-01	1.45E-02	6.93E-01	1.25E-02	8.18E-01	2.48E-01	1.00E+00	2.90E-02	1.00E+00	9.79E-01	1.00E+00	1.51E-01	1.00E+00	regulation of small GTPase mediated signa	P
GO:0051057	11	1.71E-01	1.00E+00	3.19E-01	1.00E+00	7.93E-02	1.00E+00	1.88E-01	1.00E+00	2.87E-01	1.00E+00	4.83E-01	1.00E+00	1.37E-01	1.00E+00	2.34E-01	1.00E+00	positive regulation of small GTPase mediat	P
GO:0051059	30	1.72E-02	7.02E-01	6.68E-04	6.90E-02	1.47E-01	1.00E+00	2.14E-01	1.00E+00	7.98E-03	5.39E-01	9.44E-04	5.49E-02	1.29E-01	1.00E+00	1.30E-01	1.00E+00	NF-kappaB binding	F
GO:0051082	127	1.73E-06	1.95E-03	1.10E-06	8.39E-03	3.51E-04	3.60E-02	1.44E-05	8.00E-03	1.41E-06	2.60E-03	3.25E-06	2.97E-03	1.45E-01	1.00E+00	1.73E-01	1.00E+00	unfolded protein binding	F
GO:0051084	12	1.01E-01	1.00E+00	4.45E-02	1.00E+00	9.07E-01	1.00E+00	8.69E-01	1.00E+00	3.86E-02	1.00E+00	1.42E-02	7.39E-01	1.56E-01	1.00E+00	2.88E-01	1.00E+00	posttranslational protein folding	P
GO:0051087	17	3.63E-05	1.00E-02	8.69E-02	1.00E+00	2.09E-03	2.48E-01	2.45E-01	1.00E+00	1.51E-04	1.70E-02	9.15E-02	1.00E+00	6.91E-02	1.00E+00	2.69E-01	1.00E+00	chaperone binding	F
GO:0051090	59	5.17E-04	3.37E-02	3.91E-04	6.90E-02	6.70E-03	4.60E-01	1.24E-03	1.15E-01	1.29E-03	7.80E-02	5.41E-03	2.70E-01	6.67E-03	5.44E-01	9.41E-03	4.81E-01	regulation of transcription factor activity	P
GO:0051091	36	9.69E-03	6.67E-01	4.21E-02	1.00E+00	1.20E-02	5.32E-01	1.20E-02	8.18E-01	2.47E-02	1.00E+00	1.83E-01	1.00E+00	5.04E-02	1.00E+00	4.37E-02	1.00E+00	positive regulation of transcription factor act	P
GO:0051092	28	1.49E-02	6.67E-01	4.38E-02	1.00E+00	1.71E-02	6.93E-01	9.66E-03	7.13E-01	1.94E-02	1.00E+00	1.71E-01	1.00E+00	1.13E-01	1.00E+00	5.14E-02	1.00E+00	activation of NF-kappaB transcription factor	P
GO:0051093	119	8.44E-01	1.00E+00	8.42E-01	1.00E+00	9.99E-01	1.00E+00	8.64E-01	1.00E+00	4.66E-01	1.00E+00	8.16E-01	1.00E+00	9.65E-01	1.00E+00	5.27E-01	1.00E+00	negative regulation of development	P
GO:0051094	120	8.87E-01	1.00E+00	9.61E-01	1.00E+00	9.66E-01	1.00E+00	8.20E-01	1.00E+00	7.89E-01	1.00E+00	9.70E-01	1.00E+00	9.20E-01	1.00E+00	5.49E-01	1.00E+00	positive regulation of development	P
GO:0051098	35	7.30E-03	6.34E-01	2.52E-02	1.00E+00	1.33E-02	5.53E-01	1.66E-02	8.18E-01	5.14E-03	4.18E-01	6.02E-02	1.00E+00	6.45E-01	1.00E+00	8.46E-02	1.00E+00	regulation of binding	P
GO:0051099	10	9.05E-02	1.00E+00	2.91E-01	1.00E+00	6.06E-02	1.00E+00	1.77E-01	1.00E+00	1.24E-01	1.00E+00	3.72E-01	1.00E+00	2.63E-01	1.00E+00	3.01E-01	1.00E+00	positive regulation of binding	P
GO:0051101	16	7.37E-03	6.34E-01	3.96E-03	1.97E-01	2.44E-02	1.00E+00	4.05E-02	1.00E+00	9.59E-03	5.39E-01	3.70E-03	2.70E-01	1.10E-01	1.00E+00	1.30E-01	1.00E+00	regulation of DNA binding	P
GO:0051119	46	8.51E-02	1.00E+00	2.33E-02	1.00E+00	2.00E-01	1.00E+00	2.38E-02	1.00E+00	1.06E-01	1.00E+00	7.00E-02	1.00E+00	1.69E-01	1.00E+00	2.92E-01	1.00E+00	sugar transporter activity	F
GO:0051128	120	2.28E-04	2.64E-02	2.92E-02	1.00E+00	9.40E-05	1.20E-02	1.60E-01	1.00E+00	1.46E-03	1.76E-01	2.89E-02	1.00E+00	1.52E-01	1.00E+00	2.24E-01	1.00E+00	regulation of cell organization and biogenes	P
GO:0051129	52	1.91E-03	2.02E-01	1.11E-01	1.00E+00	1.89E-04	2.40E-02	2.28E-01	1.00E+00	1.12E-02	5.39E-01	1.25E-01	1.00E+00	2.54E-01	1.00E+00	2.30E-01	1.00E+00	negative regulation of cell organization and	P
GO:0051130	27	1.37E-01	1.00E+00	4.42E-01	1.00E+00	3.06E-02	1.00E+00	3.57E-01	1.00E+00	3.56E-01	1.00E+00	4.64E-01	1.00E+00	1.52E-01	1.00E+00	7.14E-01	1.00E+00	positive regulation of cell organization and b	P
GO:0051145	13	9.51E-01	1.00E+00	9.72E-01	1.00E+00	9.72E-01	1.00E+00	5.71E-01	1.00E+00	9.48E-01	1.00E+00	9.92E-01	1.00E+00	7.37E-01	1.00E+00	3.71E-01	1.00E+00	smooth muscle cell differentiation	P
GO:0051146	29	8.08E-01	1.00E+00	7.42E-01	1.00E+00	3.25E-01	1.00E+00	2.14E-01	1.00E+00	8.66E-01	1.00E+00	6.97E-01	1.00E+00	7.87E-01	1.00E+00	9.98E-01	1.00E+00	striated muscle cell differentiation	P
GO:0051168	52	1.24E-07	1.85E-03	5.55E-06	8.39E-03	1.31E-04	1.50E-02	3.99E-03	2.41E-01	1.72E-06	2.60E-03	1.21E-06	2.97E-03	4.34E-02	1.00E+00	1.07E-03	9.16E-02	nuclear export	P
GO:0051169	148	2.54E-08	9.77E-04	1.04E-10	0.00E+00	7.46E-04	4.50E-02	3.47E-04	4.20E-02	7.64E-08	1.69E-03	6.99E-11	0.00E+00	2.16E-03	1.95E-01	1.15E-04	2.00E-02	nuclear transport	P
GO:0051170	100	3.90E-05	1.00E-02	6.90E-08	4.97E-03	3.81E-02	1.00E+00	4.82E-03	3.46E-01	3.74E-05	5.00E-03	3.06E-07	9.41E-04	3.96E-03	3.57E-01	2.29E-03	1.40E-01	nuclear import	P
GO:0051174	124	5.77E-01	1.00E+00	3.15E-01	1.00E+00	1.25E-01	1.00E+00	1.75E-01	1.00E+00	7.04E-01	1.00E+00	3.88E-01	1.00E+00	6.71E-01	1.00E+00	4.86E-01	1.00E+00	regulation of phosphorus metabolism	P
GO:0051179	3553	1.76E-18	0.00E+00	2.17E-19	0.00E+00	3.33E-10	9.34E-04	4.45E-10	0.00E+00	1.66E-18	0.00E+00	3.30E-19	0.00E+00	5.22E-03	3.57E-01	7.46E-04	9.16E-02	localization	P
GO:0051180	18	2.15E-01	1.00E+00	2.88E-01	1.00E+00	3.80E-01	1.00E+00	4.90E-01	1.00E+00	1.96E-01	1.00E+00	3.57E-01	1.00E+00	6.18E-01	1.00E+00	1.99E-01	1.00E+00	vitamin transport	P
GO:0051181	24	2.21E-01	1.00E+00	2.51E-01	1.00E+00	2.42E-01	1.00E+00	1.47E-01	1.00E+00	2.80E-01	1.00E+00	4.49E-01	1.00E+00	4.99E-01	1.00E+00	2.74E-01	1.00E+00	cofactor transport	P
GO:0051183	10	4.16E-01	1.00E+00	3.25E-01	1.00E+00	6.98E-01	1.00E+00	5.78E-01	1.00E+00	3.98E-01	1.00E+00	3.51E-01	1.00E+00	2.79E-01	1.00E+00	2.31E-01	1.00E+00	vitamin transporter activity	F
GO:0051184	24	5.96E-01	1.00E+00	3.73E-01	1.00E+00	8.00E-01	1.00E+00	5.98E-01	1.00E+00	4.98E-01	1.00E+00	4.47E-01	1.00E+00	6.63E-01	1.00E+00	2.07E-01	1.00E+00	cofactor transporter activity	F
GO:0051186	263	9.06E-06	7.00E-03	1.49E-05	9.58E-03	5.48E-06	2.66E-03	6.48E-05	1.20E-02	1.21E-04	1.70E-02	7.34E-04	5.49E-02	1.43E-01	1.00E+00	3.60E-03	1.85E-01	cofactor metabolism	P
GO:0051187	32	2.77E-02	1.00E+00	8.47E-02	1.00E+00	3.54E-03	3.27E-01	8.23E-02	1.00E+00	5.37E-02	1.00E+00	1.12E-01	1.00E+00	4.53E-01	1.00E+00	1.78E-01	1.00E+00	cofactor catabolism	P
GO:0051188	152	5.43E-04	3.37E-02	3.01E-03	1.97E-01	5.42E-04	3.60E-02	9.92E-04	8.30E-02	3.18E-03	2.85E-01	2.76E-02	1.00E+00	1.85E-01	1.00E+00	5.74E-02	1.00E+00	cofactor biosynthesis	P
GO:0051213	61	3.65E-02	1.00E+00	7.81E-04	6.90E-02	1.02E-02	4.60E-01	2.31E-01	1.00E+00	1.66E-01	1.00E+00	2.53E-04	2.60E-02	1.24E-01	1.00E+00	5.50E-02	1.00E+00	dioxygenase activity	F
GO:0051216	64	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	9.95E-01	1.00E+00	9.93E-01	1.00E+00	9.96E-01	1.00E+00	cartilage development	P
GO:0051219	15	5.80E-04	3.37E-02	3.05E-01	1.00E+00	9.39E-03	4.60E-01	3.63E-01	1.00E+00	5.43E-03	4.18E-01	3.78E-01	1.00E+00	1.64E-02	6.63E-01	3.02E-01	1.00E+00	phosphoprotein binding	F
GO:0051222	21	4.49E-03	3.28E-01	8.71E-03	5.03E-01	3.10E-02	1.00E+00	2.45E-01	1.00E+00	1.76E-03	1.76E-01	2.50E-02	1.00E+00	2.24E-01	1.00E+00	7.25E-03	4.81E-01	positive regulation of protein transport	P
GO:0051223	43	8.00E-04	8.30E-02	6.44E-04	6.90E-02	2.41E-02	1.00E+00	6.21E-02	1.00E+00	3.69E-04	2.20E-02	2.59E-03	2.39E-01	2.22E-01	1.00E+00	2.16E-03	1.40E-01	regulation of protein transport	P
GO:0051224	16	5.73E-01	1.00E+00	3.22E-01	1.00E+00	7.88E-01	1.00E+00	5.64E-01	1.00E+00	4.39E-01	1.00E+00	3.30E-01	1.00E+00	6.45E-01	1.00E+00	2.18E-01	1.00E+00	negative regulation of protein transport	P
GO:0051234	3494	1.51E-18	0.00E+00	4.82E-19	0.00E+00	3.22E-10	9.34E-04	3.14E-10	0.00E+00	1.46E-18	0.00E+00	4.31E-19	0.00E+00	5.51E-03	3.57E-01	2.31E-03	1.40E-01	establishment of localization	P
GO:0051235	50	2.28E-01	1.00E+00	1.87E-01	1.00E+00	2.42E-01	1.00E+00	2.29E-01	1.00E+00	2.65E-01	1.00E+00	2.00E-01	1.00E+00	2.53E-01	1.00E+00	5.98E-01	1.00E+00	maintenance of localization	P
GO:0051236	87	5.85E-07	1.95E-03	5.42E-10	0.00E+00	3.85E-04	3.60E-02	1.81E-05	8.00E-03	1.63E-06	2.60E-03	2.17E-09	0.00E+00	3.61E-02	1.00E+00	6.99E-04	9.16E-02	establishment of RNA localization	P
GO:0051238	12	1.91E-01	1.00E+00	2.08E-01	1.00E+00	1.98E-01	1.00E+00	3.72E-01	1.00E+00	1.62E-01	1.00E+00	1.48E-01	1.00E+00	4.71E-01	1.00E+00	6.91E-01	1.00E+00	sequestering of metal ion	P
GO:0051239	334	8.24E-01	1.00E+00	9.13E-01	1.00E+00	6.27E-01	1.00E+00	8.74E-01	1.00E+00	7.38E-01	1.00E+00	8.79E-01	1.00E+00	8.99E-01	1.00E+00	7.67E-01	1.00E+00	regulation of organismal physiological proce	P
GO:0051240	145	9.45E-01	1.00E+00	8.93E-01	1.00E+00	9.63E-01	1.00E+00	8.85E-01	1.00E+00	8.94E-01	1.00E+00	8.87E-01	1.00E+00	8.45E-01	1.00E+00	4.21E-01	1.00E+00	positive regulation of organismal physiologi	P

GO:0051241	43	8.02E-01	1.00E+00	3.53E-01	1.00E+00	4.70E-01	1.00E+00	4.96E-01	1.00E+00	8.41E-01	1.00E+00	3.44E-01	1.00E+00	7.44E-01	1.00E+00	4.30E-01	1.00E+00	negative regulation of organismal physiolog	P
GO:0051242	1055	1.86E-04	2.50E-02	2.52E-06	8.39E-03	1.21E-03	9.80E-02	1.03E-04	1.20E-02	3.39E-04	1.98E-02	2.77E-05	1.20E-02	5.82E-02	1.00E+00	6.04E-03	3.60E-01	positive regulation of cellular physiological p	P
GO:0051243	1144	7.98E-12	0.00E+00	5.50E-11	0.00E+00	4.33E-08	9.68E-04	1.26E-05	8.00E-03	2.32E-11	0.00E+00	1.13E-09	0.00E+00	1.07E-02	6.30E-01	8.10E-06	1.88E-03	negative regulation of cellular physiological	P
GO:0051244	4118	2.24E-39	0.00E+00	0.00E+00	0.00E+00	3.38E-18	0.00E+00	5.49E-23	0.00E+00	8.51E-38	0.00E+00	0.00E+00	0.00E+00	2.18E-11	0.00E+00	2.99E-21	0.00E+00	regulation of cellular physiological process	P
GO:0051246	393	1.32E-07	1.85E-03	3.44E-08	4.97E-03	1.46E-07	2.42E-03	1.46E-05	8.00E-03	8.13E-06	2.88E-03	4.76E-07	2.97E-03	1.40E-02	6.47E-01	7.69E-04	9.16E-02	regulation of protein metabolism	P
GO:0051247	117	3.23E-01	1.00E+00	8.99E-02	1.00E+00	1.63E-01	1.00E+00	1.75E-01	1.00E+00	5.12E-01	1.00E+00	9.88E-02	1.00E+00	2.34E-01	1.00E+00	9.73E-02	1.00E+00	positive regulation of protein metabolism	P
GO:0051248	114	1.85E-02	1.00E+00	2.16E-01	1.00E+00	1.00E-03	9.80E-02	4.63E-01	1.00E+00	7.18E-02	1.00E+00	1.88E-01	1.00E+00	3.51E-01	1.00E+00	2.79E-01	1.00E+00	negative regulation of protein metabolism	P
GO:0051249	94	3.23E-01	1.00E+00	1.78E-01	1.00E+00	2.55E-01	1.00E+00	4.37E-01	1.00E+00	3.26E-01	1.00E+00	1.94E-01	1.00E+00	5.08E-01	1.00E+00	1.77E-01	1.00E+00	regulation of lymphocyte activation	P
GO:0051250	30	5.98E-01	1.00E+00	7.36E-01	1.00E+00	8.44E-01	1.00E+00	9.96E-01	1.00E+00	4.95E-01	1.00E+00	5.03E-01	1.00E+00	5.13E-01	1.00E+00	7.68E-01	1.00E+00	negative regulation of lymphocyte activatior	P
GO:0051251	66	4.31E-01	1.00E+00	1.19E-01	1.00E+00	1.14E-01	1.00E+00	2.96E-01	1.00E+00	5.28E-01	1.00E+00	1.67E-01	1.00E+00	6.74E-01	1.00E+00	7.61E-02	1.00E+00	positive regulation of lymphocyte activation	P
GO:0051252	26	3.35E-02	1.00E+00	1.60E-02	1.00E+00	1.13E-01	1.00E+00	2.37E-01	1.00E+00	4.94E-02	1.00E+00	2.40E-02	1.00E+00	8.32E-02	1.00E+00	4.54E-02	1.00E+00	regulation of RNA metabolism	P
GO:0051258	86	3.01E-03	2.39E-01	1.02E-01	1.00E+00	1.30E-01	1.00E+00	7.04E-01	1.00E+00	1.51E-03	1.76E-01	5.76E-02	1.00E+00	4.62E-02	1.00E+00	2.60E-01	1.00E+00	protein polymerization	P
GO:0051259	109	1.86E-01	1.00E+00	5.15E-02	1.00E+00	5.20E-01	1.00E+00	1.48E-02	8.18E-01	1.64E-01	1.00E+00	1.04E-01	1.00E+00	1.86E-01	1.00E+00	4.91E-01	1.00E+00	protein oligomerization	P
GO:0051260	75	4.26E-01	1.00E+00	3.54E-01	1.00E+00	6.75E-01	1.00E+00	2.85E-01	1.00E+00	3.12E-01	1.00E+00	4.75E-01	1.00E+00	4.74E-01	1.00E+00	3.44E-01	1.00E+00	protein homooligomerization	P
GO:0051261	42	3.08E-02	1.00E+00	5.60E-01	1.00E+00	2.12E-03	2.48E-01	2.93E-01	1.00E+00	8.77E-02	1.00E+00	5.63E-01	1.00E+00	7.68E-01	1.00E+00	7.77E-01	1.00E+00	protein depolymerization	P
GO:0051262	24	1.37E-02	6.67E-01	4.96E-03	3.60E-01	5.53E-02	1.00E+00	3.17E-03	1.47E-01	4.52E-02	1.00E+00	9.03E-03	7.39E-01	3.12E-02	1.00E+00	6.74E-01	1.00E+00	protein tetramerization	P
GO:0051270	97	3.12E-01	1.00E+00	5.45E-01	1.00E+00	1.10E-01	1.00E+00	2.21E-01	1.00E+00	3.26E-01	1.00E+00	7.36E-01	1.00E+00	7.38E-01	1.00E+00	4.68E-01	1.00E+00	regulation of cell motility	P
GO:0051271	30	1.31E-01	1.00E+00	1.91E-01	1.00E+00	2.24E-01	1.00E+00	4.20E-02	1.00E+00	8.76E-02	1.00E+00	4.22E-01	1.00E+00	2.61E-01	1.00E+00	2.70E-01	1.00E+00	negative regulation of cell motility	P
GO:0051272	40	4.94E-01	1.00E+00	7.26E-01	1.00E+00	1.82E-01	1.00E+00	6.11E-01	1.00E+00	5.80E-01	1.00E+00	8.52E-01	1.00E+00	8.24E-01	1.00E+00	1.72E-01	1.00E+00	positive regulation of cell motility	P
GO:0051276	472	6.57E-12	0.00E+00	3.70E-15	0.00E+00	6.21E-04	3.60E-02	2.24E-04	2.70E-02	4.80E-12	0.00E+00	3.23E-14	0.00E+00	2.33E-04	3.40E-02	2.49E-08	7.71E-04	chromosome organization and biogenesis	P
GO:0051287	38	2.17E-03	2.02E-01	1.02E-01	1.00E+00	2.18E-02	1.00E+00	1.55E-02	8.18E-01	1.18E-02	5.39E-01	3.01E-01	1.00E+00	1.14E-01	1.00E+00	1.60E-01	1.00E+00	NAD binding	F
GO:0051289	10	4.98E-02	1.00E+00	1.48E-01	1.00E+00	2.48E-01	1.00E+00	2.10E-01	1.00E+00	5.21E-02	1.00E+00	1.48E-01	1.00E+00	2.41E-01	1.00E+00	4.23E-01	1.00E+00	protein homotetramerization	P
GO:0051297	19	2.41E-02	1.00E+00	7.24E-02	1.00E+00	4.81E-02	1.00E+00	1.01E-01	1.00E+00	1.72E-02	1.00E+00	1.15E-01	1.00E+00	6.23E-01	1.00E+00	1.71E-01	1.00E+00	centrosome organization and biogenesis	P
GO:0051301	244	3.82E-06	7.00E-03	7.38E-09	4.97E-03	2.01E-03	2.48E-01	1.66E-05	8.00E-03	7.74E-06	2.88E-03	9.45E-08	8.37E-04	2.58E-02	1.00E+00	1.60E-03	9.16E-02	cell division	P
GO:0051318	18	1.51E-01	1.00E+00	3.67E-02	1.00E+00	7.19E-01	1.00E+00	1.30E-01	1.00E+00	1.27E-01	1.00E+00	4.83E-02	1.00E+00	9.29E-02	1.00E+00	4.64E-02	1.00E+00	G1 phase	P
GO:0051320	16	7.20E-02	1.00E+00	7.58E-02	1.00E+00	1.22E-01	1.00E+00	4.24E-01	1.00E+00	8.76E-02	1.00E+00	1.28E-01	1.00E+00	1.22E-01	1.00E+00	2.98E-02	1.00E+00	S phase	P
GO:0051321	88	1.56E-02	6.67E-01	1.02E-03	9.10E-02	4.02E-02	1.00E+00	1.45E-02	8.18E-01	1.88E-02	1.00E+00	2.00E-03	1.61E-01	3.52E-01	1.00E+00	6.43E-02	1.00E+00	meiotic cell cycle	P
GO:0051324	10	1.75E-01	1.00E+00	5.11E-02	1.00E+00	1.80E-01	1.00E+00	2.69E-01	1.00E+00	1.73E-01	1.00E+00	8.48E-03	7.39E-01	5.70E-01	1.00E+00	5.12E-01	1.00E+00	prophase	P
GO:0051325	100	5.41E-04	3.37E-02	1.24E-04	1.50E-02	1.76E-02	6.93E-01	4.19E-04	4.20E-02	5.61E-04	4.00E-02	1.10E-03	5.49E-02	6.04E-02	1.00E+00	2.76E-02	1.00E+00	interphase	P
GO:0051327	86	3.10E-02	1.00E+00	1.13E-03	9.10E-02	7.51E-02	1.00E+00	1.38E-02	8.18E-01	3.04E-02	1.00E+00	2.35E-03	1.64E-01	5.52E-01	1.00E+00	6.21E-02	1.00E+00	M phase of meiotic cell cycle	P
GO:0051329	98	3.31E-04	3.37E-02	1.01E-04	1.50E-02	1.27E-02	5.32E-01	6.73E-04	4.70E-02	3.96E-04	2.20E-02	6.27E-04	5.49E-02	5.22E-02	1.00E+00	2.26E-02	1.00E+00	interphase of mitotic cell cycle	P
GO:0051336	211	1.29E-07	1.85E-03	1.35E-05	9.58E-03	6.11E-05	1.20E-02	9.18E-02	1.00E+00	2.04E-06	2.60E-03	5.47E-05	1.70E-02	2.47E-04	3.40E-02	9.70E-05	2.00E-02	regulation of hydrolase activity	P
GO:0051338	261	6.69E-04	3.44E-02	1.10E-04	1.50E-02	1.42E-02	6.93E-01	1.56E-02	8.18E-01	3.10E-04	1.98E-02	1.36E-04	1.70E-02	2.16E-01	1.00E+00	9.18E-03	4.81E-01	regulation of transferase activity	P
GO:0051339	46	9.32E-01	1.00E+00	7.87E-01	1.00E+00	9.58E-01	1.00E+00	5.16E-01	1.00E+00	8.68E-01	1.00E+00	8.61E-01	1.00E+00	8.01E-01	1.00E+00	3.78E-01	1.00E+00	regulation of lyase activity	P
GO:0051340	79	1.73E-04	2.50E-02	1.20E-04	1.50E-02	9.07E-02	1.00E+00	8.61E-03	7.13E-01	2.34E-04	1.70E-02	3.10E-04	3.07E-02	4.30E-03	3.57E-01	6.79E-03	4.81E-01	regulation of ligase activity	P
GO:0051341	15	4.77E-01	1.00E+00	1.36E-01	1.00E+00	2.11E-01	1.00E+00	2.93E-01	1.00E+00	7.47E-01	1.00E+00	1.29E-01	1.00E+00	4.50E-01	1.00E+00	2.61E-01	1.00E+00	regulation of oxidoreductase activity	P
GO:0051345	64	3.50E-05	1.00E-02	4.03E-04	6.90E-02	8.56E-04	7.56E-02	1.85E-01	1.00E+00	1.15E-04	1.70E-02	2.80E-04	2.60E-02	1.05E-02	6.30E-01	1.96E-03	1.40E-01	positive regulation of hydrolase activity	P
GO:0051347	159	3.88E-02	1.00E+00	1.78E-02	1.00E+00	1.07E-01	1.00E+00	9.04E-02	1.00E+00	2.69E-02	1.00E+00	1.73E-02	8.81E-01	2.95E-01	1.00E+00	4.28E-02	1.00E+00	positive regulation of transferase activity	P
GO:0051348	66	6.79E-03	5.17E-01	3.14E-03	1.97E-01	7.66E-02	1.00E+00	8.95E-02	1.00E+00	4.37E-03	3.60E-01	2.83E-03	2.39E-01	2.27E-01	1.00E+00	1.78E-01	1.00E+00	negative regulation of transferase activity	P
GO:0051349	28	6.55E-01	1.00E+00	5.67E-01	1.00E+00	5.56E-01	1.00E+00	1.90E-01	1.00E+00	7.19E-01	1.00E+00	8.38E-01	1.00E+00	3.89E-01	1.00E+00	1.54E-01	1.00E+00	positive regulation of lyase activity	P
GO:0051350	16	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	negative regulation of lyase activity	P
GO:0051351	72	7.51E-05	1.24E-02	6.88E-05	1.00E-02	9.33E-02	1.00E+00	9.07E-03	7.13E-01	6.39E-05	1.70E-02	2.27E-04	2.60E-02	6.27E-03	3.57E-01	1.82E-02	1.00E+00	positive regulation of ligase activity	P
GO:0051352	66	8.53E-04	8.30E-02	5.48E-04	6.90E-02	2.39E-01	1.00E+00	5.30E-02	1.00E+00	3.98E-04	2.20E-02	1.35E-03	6.40E-02	2.02E-02	9.11E-01	2.82E-03	1.85E-01	negative regulation of ligase activity	P
GO:0051384	21	6.49E-01	1.00E+00	5.24E-01	1.00E+00	9.81E-01	1.00E+00	8.77E-01	1.00E+00	4.49E-01	1.00E+00	4.62E-01	1.00E+00	6.97E-01	1.00E+00	1.16E-01	1.00E+00	response to glucocorticoid stimulus	P
GO:0051402	58	2.38E-02	1.00E+00	1.87E-02	1.00E+00	4.30E-02	1.00E+00	2.23E-02	1.00E+00	2.02E-02	1.00E+00	4.59E-02	1.00E+00	1.34E-01	1.00E+00	7.96E-02	1.00E+00	neuron apoptosis	P
GO:0051427	69	1.22E-02	6.67E-01	4.71E-04	6.90E-02	1.48E-02	6.93E-01	2.45E-02	1.00E+00	1.74E-02	1.00E+00	8.03E-04	5.49E-02	7.65E-01	1.00E+00	3.78E-02	1.00E+00	hormone receptor binding	F
GO:0051436	65	4.51E-04	3.37E-02	3.89E-04	6.90E-02	2.08E-01	1.00E+00	4.24E-02	1.00E+00	2.28E-04	1.70E-02	1.10E-03	5.49E-02	1.59E-02	6.47E-01	2.70E-03	1.85E-01	negative regulation of ubiquitin ligase activit	P
GO:0051437	68	4.72E-05	1.00E-02	5.45E-05	9.58E-03	9.95E-02	1.00E+00	1.34E-02	8.18E-01	3.46E-05	5.00E-03	1.62E-04	1.70E-02	5.42E-03	3.57E-01	7.26E-03	4.81E-01	positive regulation of ubiquitin ligase activity	P
GO:0051438	76	8.00E-05	1.24E-02	7.48E-05	1.00E-02	7.25E-02	1.00E+00	9.41E-03	7.13E-01	1.33E-04	1.70E-02	1.81E-04	2.60E-02	3.02E-03	1.95E-01	3.33E-03	1.85E-01	regulation of ubiquitin ligase activity	P
GO:0051439	71	1.38E-04	2.50E-02	1.82E-04	1.50E-02	1.14E-01	1.00E+00	2.26E-02	1.00E+00	1.54E-04	1.70E-02	4.63E-04	4.10E-02	5.01E-03	3.57E-01	6.71E-03	4.81E-01	regulation of ubiquitin ligase activity during	P
GO:0051443	69	2.99E-05	1.00E-02	3.74E-05	9.58E-03	7.34E-02	1.00E+00	9.90E-03	7.13E-01	3.18E-05	5.00E-03	1.13E-04	1.70E-02	4.36E-03	3.57E-01	9.29E-03	4.81E-01	positive regulation of ubiquitin ligase activity	P
GO:0051444	66	8.53E-04	8.30E-02	5.48E-04	6.90E-02	2.39E-01	1.00E+00	5.30E-02	1.00E+00	3.98E-04	2.20E-02	1.35E-03	6.40E-02	2.02E-02	9.11E-01	2.82E-03	1.85E-01	negative regulation of ubiquitin ligase activit	P
GO:0051480	77	6.36E-01	1.00E+00	7.34E-01	1.00E+00	4.99E-01	1.00E+00	8.02E-01	1.00E+00	6.12E-01	1.00E+00	5.51E-01	1.00E+00	5.41E-01	1.00E+00	9.46E-01	1.00E+00	cytosolic calcium ion homeostasis	P
GO:0051493	13	3.49E-01	1.00E+00	5.29E-01	1.00E+00	4.55E-02	1.00E+00	2.35E-01	1.00E+00	5.37E-01	1.00E+00	6.08E-01	1.00E+00	8.17E-01	1.00E+00	8.35E-01	1.00E+00	regulation of cytoskeleton organization and	P
GO:0051536	53	1.73E-01	1.00E+00	2.68E-01	1.00E+00	4.74E-02	1.00E+00	2.83E-01	1.00E+00	2.52E-01	1.00E+00	2.57E-01	1.00E+00	9.83E-01	1.00E+00	4.49E-01	1.00E+00	iron-sulfur cluster binding	F
GO:0051537	14	5.52E-01	1.00E+00	5.85E-01	1.00E+00	2.91E-01	1.00E+00	3.22E-01	1.00E+00	5.59E-01	1.00E+00	7.61E-01	1.00E+00	9.90E-01	1.00E+00	3.98E-01	1.00E+00	2 iron, 2 sulfur cluster binding	F
GO:0051539	21	4.44E-02	1.00E+00	2.04E-01	1.00E+00	1.14E-01	1.00E+00	2.12E-01	1.00E+00	1.89E-02	1.00E+00	1.32E-01	1.00E+00	9.98E-01	1.00E+00	7.88E-01	1.00E+00	4 iron, 4 sulfur cluster binding	F
GO:0051540	53	1.73E-01	1.00E+00	2.68E-01	1.00E+00	4.74E-02	1.00E+00	2.83E-01	1.00E+00	2.52E-01	1.00E+00	2.57E-01	1.00E+00	9.83E-01	1.00E+00	4.49E-01	1.00E+00	metal cluster binding	F
GO:0051591	14	8.26E-01	1.00E+00	6.97E-01	1.00E+00	9.89E-01	1.00E+00	9.88E-01	1.00E+00	5.53E-01	1.00E+00	4.12E-01	1.00E+00	6.70E-01	1.00E+00	8.76E-01	1.00E+00	response to cAMP	P
GO:0051592	15	9.95E-01	1.00E+00	9.26E-01	1.00E+00	3.36E-01	1.00E+00	9.28E-01	1.00E+00	9.96E-01	1.00E+00	7.30E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	response to calcium ion	P
GO:0051603	255	2.05E-05	8.00E-03	1.73E-09	4.97E-03	3.83E-03	3.27E-01	7.71E-06	8.00E-03	1.94E-04	1.70E-02	2.86E-08	8.37E-04	2.91E-03	1.95E-01	3.88E-04	2.70E-02	proteolysis during cellular protein catabolisr	P
GO:0051604	13	6.39E-01	1.00E+00	8.04E-01	1.00E+00	5.59E-01	1.00E+00	8.17E-01	1.00E+00	7.16E-01	1.00E+00	7.80E-01	1.00E+00	3.83E-01	1.00E+00	5.65E-01	1.00E+00	protein maturation	P
GO:0051605	12	5.32E-01	1.00E+00	7.17E-01	1.00E+00	4.63E-01	1.00E+00	7.39E-01	1.00E+00	6.28E-01	1.00E+00	6.76E-01	1.00E+00	3.16E-01	1.00E+00	6.33E-01	1.00E+00	proteolysis during protein maturation	P
GO:0051606	91	8.56E-01	1.00E+00	8.15E-01	1.00E+00	2.87E-01	1.00E+00	7.49E-01	1.00E+00	7.64E-01	1.00E+00	6.57E-01	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	detection of stimulus	P
GO:0051607	21	8.69E-02	1.00E+00	3.91E-01	1.00E+00	9.35E-02	1.00E+00	6.68E-01	1.00E+00	9.47E-02	1.00E+00	3.94E-01	1.00E+00	3.41E-01	1.00E+00	2.46E-01	1.00E+00	defense response to virus	P
GO:0051640	36	2.72E-03	2.39E-01	9.64E-05	1.50E-02	6.22E-03	4.60E-01	8.98E-03	7.13E-01	5.92E-03	5.39E-01	1.10E-04	1.70E-02	3.99E-01	1.00E+00	1.34E-02	6.47E-01	organelle localization	P
GO:0051641	868	1.56E-25	0.00E+00	1.36E-24	0.00E+00	2.23E-15	0.00E+00	1.05E-09	0.00E+00	8.46E-23	0.00E+00	3.55E-24	0.00E+00	5.20E-05	6.00E-03	6.87E-07	1.88E-03	cellular localization	P
GO:0051649	847	3.12E-26	0.00E+00	7.63E-25	0.00E+00	2.76E-15	0.00E+00	2.91E-10	0.00E+00	1.85E-23	0.00E+00	2.63E-24	0.00E+00	2.11E-05	5.44E-03	9.22E-07	1.88E-03	establishment of cellular localization	P
GO:0051656	24	5.61E-04	3.37E-02	4.94E-05	9.58E-03	8.45E-03	4.60E-01	9.99E-04	8.30E-02	3.92E-03	2.85E-01	5.96E-05	1.70E-02	1.46E-01	1.00E+00	1.47E-02	8.49E-01	establishment of organelle localization	P
GO:0051668	14	3.41E-01	1.00E+00	4.44E-01	1.00E+00	1.77E-01	1.00E+00	6.70E-01	1.00E+00	4.38E-01	1.00E+00	4.10E-01	1.00E+00	4.41E-01	1.00E+00	5.24E-01	1.00E+00	localization within membrane	P
GO:0051674	513	6.78E-01	1.00E+00	3.90E-01	1.00E+00	1.82E-01	1.00E+00	1.88E-01	1.00E+00	8.01E-01	1.00E+00	6.07E-01	1.00E+00	6.16E-01	1.00E+00	2.43E-01	1.00E+00	localization of cell	P
GO:0051693	21	1.96E-01	1.00E+00	5.36E-01	1.00E+00	1.58E-01	1.00E+00	3.93E-01	1.00E+00	2.23E-01	1.00E+00	6.58E-01	1.00E+00	8.35E-01	1.00E+00	4.73E-01	1.00E+00	actin filament capping	P
GO:0051701	25	1.00E-01	1.00E+00	1.44E-01	1.00E+00	3.51E-01	1.00E+00	3.16E-01	1.00E+00	9.72E-02	1.00E+00	1.01E-01	1.00E+00	1.20E-01	1.00E+00	6.63E-01	1.00E+00	interaction with host	P
GO:0051704	369	3.11E-06	7.00E-03	2.46E-06	8.39E-03	4.26E-04	3.60E-02	1.98E-02	1.00E+00	1.53E-05	4.00E-03	1.18E-06	2.97E-03	6.58E-04	6.50E-02	7.20E-03	4.81E-01	interaction between organisms	P
GO:0051705	29	7.91E-01	1.00E+00	9.58E-01	1.00E+00	7.31E-01	1.00E+00	7.63E-01	1.00E+00	8.23E-01	1.00E+00	9.48E-01	1.00E+00	2.35E-01	1.00E+00	5.05E-01	1.00E+00	behavioral interaction between organisms	P

GO:0051706	82	9.11E-01	1.00E+00	1.00E+00	1.00E+00	7.20E-01	1.00E+00	9.75E-01	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	2.85E-01	1.00E+00	9.18E-01	1.00E+00	physiological interaction between organisms	P
GO:0051707	241	7.77E-01	1.00E+00	9.08E-01	1.00E+00	7.41E-01	1.00E+00	9.63E-01	1.00E+00	6.91E-01	1.00E+00	8.22E-01	1.00E+00	8.73E-01	1.00E+00	7.05E-01	1.00E+00	response to other organism	P
GO:0051716	20	6.91E-02	1.00E+00	3.85E-01	1.00E+00	8.85E-02	1.00E+00	4.37E-01	1.00E+00	8.46E-02	1.00E+00	2.90E-01	1.00E+00	1.07E-01	1.00E+00	7.92E-01	1.00E+00	cellular response to stimulus	P
GO:0051726	385	6.11E-06	7.00E-03	7.26E-07	8.39E-03	2.43E-03	2.48E-01	7.01E-04	4.70E-02	9.80E-06	4.00E-03	1.05E-05	4.88E-03	2.82E-02	1.00E+00	4.59E-05	9.00E-03	regulation of cell cycle	P
GO:0051789	78	6.05E-05	1.10E-02	1.94E-05	9.58E-03	1.47E-02	6.93E-01	9.06E-02	1.00E+00	2.24E-05	5.00E-03	3.85E-06	2.97E-03	8.94E-02	1.00E+00	1.02E-01	1.00E+00	response to protein stimulus	P
GO:0051806	11	6.16E-01	1.00E+00	2.35E-01	1.00E+00	9.19E-01	1.00E+00	3.58E-01	1.00E+00	5.71E-01	1.00E+00	2.09E-01	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	entry into cell of other organism during sym	P
GO:0051828	11	6.16E-01	1.00E+00	2.35E-01	1.00E+00	9.19E-01	1.00E+00	3.58E-01	1.00E+00	5.71E-01	1.00E+00	2.09E-01	1.00E+00	2.94E-01	1.00E+00	3.08E-01	1.00E+00	entry into other organism during symbiotic i	P
GO:0051869	1924	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	physiological response to stimulus	P
GO:0051881	11	5.89E-03	3.50E-01	1.42E-01	1.00E+00	3.25E-02	1.00E+00	4.67E-02	1.00E+00	2.34E-03	2.85E-01	3.33E-01	1.00E+00	1.08E-01	1.00E+00	4.20E-01	1.00E+00	regulation of mitochondrial membrane potei	P
GO:0051899	14	6.94E-02	1.00E+00	2.34E-01	1.00E+00	1.68E-01	1.00E+00	6.78E-02	1.00E+00	2.14E-01	1.00E+00	4.29E-01	1.00E+00	1.08E-01	1.00E+00	7.79E-01	1.00E+00	membrane depolarization	P
GO:0051924	22	4.42E-01	1.00E+00	3.45E-01	1.00E+00	4.45E-01	1.00E+00	9.70E-01	1.00E+00	5.55E-01	1.00E+00	2.87E-01	1.00E+00	2.08E-01	1.00E+00	1.71E-01	1.00E+00	regulation of calcium ion transport	P
GO:0051969	66	1.27E-01	1.00E+00	5.61E-01	1.00E+00	2.53E-01	1.00E+00	2.56E-01	1.00E+00	6.20E-02	1.00E+00	5.91E-01	1.00E+00	5.40E-01	1.00E+00	8.65E-01	1.00E+00	regulation of transmission of nerve impulse	P
GO:0051970	10	6.57E-01	1.00E+00	9.98E-01	1.00E+00	7.70E-01	1.00E+00	9.19E-01	1.00E+00	4.33E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	negative regulation of transmission of nerve	P
GO:0051971	20	5.51E-02	1.00E+00	1.85E-01	1.00E+00	1.04E-01	1.00E+00	2.22E-01	1.00E+00	4.39E-02	1.00E+00	2.50E-01	1.00E+00	2.34E-01	1.00E+00	2.20E-01	1.00E+00	positive regulation of transmission of nerve	P
GO:0055001	17	9.24E-01	1.00E+00	6.47E-02	1.00E+00	2.77E-01	1.00E+00	1.87E-02	1.00E+00	9.90E-01	1.00E+00	1.42E-01	1.00E+00	9.96E-01	1.00E+00	8.32E-01	1.00E+00	muscle cell development	P
GO:0055002	16	8.56E-01	1.00E+00	6.97E-02	1.00E+00	2.67E-01	1.00E+00	3.82E-02	1.00E+00	9.77E-01	1.00E+00	1.20E-01	1.00E+00	9.92E-01	1.00E+00	7.71E-01	1.00E+00	striated muscle cell development	P
GO:0055008	18	9.62E-01	1.00E+00	8.79E-01	1.00E+00	9.82E-01	1.00E+00	6.10E-01	1.00E+00	9.52E-01	1.00E+00	6.82E-01	1.00E+00	5.42E-01	1.00E+00	1.00E+00	1.00E+00	cardiac muscle morphogensis	P
GO:0055010	16	9.22E-01	1.00E+00	8.76E-01	1.00E+00	9.82E-01	1.00E+00	7.22E-01	1.00E+00	9.12E-01	1.00E+00	6.71E-01	1.00E+00	4.06E-01	1.00E+00	9.99E-01	1.00E+00	ventricular cardiac muscle morphogenesis	P

		Alu+		Alu-		AluJ+		AluJ-		AluS+		AluS-		AluY+		AluY-			
GO term id	genes	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	GO term description	GO term catecory
GO:0000003	491	9.97E-01	1.00E+00	9.79E-01	1.00E+00	7.79E-01	1.00E+00	6.59E-01	1.00E+00	9.97E-01	1.00E+00	9.54E-01	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	reproduction	P
GO:0000018	11	4.82E-01	1.00E+00	9.22E-02	1.00E+00	4.65E-01	1.00E+00	2.63E-01	1.00E+00	3.64E-01	1.00E+00	8.24E-02	1.00E+00	8.73E-01	1.00E+00	4.22E-01	1.00E+00	regulation of DNA recombination	P
GO:0000030	14	2.56E-01	1.00E+00	5.28E-02	1.00E+00	8.35E-01	1.00E+00	3.35E-01	1.00E+00	1.41E-01	1.00E+00	4.16E-02	1.00E+00	2.58E-01	1.00E+00	4.61E-01	1.00E+00	mannosyltransferase activity	F
GO:0000041	74	7.08E-01	1.00E+00	3.67E-01	1.00E+00	5.68E-01	1.00E+00	4.47E-01	1.00E+00	6.85E-01	1.00E+00	2.06E-01	1.00E+00	8.18E-01	1.00E+00	9.55E-01	1.00E+00	transition metal ion transport	P
GO:0000045	11	2.82E-01	1.00E+00	2.11E-01	1.00E+00	5.79E-01	1.00E+00	8.70E-01	1.00E+00	2.43E-01	1.00E+00	8.99E-02	1.00E+00	3.26E-01	1.00E+00	5.49E-01	1.00E+00	autophagic vacuole formation	P
GO:0000049	21	1.77E-01	1.00E+00	1.27E-02	3.84E-01	2.23E-01	1.00E+00	4.17E-02	1.00E+00	2.40E-01	1.00E+00	5.56E-02	1.00E+00	4.21E-01	1.00E+00	4.52E-02	8.10E-01	tRNA binding	F
GO:0000051	22	7.41E-01	1.00E+00	9.70E-01	1.00E+00	5.70E-01	1.00E+00	9.43E-01	1.00E+00	5.52E-01	1.00E+00	9.46E-01	1.00E+00	1.00E+00	1.00E+00	8.40E-01	1.00E+00	urea cycle intermediate metabolism	P
GO:0000059	17	4.16E-02	1.00E+00	1.34E-02	3.84E-01	3.08E-02	5.65E-01	3.41E-02	5.42E-01	7.43E-02	1.00E+00	9.45E-03	1.43E-01	1.63E-01	1.00E+00	2.85E-01	1.00E+00	protein import into nucleus, docking	P
GO:0000060	24	4.11E-01	1.00E+00	6.55E-01	1.00E+00	6.50E-01	1.00E+00	2.04E-01	1.00E+00	2.36E-01	1.00E+00	5.59E-01	1.00E+00	9.49E-01	1.00E+00	1.00E+00	1.00E+00	protein import into nucleus, translocation	P
GO:0000062	12	7.57E-04	1.60E-02	6.61E-03	1.50E-01	6.53E-02	1.00E+00	1.19E-01	1.00E+00	8.78E-05	2.00E-03	1.97E-03	5.10E-02	7.38E-01	1.00E+00	9.38E-01	1.00E+00	acyl-CoA binding	F
GO:0000070	31	3.97E-01	1.00E+00	1.59E-01	1.00E+00	4.43E-01	1.00E+00	2.98E-01	1.00E+00	6.57E-01	1.00E+00	3.27E-01	1.00E+00	1.10E-01	1.00E+00	1.39E-01	1.00E+00	mitotic sister chromatid segregation	P
GO:0000074	363	2.33E-01	1.00E+00	3.45E-01	1.00E+00	1.86E-03	1.80E-02	1.96E-02	4.10E-01	4.73E-01	1.00E+00	7.44E-01	1.00E+00	9.62E-01	1.00E+00	4.93E-01	1.00E+00	regulation of progression through cell cycle	P
GO:0000075	68	2.31E-02	1.00E+00	6.56E-04	1.90E-02	1.16E-03	1.25E-02	2.91E-03	5.60E-02	1.10E-01	1.00E+00	1.52E-03	3.00E-02	2.32E-01	1.00E+00	1.14E-01	1.00E+00	cell cycle checkpoint	P
GO:0000077	33	6.80E-02	1.00E+00	1.97E-02	9.24E-01	1.62E-02	1.92E-01	1.96E-02	4.10E-01	1.05E-01	1.00E+00	4.65E-02	1.00E+00	4.04E-01	1.00E+00	2.71E-01	1.00E+00	DNA damage checkpoint	P
GO:0000079	47	2.76E-01	1.00E+00	1.28E-01	1.00E+00	1.75E-01	1.00E+00	1.44E-02	2.81E-01	2.92E-01	1.00E+00	4.65E-01	1.00E+00	9.56E-01	1.00E+00	3.32E-01	1.00E+00	regulation of cyclin-dependent protein kinas	P
GO:0000080	16	1.55E-01	1.00E+00	1.35E-01	1.00E+00	3.08E-02	5.65E-01	6.19E-02	1.00E+00	2.49E-01	1.00E+00	2.55E-01	1.00E+00	3.91E-01	1.00E+00	2.79E-01	1.00E+00	G1 phase of mitotic cell cycle	P
GO:0000082	45	2.59E-01	1.00E+00	5.44E-01	1.00E+00	1.34E-01	1.00E+00	8.68E-02	1.00E+00	2.07E-01	1.00E+00	8.93E-01	1.00E+00	9.26E-01	1.00E+00	5.32E-01	1.00E+00	G1/S transition of mitotic cell cycle	P
GO:0000084	15	3.73E-01	1.00E+00	3.20E-01	1.00E+00	5.03E-01	1.00E+00	5.80E-01	1.00E+00	5.11E-01	1.00E+00	3.07E-01	1.00E+00	1.58E-01	1.00E+00	2.13E-01	1.00E+00	S phase of mitotic cell cycle	P
GO:0000086	20	6.93E-02	1.00E+00	3.78E-02	1.00E+00	3.48E-02	5.87E-01	1.25E-02	1.57E-01	1.25E-01	1.00E+00	9.19E-02	1.00E+00	1.72E-01	1.00E+00	2.34E-01	1.00E+00	G2/M transition of mitotic cell cycle	P
GO:0000087	226	6.46E-03	1.37E-01	5.38E-07	1.00E-03	7.15E-04	1.25E-02	5.71E-06	8.32E-04	7.04E-02	1.00E+00	1.97E-05	2.29E-03	4.30E-01	1.00E+00	6.24E-03	6.60E-02	M phase of mitotic cell cycle	P
GO:0000096	20	3.83E-01	1.00E+00	4.05E-01	1.00E+00	1.87E-01	1.00E+00	1.42E-01	1.00E+00	5.21E-01	1.00E+00	4.55E-01	1.00E+00	6.82E-01	1.00E+00	7.97E-01	1.00E+00	sulfur amino acid metabolism	P
GO:0000097	13	7.29E-01	1.00E+00	6.67E-01	1.00E+00	2.09E-01	1.00E+00	2.39E-01	1.00E+00	9.29E-01	1.00E+00	7.20E-01	1.00E+00	7.91E-01	1.00E+00	9.98E-01	1.00E+00	sulfur amino acid biosynthesis	P
GO:0000118	27	1.86E-01	1.00E+00	7.09E-02	1.00E+00	1.48E-01	1.00E+00	3.13E-01	1.00E+00	2.65E-01	1.00E+00	9.46E-02	1.00E+00	4.32E-01	1.00E+00	1.66E-01	1.00E+00	histone deacetylase complex	C
GO:0000119	25	1.35E-01	1.00E+00	3.08E-02	1.00E+00	2.66E-01	1.00E+00	2.12E-01	1.00E+00	1.45E-01	1.00E+00	1.60E-02	5.65E-01	6.24E-01	1.00E+00	1.19E-01	1.00E+00	mediator complex	C
GO:0000122	190	9.97E-01	1.00E+00	9.81E-01	1.00E+00	8.66E-01	1.00E+00	7.84E-01	1.00E+00	9.91E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	negative regulation of transcription from RN	P
GO:0000123	12	2.62E-01	1.00E+00	4.14E-01	1.00E+00	9.66E-02	1.00E+00	1.36E-01	1.00E+00	3.55E-01	1.00E+00	6.61E-01	1.00E+00	4.74E-01	1.00E+00	3.85E-01	1.00E+00	histone acetyltransferase complex	C
GO:0000139	348	4.77E-01	1.00E+00	2.93E-01	1.00E+00	7.76E-04	1.25E-02	2.03E-02	4.10E-01	7.40E-01	1.00E+00	4.26E-01	1.00E+00	9.97E-01	1.00E+00	9.61E-01	1.00E+00	Golgi membrane	C
GO:0000146	15	6.12E-01	1.00E+00	9.32E-01	1.00E+00	4.84E-01	1.00E+00	8.89E-01	1.00E+00	6.86E-01	1.00E+00	8.86E-01	1.00E+00	4.77E-01	1.00E+00	9.77E-01	1.00E+00	microfilament motor activity	F
GO:0000149	29	9.78E-01	1.00E+00	7.81E-01	1.00E+00	3.63E-01	1.00E+00	1.50E-01	1.00E+00	9.75E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	SNARE binding	F
GO:0000151	96	1.50E-01	1.00E+00	1.29E-01	1.00E+00	1.08E-02	1.57E-01	1.80E-03	2.70E-02	5.02E-01	1.00E+00	3.57E-01	1.00E+00	2.90E-01	1.00E+00	8.10E-01	1.00E+00	ubiquitin ligase complex	C
GO:0000152	16	1.07E-01	1.00E+00	3.62E-02	1.00E+00	5.47E-02	1.00E+00	3.00E-02	5.42E-01	1.06E-01	1.00E+00	5.36E-02	1.00E+00	8.82E-01	1.00E+00	5.55E-01	1.00E+00	nuclear ubiquitin ligase complex	C
GO:0000155	13	7.13E-01	1.00E+00	9.92E-01	1.00E+00	5.06E-01	1.00E+00	9.49E-01	1.00E+00	7.73E-01	1.00E+00	9.55E-01	1.00E+00	5.62E-01	1.00E+00	9.66E-01	1.00E+00	two-component sensor activity	F
GO:0000159	23	5.51E-01	1.00E+00	5.10E-01	1.00E+00	3.73E-01	1.00E+00	2.12E-01	1.00E+00	6.95E-01	1.00E+00	4.91E-01	1.00E+00	4.14E-01	1.00E+00	8.19E-01	1.00E+00	protein phosphatase type 2A complex	C
GO:0000160	11	7.23E-01	1.00E+00	1.00E+00	1.00E+00	8.36E-01	1.00E+00	9.88E-01	1.00E+00	7.99E-01	1.00E+00	1.00E+00	1.00E+00	6.07E-01	1.00E+00	7.55E-01	1.00E+00	two-component signal transduction system	P
GO:0000165	187	9.88E-01	1.00E+00	9.99E-01	1.00E+00	9.35E-01	1.00E+00	5.68E-01	1.00E+00	9.72E-01	1.00E+00	9.99E-01	1.00E+00	9.80E-01	1.00E+00	9.99E-01	1.00E+00	MAPKKK cascade	P
GO:0000166	2323	5.32E-03	1.37E-01	4.95E-06	1.41E-03	6.07E-11	0.00E+00	7.84E-08	0.00E+00	2.28E-01	1.00E+00	5.96E-04	1.02E-02	9.55E-01	1.00E+00	7.30E-01	1.00E+00	nucleotide binding	F
GO:0000178	11	2.21E-01	1.00E+00	2.94E-01	1.00E+00	1.37E-01	1.00E+00	1.88E-01	1.00E+00	1.42E-01	1.00E+00	2.24E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	exosome (RNase complex)	C
GO:0000184	21	1.56E-03	4.90E-02	3.15E-05	3.00E-03	3.17E-04	7.18E-03	1.57E-05	2.00E-03	4.40E-02	1.00E+00	1.53E-04	2.29E-03	7.19E-03	2.07E-01	3.09E-01	1.00E+00	mRNA catabolism, nonsense-mediated dec	P
GO:0000186	16	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	7.41E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	activation of MAPKK activity	P
GO:0000187	69	8.27E-01	1.00E+00	8.11E-01	1.00E+00	9.77E-01	1.00E+00	4.87E-01	1.00E+00	6.59E-01	1.00E+00	7.93E-01	1.00E+00	7.40E-01	1.00E+00	9.77E-01	1.00E+00	activation of MAPK activity	P
GO:0000188	20	9.98E-01	1.00E+00	9.96E-01	1.00E+00	7.84E-01	1.00E+00	9.95E-01	1.00E+00	9.94E-01	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inactivation of MAPK activity	P
GO:0000209	15	3.29E-01	1.00E+00	3.01E-02	1.00E+00	1.64E-01	1.00E+00	1.34E-02	2.81E-01	3.87E-01	1.00E+00	4.33E-02	1.00E+00	4.23E-01	1.00E+00	1.42E-01	1.00E+00	protein polyubiquitination	P
GO:0000226	106	1.77E-01	1.00E+00	9.07E-02	1.00E+00	4.06E-02	5.87E-01	6.21E-02	1.00E+00	2.73E-01	1.00E+00	9.03E-02	1.00E+00	5.20E-01	1.00E+00	6.93E-01	1.00E+00	microtubule cytoskeleton organization and b	P
GO:0000228	110	6.56E-02	1.00E+00	2.85E-03	5.10E-02	3.22E-02	5.87E-01	2.09E-02	4.10E-01	8.73E-02	1.00E+00	7.86E-03	1.05E-01	7.20E-01	1.00E+00	7.66E-02	1.00E+00	nuclear chromosome	C
GO:0000242	12	1.19E-02	2.72E-01	3.07E-02	1.00E+00	1.33E-02	1.92E-01	3.81E-02	1.00E+00	6.60E-02	1.00E+00	1.22E-01	1.00E+00	2.54E-01	1.00E+00	1.15E-01	1.00E+00	pericentriolar material	C
GO:0000245	36	3.98E-02	1.00E+00	1.22E-02	3.84E-01	1.52E-02	1.92E-01	1.44E-02	2.81E-01	1.73E-01	1.00E+00	3.02E-02	1.00E+00	2.06E-01	1.00E+00	2.48E-01	1.00E+00	spliceosome assembly	P
GO:0000267	855	1.00E+00	1.00E+00	9.84E-01	1.00E+00	7.68E-01	1.00E+00	1.32E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell fraction	C
GO:0000271	47	4.67E-01	1.00E+00	8.08E-01	1.00E+00	8.89E-02	1.00E+00	4.33E-01	1.00E+00	6.00E-01	1.00E+00	7.41E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	polysaccharide biosynthesis	P
GO:0000272	16	9.49E-01	1.00E+00	9.71E-01	1.00E+00	4.63E-01	1.00E+00	6.18E-01	1.00E+00	9.84E-01	1.00E+00	9.92E-01	1.00E+00	9.80E-01	1.00E+00	8.48E-01	1.00E+00	polysaccharide catabolism	P
GO:0000278	387	6.92E-03	1.37E-01	2.68E-06	1.41E-03	4.11E-04	1.25E-02	3.67E-07	0.00E+00	2.95E-02	6.55E-01	2.06E-04	2.90E-03	7.99E-01	1.00E+00	4.36E-02	8.10E-01	mitotic cell cycle	P
GO:0000279	299	4.22E-03	1.37E-01	1.19E-08	1.00E-03	1.52E-03	1.60E-02	2.45E-06	0.00E+00	3.50E-02	6.55E-01	1.34E-06	1.67E-03	3.45E-01	1.00E+00	7.43E-04	9.50E-03	M phase	P
GO:0000287	416	2.76E-01	1.00E+00	1.06E-01	1.00E+00	7.11E-04	1.25E-02	4.28E-03	6.84E-02	6.41E-01	1.00E+00	3.91E-01	1.00E+00	9.91E-01	1.00E+00	5.26E-01	1.00E+00	magnesium ion binding	F
GO:0000299	12	6.45E-01	1.00E+00	2.04E-01	1.00E+00	2.71E-01	1.00E+00	4.25E-02	1.00E+00	6.34E-01	1.00E+00	2.88E-01	1.00E+00	1.00E+00	1.00E+00	6.23E-01	1.00E+00	integral to membrane of membrane fraction	C
GO:0000302	36	5.40E-01	1.00E+00	6.24E-01	1.00E+00	4.32E-01	1.00E+00	8.34E-01	1.00E+00	6.41E-01	1.00E+00	4.71E-01	1.00E+00	3.55E-01	1.00E+00	8.22E-01	1.00E+00	response to reactive oxygen species	P
GO:0000313	50	1.09E-01	1.00E+00	2.79E-01	1.00E+00	9.73E-01	1.00E+00	1.14E-01	1.00E+00	1.91E-02	3.81E-01	4.39E-01	1.00E+00	7.50E-01	1.00E+00	7.29E-01	1.00E+00	organellar ribosome	C
GO:0000314	20	2.25E-02	1.00E+00	5.77E-01	1.00E+00	9.96E-01	1.00E+00	3.84E-01	1.00E+00	8.70E-03	2.02E-01	7.64E-01	1.00E+00	1.80E-01	1.00E+00	3.40E-01	1.00E+00	organellar small ribosomal subunit	C
GO:0000315	17	8.38E-01	1.00E+00	6.91E-01	1.00E+00	9.97E-01	1.00E+00	3.45E-01	1.00E+00	3.76E-01	1.00E+00	6.68E-01	1.00E+00	1.00E+00	1.00E+00	8.86E-01	1.00E+00	organellar large ribosomal subunit	C
GO:0000323	213	2.20E-01	1.00E+00	8.04E-02	1.00E+00	4.54E-02	8.68E-01	9.39E-03	1.12E-01	3.08E-01	1.00E+00	1.28E-01	1.00E+00	7.37E-01	1.00E+00	7.55E-01	1.00E+00	lytic vacuole	C
GO:0000375	158	1.58E-05	5.00E-03	7.30E-07	1.00E-03	3.12E-04	7.18E-03	3.78E-04	7.17E-03	1.90E-03	4.30E-02	1.53E-05	2.29E-03	2.57E-02	2.56E-01	8.93E-03	6.60E-02	RNA splicing, via transesterification reactior	P
GO:0000377	158	1.58E-05	5.00E-03	7.30E-07	1.00E-03	3.12E-04	7.18E-03	3.78E-04	7.17E-03	1.90E-03	4.30E-02	1.53E-05	2.29E-03	2.57E-02	2.56E-01	8.93E-03	6.60E-02	RNA splicing, via transesterification reactior	P
GO:0000387	28	1.07E-04	5.00E-03	4.30E-04	1.90E-02	1.91E-02	2.36E-01	7.88E-04	1.03E-02	1.24E-02	3.01E-01	3.96E-03	7.40E-02	1.70E-02	2.07E-01	1.85E-01	1.00E+00	spliceosomal snRNP biogenesis	P
GO:0000398	158	1.58E-05	5.00E-03	7.30E-07	1.00E-03	3.12E-04	7.18E-03	3.78E-04	7.17E-03	1.90E-03	4.30E-02	1.53E-05	2.29E-03	2.57E-02	2.56E-01	8.93E-03	6.60E-02	nuclear mRNA splicing, via spliceosome	P
GO:0000502	51	9.44E-02	1.00E+00	2.80E-01	1.00E+00	2.89E-01	1.00E+00	1.48E-02	2.81E-01	8.30E-02	1.00E+00	4.63E-01	1.00E+00	3.94E-01	1.00E+00	7.58E-01	1.00E+00	proteasome complex (sensu Eukaryota)	C
GO:0000718	23	4.81E-02	1.00E+00	1.05E-01	1.00E+00	1.70E-01	1.00E+00	1.03E-01	1.00E+00	4.25E-02	1.00E+00	1.13E-01	1.00E+00	3.24E-01	1.00E+00	5.25E-01	1.00E+00	nucleotide-excision repair, DNA damage rer	P
GO:0000723	28	2.57E-01	1.00E+00	9.08E-02	1.00E+00	2.01E-01	1.00E+00	9.74E-02	1.00E+00	2.18E-01	1.00E+00	3.05E-01	1.00E+00	7.83E-01	1.00E+00	7.58E-02	1.00E+00	telomere maintenance	P
GO:0000724	15	4.65E-01	1.00E+00	7.54E-02	1.00E+00	3.39E-01	1.00E+00	5.90E-02	1.00E+00	4.79E-01	1.00E+00	1.15E-01	1.00E+00	6.96E-01	1.00E+00	6.59E-02	1.00E+00	double-strand break repair via homologous	P
GO:0000725	15	4.65E-01	1.00E+00	7.54E-02	1.00E+00	3.39E-01	1.00E+00	5.90E-02	1.00E+00	4.79E-01	1.00E+00	1.15E-01	1.00E+00	6.96E-01	1.00E+00	6.59E-02	1.00E+00	recombinational repair	P
GO:0000726	12	5.46E-01	1.00E+00	3.59E-02	1.00E+00	4.67E-01	1.00E+00	3.96E-02	1.00E+00	5.69E-01	1.00E+00	5.16E-02	1.00E+00	6.26E-01	1.00E+00	1.46E-01	1.00E+00	non-recombinational repair	P
GO:0000775	83	6.16E-03	1.37E-01	1.46E-05	2.21E-03	2.46E-03	1.80E-02	8.76E-05	3.91E-03	3.37E-02	6.55E-01	3.84E-05	2.29E-03	2.83E-01	1.00E+00	1.79E-02	1.77E-01	chromosome, pericentric region	C
GO:0000776	46	1.42E-02	2.72E-01	3.53E-05	3.00E-03	1.53E-05	9.71E-04	1.70E-05	2.00E-03	7.55E-02	1.00E+00	1.66E-04	2.29E-03	8.29E-01	1.00E+00	1.32E-02	1.38E-01	kinetochore	C
GO:0000777	29	5.49E-02	1.00E+00	2.69E-03	5.10E-02	5.30E-05	4.57E-03	1.21E-03	1.30E-02	2.30E-01	1.00E+00	6.97E-03	1.05E-01	9.00E-01	1.00E+00	3.46E-02	4.55E-01	condensed chromosome kinetochore	C
GO:0000779	34	1.14E-01	1.00E+00	2.69E-03	5.10E-02	4.49E-04	1.25E-02	2.02E-03	2.70E-02	4.19E-01	1.00E+00	7.27E-03	1.05E-01	8.19E-01	1.00E+00	5.14E-02	8.10E-01	condensed chromosome, pericentric region	C
GO:0000781	24	3.43E-01	1.00E+00	9.54E-02	1.00E+00	3.75E-01	1.00E+00	1.59E-01	1.00E+00	2.61E-01	1.00E+00	1.39E-01	1.00E+00	6.36E-01	1.00E+00	2.52E-01	1.00E+00	chromosome, telomeric region	C

GO:0000785	229	2.91E-01	1.00E+00	2.00E-01	1.00E+00	3.99E-01	1.00E+00	3.04E-01	1.00E+00	1.73E-01	1.00E+00	1.60E-01	1.00E+00	9.96E-01	1.00E+00	8.34E-01	1.00E+00	chromatin	C
GO:0000786	89	4.17E-01	1.00E+00	6.77E-01	1.00E+00	6.53E-01	1.00E+00	6.40E-01	1.00E+00	2.87E-01	1.00E+00	5.30E-01	1.00E+00	9.71E-01	1.00E+00	9.91E-01	1.00E+00	nucleosome	C
GO:0000790	33	1.59E-01	1.00E+00	2.08E-02	9.24E-01	1.40E-01	1.00E+00	1.31E-01	1.00E+00	1.33E-01	1.00E+00	2.37E-02	7.69E-01	9.43E-01	1.00E+00	5.69E-02	1.00E+00	nuclear chromatin	C
GO:0000792	37	7.00E-01	1.00E+00	1.24E-01	1.00E+00	3.11E-01	1.00E+00	2.23E-01	1.00E+00	6.35E-01	1.00E+00	1.65E-01	1.00E+00	1.00E+00	1.00E+00	6.66E-02	1.00E+00	heterochromatin	C
GO:0000793	83	1.00E-02	1.77E-01	1.06E-05	1.41E-03	5.32E-05	4.57E-03	5.57E-04	7.17E-03	9.15E-02	1.00E+00	6.77E-05	2.29E-03	2.79E-01	1.00E+00	1.14E-02	1.38E-01	condensed chromosome	C
GO:0000794	39	1.41E-01	1.00E+00	2.26E-03	5.10E-02	2.45E-01	1.00E+00	6.90E-02	1.00E+00	2.53E-01	1.00E+00	5.30E-03	7.40E-02	1.42E-01	1.00E+00	8.36E-02	1.00E+00	condensed nuclear chromosome	C
GO:0000795	17	1.22E-01	1.00E+00	1.58E-02	3.84E-01	3.96E-01	1.00E+00	1.41E-01	1.00E+00	1.05E-01	1.00E+00	1.60E-02	5.65E-01	1.98E-01	1.00E+00	2.47E-01	1.00E+00	synaptonemal complex	C
GO:0000803	13	7.27E-01	1.00E+00	5.46E-01	1.00E+00	3.35E-01	1.00E+00	6.64E-01	1.00E+00	7.80E-01	1.00E+00	6.35E-01	1.00E+00	9.83E-01	1.00E+00	2.62E-01	1.00E+00	sex chromosome	C
GO:0000819	32	2.62E-01	1.00E+00	1.21E-01	1.00E+00	3.31E-01	1.00E+00	2.45E-01	1.00E+00	4.69E-01	1.00E+00	2.56E-01	1.00E+00	1.01E-01	1.00E+00	1.38E-01	1.00E+00	sister chromatid segregation	P
GO:0000902	590	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell morphogenesis	P
GO:0000904	194	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cellular morphogenesis during differentiatio	P
GO:0000910	34	2.79E-01	1.00E+00	2.45E-01	1.00E+00	1.62E-01	1.00E+00	5.87E-01	1.00E+00	4.37E-01	1.00E+00	2.14E-01	1.00E+00	1.72E-01	1.00E+00	4.73E-01	1.00E+00	cytokinesis	P
GO:0000922	24	1.65E-01	1.00E+00	2.74E-04	8.26E-03	3.74E-02	5.87E-01	1.19E-02	1.27E-01	2.30E-01	1.00E+00	4.97E-04	1.02E-02	9.72E-01	1.00E+00	4.61E-03	6.60E-02	spindle pole	C
GO:0000930	10	3.16E-02	1.00E+00	1.14E-02	3.84E-01	1.87E-02	2.36E-01	6.84E-02	1.00E+00	3.68E-02	1.00E+00	2.35E-02	7.69E-01	5.09E-01	1.00E+00	5.50E-02	1.00E+00	gamma-tubulin complex	C
GO:0001501	312	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	skeletal development	P
GO:0001502	16	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cartilage condensation	P
GO:0001503	141	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.80E-01	1.00E+00	9.61E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	ossification	P
GO:0001505	102	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.42E-01	1.00E+00	5.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of neurotransmitter levels	P
GO:0001508	47	6.70E-01	1.00E+00	9.53E-01	1.00E+00	1.51E-01	1.00E+00	6.69E-01	1.00E+00	8.75E-01	1.00E+00	9.06E-01	1.00E+00	9.56E-01	1.00E+00	9.76E-01	1.00E+00	regulation of action potential	P
GO:0001518	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.67E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	voltage-gated sodium channel complex	C
GO:0001522	14	4.35E-02	1.00E+00	1.56E-01	1.00E+00	2.80E-02	4.97E-01	1.15E-01	1.00E+00	1.09E-01	1.00E+00	6.80E-01	1.00E+00	2.95E-01	1.00E+00	1.31E-01	1.00E+00	pseudouridine synthesis	P
GO:0001523	13	8.14E-01	1.00E+00	9.86E-01	1.00E+00	7.36E-01	1.00E+00	9.96E-01	1.00E+00	7.68E-01	1.00E+00	9.57E-01	1.00E+00	9.74E-01	1.00E+00	9.19E-01	1.00E+00	retinoid metabolism	P
GO:0001525	156	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.22E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	angiogenesis	P
GO:0001533	19	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.06E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cornified envelope	C
GO:0001539	43	8.18E-01	1.00E+00	9.61E-01	1.00E+00	5.60E-01	1.00E+00	8.31E-01	1.00E+00	6.70E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ciliary or flagellar motility	P
GO:0001540	11	9.93E-01	1.00E+00	9.98E-01	1.00E+00	2.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	beta-amyloid binding	F
GO:0001541	22	2.92E-01	1.00E+00	8.23E-01	1.00E+00	2.56E-01	1.00E+00	6.68E-01	1.00E+00	8.52E-01	1.00E+00	8.01E-01	1.00E+00	8.62E-02	1.00E+00	7.95E-01	1.00E+00	ovarian follicle development	P
GO:0001558	163	9.97E-01	1.00E+00	1.00E+00	1.00E+00	6.63E-01	1.00E+00	8.79E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	regulation of cell growth	P
GO:0001565	15	1.00E-01	1.00E+00	2.02E-01	1.00E+00	8.80E-02	1.00E+00	1.94E-01	1.00E+00	1.05E-01	1.00E+00	2.00E-01	1.00E+00	5.16E-01	1.00E+00	3.98E-01	1.00E+00	phorbol ester receptor activity	F
GO:0001568	221	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	blood vessel development	P
GO:0001569	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	patterning of blood vessels	P
GO:0001570	24	8.76E-01	1.00E+00	9.41E-01	1.00E+00	4.71E-01	1.00E+00	9.33E-01	1.00E+00	9.56E-01	1.00E+00	9.18E-01	1.00E+00	7.37E-01	1.00E+00	9.44E-01	1.00E+00	vasculogenesis	P
GO:0001584	654	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	rhodopsin-like receptor activity	F
GO:0001595	61	9.90E-01	1.00E+00	9.92E-01	1.00E+00	9.86E-01	1.00E+00	5.60E-01	1.00E+00	9.50E-01	1.00E+00	9.76E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	angiotensin receptor activity	F
GO:0001603	18	9.21E-01	1.00E+00	6.34E-01	1.00E+00	6.09E-01	1.00E+00	7.30E-01	1.00E+00	8.74E-01	1.00E+00	4.85E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	vasopressin-like receptor activity	F
GO:0001608	100	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.44E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	nucleotide receptor activity, G-protein coupl	F
GO:0001614	107	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.69E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	purinergic nucleotide receptor activity	F
GO:0001619	20	9.79E-01	1.00E+00	7.46E-01	1.00E+00	9.99E-01	1.00E+00	1.95E-01	1.00E+00	8.27E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	6.45E-01	1.00E+00	lysosphingolipid and lysophosphatidic acid r	F
GO:0001633	36	9.67E-01	1.00E+00	1.00E+00	1.00E+00	8.46E-01	1.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	9.98E-01	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	secretin-like receptor activity	F
GO:0001637	56	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	7.11E-01	1.00E+00	9.94E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	G-protein chemoattractant receptor activity	F
GO:0001649	45	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.99E-01	1.00E+00	osteoblast differentiation	P
GO:0001653	261	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.70E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity	F
GO:0001654	72	9.67E-01	1.00E+00	9.75E-01	1.00E+00	4.67E-01	1.00E+00	9.95E-01	1.00E+00	9.77E-01	1.00E+00	9.62E-01	1.00E+00	9.32E-01	1.00E+00	8.12E-01	1.00E+00	eye development	P
GO:0001655	78	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	urogenital system development	P
GO:0001656	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	metanephros development	P
GO:0001657	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ureteric bud development	P
GO:0001658	20	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ureteric bud branching	P
GO:0001659	204	9.99E-01	1.00E+00	9.98E-01	1.00E+00	4.23E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	thermoregulation	P
GO:0001662	10	9.01E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	9.15E-01	1.00E+00	8.41E-01	1.00E+00	9.96E-01	1.00E+00	6.35E-01	1.00E+00	9.45E-01	1.00E+00	behavioral fear response	P
GO:0001664	88	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein-coupled receptor binding	F
GO:0001666	72	4.36E-01	1.00E+00	9.28E-01	1.00E+00	6.09E-02	1.00E+00	8.51E-01	1.00E+00	4.99E-01	1.00E+00	9.03E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	response to hypoxia	P
GO:0001669	31	7.56E-01	1.00E+00	8.43E-01	1.00E+00	9.78E-01	1.00E+00	8.40E-01	1.00E+00	7.18E-01	1.00E+00	8.53E-01	1.00E+00	2.76E-01	1.00E+00	6.15E-01	1.00E+00	acrosome	C
GO:0001701	109	7.46E-01	1.00E+00	3.75E-01	1.00E+00	8.48E-01	1.00E+00	1.51E-01	1.00E+00	6.87E-01	1.00E+00	7.97E-01	1.00E+00	7.31E-01	1.00E+00	6.93E-02	1.00E+00	embryonic development (sensu Mammalia)	P
GO:0001702	14	4.78E-01	1.00E+00	4.31E-01	1.00E+00	2.46E-01	1.00E+00	7.47E-02	1.00E+00	4.47E-01	1.00E+00	5.33E-01	1.00E+00	9.78E-01	1.00E+00	9.51E-01	1.00E+00	gastrulation (sensu Deuterostomia)	P
GO:0001704	37	9.89E-01	1.00E+00	9.78E-01	1.00E+00	9.92E-01	1.00E+00	4.69E-01	1.00E+00	9.54E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	formation of primary germ layer	P
GO:0001707	33	9.48E-01	1.00E+00	9.73E-01	1.00E+00	9.65E-01	1.00E+00	3.40E-01	1.00E+00	8.53E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mesoderm formation	P
GO:0001708	26	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell fate specification	P
GO:0001709	35	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell fate determination	P
GO:0001725	18	8.12E-01	1.00E+00	4.52E-01	1.00E+00	6.32E-01	1.00E+00	3.16E-01	1.00E+00	9.35E-01	1.00E+00	3.39E-01	1.00E+00	4.86E-01	1.00E+00	8.84E-01	1.00E+00	stress fiber	C
GO:0001726	46	5.35E-01	1.00E+00	5.93E-01	1.00E+00	1.09E-01	1.00E+00	3.05E-01	1.00E+00	5.56E-01	1.00E+00	5.21E-01	1.00E+00	9.97E-01	1.00E+00	9.66E-01	1.00E+00	ruffle	C
GO:0001727	25	1.34E-01	1.00E+00	2.90E-01	1.00E+00	7.11E-02	1.00E+00	3.43E-01	1.00E+00	1.79E-01	1.00E+00	2.30E-01	1.00E+00	4.79E-01	1.00E+00	9.27E-01	1.00E+00	lipid kinase activity	F
GO:0001739	13	7.27E-01	1.00E+00	5.46E-01	1.00E+00	3.35E-01	1.00E+00	6.64E-01	1.00E+00	7.80E-01	1.00E+00	6.35E-01	1.00E+00	9.83E-01	1.00E+00	2.62E-01	1.00E+00	sex chromatin	C
GO:0001750	13	9.95E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.94E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	photoreceptor outer segment	C
GO:0001755	19	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.25E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	5.89E-01	1.00E+00	1.00E+00	1.00E+00	neural crest cell migration	P
GO:0001756	27	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	9.56E-01	1.00E+00	somitogenesis	P
GO:0001759	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	induction of an organ	P
GO:0001763	59	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	morphogenesis of a branching structure	P
GO:0001764	55	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.07E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	neuron migration	P
GO:0001772	24	1.97E-01	1.00E+00	9.97E-01	1.00E+00	1.21E-02	1.92E-01	6.98E-01	1.00E+00	6.60E-01	1.00E+00	1.00E+00	1.00E+00	8.47E-01	1.00E+00	8.87E-01	1.00E+00	immunological synapse	C
GO:0001775	289	8.28E-01	1.00E+00	9.99E-01	1.00E+00	3.82E-01	1.00E+00	9.97E-01	1.00E+00	7.82E-01	1.00E+00	9.83E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cell activation	P
GO:0001776	30	5.59E-01	1.00E+00	3.55E-01	1.00E+00	3.03E-01	1.00E+00	1.95E-01	1.00E+00	7.08E-01	1.00E+00	3.94E-01	1.00E+00	7.45E-01	1.00E+00	6.60E-01	1.00E+00	leukocyte homeostasis	P
GO:0001782	10	3.31E-01	1.00E+00	4.31E-01	1.00E+00	6.62E-02	1.00E+00	2.77E-01	1.00E+00	6.53E-01	1.00E+00	5.08E-01	1.00E+00	9.90E-01	1.00E+00	3.64E-01	1.00E+00	B cell homeostasis	P
GO:0001816	133	7.62E-01	1.00E+00	9.94E-01	1.00E+00	4.34E-01	1.00E+00	9.68E-01	1.00E+00	7.40E-01	1.00E+00	9.76E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	cytokine production	P
GO:0001817	18	9.06E-01	1.00E+00	9.77E-01	1.00E+00	7.25E-01	1.00E+00	8.95E-01	1.00E+00	9.55E-01	1.00E+00	9.87E-01	1.00E+00	6.77E-01	1.00E+00	6.67E-01	1.00E+00	regulation of cytokine production	P
GO:0001819	12	4.92E-01	1.00E+00	7.25E-01	1.00E+00	4.99E-01	1.00E+00	6.19E-01	1.00E+00	7.39E-01	1.00E+00	8.08E-01	1.00E+00	2.94E-01	1.00E+00	2.85E-01	1.00E+00	positive regulation of cytokine production	P

GO:0001822	68	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	kidney development	P
GO:0001824	30	8.04E-02	1.00E+00	2.02E-02	9.24E-01	4.03E-01	1.00E+00	1.59E-01	1.00E+00	5.99E-02	1.00E+00	3.96E-02	1.00E+00	2.71E-01	1.00E+00	4.81E-02	8.10E-01	blastocyst development	P
GO:0001825	10	1.12E-01	1.00E+00	1.81E-01	1.00E+00	2.25E-01	1.00E+00	5.85E-01	1.00E+00	1.32E-01	1.00E+00	1.46E-01	1.00E+00	1.98E-01	1.00E+00	3.04E-01	1.00E+00	blastocyst formation	P
GO:0001832	10	2.91E-01	1.00E+00	7.90E-02	1.00E+00	2.97E-01	1.00E+00	7.72E-01	1.00E+00	2.42E-01	1.00E+00	4.82E-02	1.00E+00	7.01E-01	1.00E+00	1.82E-01	1.00E+00	blastocyst growth	P
GO:0001836	15	3.06E-01	1.00E+00	8.63E-02	1.00E+00	3.03E-01	1.00E+00	2.36E-01	1.00E+00	3.89E-01	1.00E+00	1.11E-01	1.00E+00	1.91E-01	1.00E+00	3.33E-01	1.00E+00	release of cytochrome c from mitochondria	P
GO:0001837	13	9.27E-01	1.00E+00	9.90E-01	1.00E+00	8.90E-01	1.00E+00	5.31E-01	1.00E+00	8.48E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	epithelial to mesenchymal transition	P
GO:0001838	40	8.28E-01	1.00E+00	8.53E-01	1.00E+00	6.69E-01	1.00E+00	5.71E-01	1.00E+00	7.42E-01	1.00E+00	9.23E-01	1.00E+00	9.58E-01	1.00E+00	6.69E-01	1.00E+00	embryonic epithelial tube formation	P
GO:0001839	39	7.83E-01	1.00E+00	7.85E-01	1.00E+00	5.90E-01	1.00E+00	5.15E-01	1.00E+00	7.01E-01	1.00E+00	8.65E-01	1.00E+00	9.54E-01	1.00E+00	6.27E-01	1.00E+00	neural plate morphogenesis	P
GO:0001841	37	6.91E-01	1.00E+00	7.17E-01	1.00E+00	5.52E-01	1.00E+00	4.08E-01	1.00E+00	5.89E-01	1.00E+00	8.38E-01	1.00E+00	9.33E-01	1.00E+00	5.23E-01	1.00E+00	neural tube formation	P
GO:0001843	27	8.24E-01	1.00E+00	6.84E-01	1.00E+00	5.62E-01	1.00E+00	4.15E-01	1.00E+00	7.64E-01	1.00E+00	8.08E-01	1.00E+00	9.52E-01	1.00E+00	5.85E-01	1.00E+00	neural tube closure	P
GO:0001871	128	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	pattern binding	F
GO:0001889	26	4.79E-01	1.00E+00	4.70E-01	1.00E+00	2.70E-01	1.00E+00	3.75E-01	1.00E+00	5.45E-01	1.00E+00	6.12E-01	1.00E+00	7.12E-01	1.00E+00	2.49E-01	1.00E+00	liver development	P
GO:0001890	31	8.40E-01	1.00E+00	7.31E-01	1.00E+00	2.12E-01	1.00E+00	7.03E-01	1.00E+00	9.54E-01	1.00E+00	7.60E-01	1.00E+00	5.33E-01	1.00E+00	4.93E-01	1.00E+00	placenta development	P
GO:0001892	11	2.79E-01	1.00E+00	2.29E-01	1.00E+00	1.41E-01	1.00E+00	3.42E-01	1.00E+00	2.87E-01	1.00E+00	1.90E-01	1.00E+00	6.26E-01	1.00E+00	4.47E-01	1.00E+00	embryonic placenta development	P
GO:0001894	40	6.41E-01	1.00E+00	3.76E-01	1.00E+00	4.41E-01	1.00E+00	1.87E-01	1.00E+00	7.11E-01	1.00E+00	3.42E-01	1.00E+00	8.15E-01	1.00E+00	9.01E-01	1.00E+00	tissue homeostasis	P
GO:0001906	25	6.78E-01	1.00E+00	9.86E-01	1.00E+00	7.41E-01	1.00E+00	1.00E+00	1.00E+00	5.31E-01	1.00E+00	9.71E-01	1.00E+00	7.94E-01	1.00E+00	7.43E-01	1.00E+00	cell killing	P
GO:0001909	22	5.64E-01	1.00E+00	9.63E-01	1.00E+00	7.28E-01	1.00E+00	9.98E-01	1.00E+00	3.58E-01	1.00E+00	9.23E-01	1.00E+00	9.33E-01	1.00E+00	8.57E-01	1.00E+00	leukocyte mediated cytotoxicity	P
GO:0001910	12	4.11E-01	1.00E+00	9.29E-01	1.00E+00	8.91E-01	1.00E+00	9.40E-01	1.00E+00	2.78E-01	1.00E+00	8.73E-01	1.00E+00	7.07E-01	1.00E+00	9.32E-01	1.00E+00	regulation of leukocyte mediated cytotoxicity	P
GO:0001932	90	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.49E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of protein amino acid phosphoryl	P
GO:0001933	12	3.68E-01	1.00E+00	4.06E-01	1.00E+00	1.43E-01	1.00E+00	3.37E-01	1.00E+00	3.94E-01	1.00E+00	5.03E-01	1.00E+00	8.50E-01	1.00E+00	3.68E-01	1.00E+00	negative regulation of protein amino acid ph	P
GO:0001934	44	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.35E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of protein amino acid ph	P
GO:0001935	29	1.00E+00	1.00E+00	4.91E-01	1.00E+00	6.39E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	7.10E-01	1.00E+00	9.97E-01	1.00E+00	1.75E-01	1.00E+00	endothelial cell proliferation	P
GO:0001936	24	9.99E-01	1.00E+00	6.90E-01	1.00E+00	6.01E-01	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	8.44E-01	1.00E+00	9.97E-01	1.00E+00	2.39E-01	1.00E+00	regulation of endothelial cell proliferation	P
GO:0001937	15	9.99E-01	1.00E+00	8.44E-01	1.00E+00	3.90E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	7.49E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of endothelial cell prolife	P
GO:0001938	10	9.59E-01	1.00E+00	4.31E-01	1.00E+00	9.88E-01	1.00E+00	7.71E-01	1.00E+00	8.52E-01	1.00E+00	9.16E-01	1.00E+00	8.61E-01	1.00E+00	1.35E-01	1.00E+00	positive regulation of endothelial cell prolife	P
GO:0001942	31	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	hair follicle development	P
GO:0001944	225	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.02E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	vasculature development	P
GO:0001947	14	8.21E-01	1.00E+00	9.89E-01	1.00E+00	6.99E-01	1.00E+00	9.96E-01	1.00E+00	7.84E-01	1.00E+00	9.51E-01	1.00E+00	8.67E-01	1.00E+00	6.51E-01	1.00E+00	heart looping	P
GO:0001948	14	4.46E-01	1.00E+00	4.01E-01	1.00E+00	4.68E-01	1.00E+00	2.85E-01	1.00E+00	4.85E-01	1.00E+00	4.64E-01	1.00E+00	3.81E-01	1.00E+00	6.75E-01	1.00E+00	glycoprotein binding	F
GO:0001952	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	6.00E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	regulation of cell-matrix adhesion	P
GO:0001974	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.04E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	blood vessel remodeling	P
GO:0001976	17	9.94E-01	1.00E+00	1.00E+00	1.00E+00	6.38E-01	1.00E+00	9.85E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	fast regulation of arterial pressure	P
GO:0001990	14	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	9.12E-01	1.00E+00	9.92E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of blood pressure by hormones	P
GO:0002009	116	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	morphogenesis of an epithelium	P
GO:0002026	10	9.90E-01	1.00E+00	9.76E-01	1.00E+00	4.46E-01	1.00E+00	9.12E-01	1.00E+00	9.63E-01	1.00E+00	9.65E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	cardiac inotropy	P
GO:0002053	10	8.70E-01	1.00E+00	9.88E-01	1.00E+00	7.98E-01	1.00E+00	7.77E-01	1.00E+00	7.79E-01	1.00E+00	9.73E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of mesenchymal cell pro	P
GO:0002062	19	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chondrocyte differentiation	P
GO:0002064	11	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.74E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.96E-01	1.00E+00	epithelial cell development	P
GO:0002088	11	7.73E-01	1.00E+00	6.41E-01	1.00E+00	2.99E-01	1.00E+00	9.73E-01	1.00E+00	9.09E-01	1.00E+00	7.40E-01	1.00E+00	9.25E-01	1.00E+00	3.75E-01	1.00E+00	lens development (sensu Vertebrata)	P
GO:0002200	29	3.20E-01	1.00E+00	3.48E-01	1.00E+00	4.81E-01	1.00E+00	4.81E-01	1.00E+00	1.80E-01	1.00E+00	2.82E-01	1.00E+00	8.54E-01	1.00E+00	6.74E-01	1.00E+00	somatic diversification of immune receptors	P
GO:0002204	24	4.11E-01	1.00E+00	2.86E-01	1.00E+00	6.71E-01	1.00E+00	5.21E-01	1.00E+00	2.27E-01	1.00E+00	2.25E-01	1.00E+00	9.19E-01	1.00E+00	5.19E-01	1.00E+00	somatic recombination of immunoglobulin g	P
GO:0002208	24	4.11E-01	1.00E+00	2.86E-01	1.00E+00	6.71E-01	1.00E+00	5.21E-01	1.00E+00	2.27E-01	1.00E+00	2.25E-01	1.00E+00	9.19E-01	1.00E+00	5.19E-01	1.00E+00	somatic diversification of immunoglobulins	P
GO:0002209	10	9.01E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	9.15E-01	1.00E+00	8.41E-01	1.00E+00	9.96E-01	1.00E+00	6.35E-01	1.00E+00	9.45E-01	1.00E+00	behavioral defense response	P
GO:0002217	582	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	physiological defense response	P
GO:0002228	18	5.97E-01	1.00E+00	9.71E-01	1.00E+00	6.93E-01	1.00E+00	9.98E-01	1.00E+00	4.13E-01	1.00E+00	9.52E-01	1.00E+00	9.02E-01	1.00E+00	7.59E-01	1.00E+00	natural killer cell mediated immunity	P
GO:0002245	546	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	physiological response to wounding	P
GO:0002250	147	9.27E-01	1.00E+00	9.99E-01	1.00E+00	5.56E-01	1.00E+00	9.96E-01	1.00E+00	8.77E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	adaptive immune response	P
GO:0002252	189	9.51E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	9.99E-01	1.00E+00	8.06E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	immune effector process	P
GO:0002253	83	9.90E-01	1.00E+00	9.95E-01	1.00E+00	5.91E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	activation of immune response	P
GO:0002260	22	1.52E-01	1.00E+00	1.25E-01	1.00E+00	9.56E-02	1.00E+00	1.59E-01	1.00E+00	2.50E-01	1.00E+00	1.02E-01	1.00E+00	6.54E-01	1.00E+00	8.14E-01	1.00E+00	lymphocyte homeostasis	P
GO:0002263	17	2.76E-01	1.00E+00	4.02E-01	1.00E+00	2.46E-01	1.00E+00	5.60E-01	1.00E+00	1.70E-01	1.00E+00	2.66E-01	1.00E+00	9.84E-01	1.00E+00	8.80E-01	1.00E+00	cell activation during immune response	P
GO:0002274	36	2.31E-01	1.00E+00	4.13E-01	1.00E+00	1.88E-01	1.00E+00	8.09E-01	1.00E+00	2.24E-01	1.00E+00	2.22E-01	1.00E+00	8.36E-01	1.00E+00	8.29E-01	1.00E+00	myeloid leukocyte activation	P
GO:0002285	15	4.64E-01	1.00E+00	6.77E-01	1.00E+00	3.14E-01	1.00E+00	7.94E-01	1.00E+00	3.76E-01	1.00E+00	5.24E-01	1.00E+00	9.72E-01	1.00E+00	9.23E-01	1.00E+00	lymphocyte activation during immune respo	P
GO:0002286	13	3.45E-01	1.00E+00	6.14E-01	1.00E+00	2.36E-01	1.00E+00	7.79E-01	1.00E+00	2.80E-01	1.00E+00	4.28E-01	1.00E+00	9.35E-01	1.00E+00	9.48E-01	1.00E+00	T cell activation during immune response	P
GO:0002292	13	3.45E-01	1.00E+00	6.14E-01	1.00E+00	2.36E-01	1.00E+00	7.79E-01	1.00E+00	2.80E-01	1.00E+00	4.28E-01	1.00E+00	9.35E-01	1.00E+00	9.48E-01	1.00E+00	T cell differentiation during immune respons	P
GO:0002293	13	3.45E-01	1.00E+00	6.14E-01	1.00E+00	2.36E-01	1.00E+00	7.79E-01	1.00E+00	2.80E-01	1.00E+00	4.28E-01	1.00E+00	9.35E-01	1.00E+00	9.48E-01	1.00E+00	alpha-beta T cell differentiation during immu	P
GO:0002294	13	3.45E-01	1.00E+00	6.14E-01	1.00E+00	2.36E-01	1.00E+00	7.79E-01	1.00E+00	2.80E-01	1.00E+00	4.28E-01	1.00E+00	9.35E-01	1.00E+00	9.48E-01	1.00E+00	CD4-positive, alpha-beta T cell differentiatic	P
GO:0002366	17	2.76E-01	1.00E+00	4.02E-01	1.00E+00	2.46E-01	1.00E+00	5.60E-01	1.00E+00	1.70E-01	1.00E+00	2.66E-01	1.00E+00	9.84E-01	1.00E+00	8.80E-01	1.00E+00	leukocyte activation during immune respons	P
GO:0002367	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.21E-01	1.00E+00	cytokine production during immune respons	P
GO:0002376	1064	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	immune system process	P
GO:0002377	41	5.04E-01	1.00E+00	6.02E-01	1.00E+00	8.12E-01	1.00E+00	6.46E-01	1.00E+00	2.76E-01	1.00E+00	4.75E-01	1.00E+00	9.33E-01	1.00E+00	8.95E-01	1.00E+00	immunoglobulin production	P
GO:0002381	25	4.48E-01	1.00E+00	2.97E-01	1.00E+00	6.98E-01	1.00E+00	4.85E-01	1.00E+00	2.61E-01	1.00E+00	2.42E-01	1.00E+00	9.17E-01	1.00E+00	5.32E-01	1.00E+00	immunoglobulin production during immune	P
GO:0002429	38	3.42E-01	1.00E+00	6.62E-01	1.00E+00	3.79E-02	5.87E-01	8.40E-01	1.00E+00	4.52E-01	1.00E+00	5.08E-01	1.00E+00	1.00E+00	1.00E+00	9.27E-01	1.00E+00	immune response-activating cell surface re	P
GO:0002437	54	9.97E-01	1.00E+00	1.00E+00	1.00E+00	6.14E-01	1.00E+00	9.66E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	inflammatory response to antigenic stimulus	P
GO:0002438	48	9.91E-01	1.00E+00	9.98E-01	1.00E+00	8.34E-01	1.00E+00	8.99E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.53E-01	1.00E+00	9.93E-01	1.00E+00	acute inflammatory response to antigenic st	P
GO:0002440	50	3.68E-01	1.00E+00	8.60E-01	1.00E+00	9.31E-01	1.00E+00	9.02E-01	1.00E+00	1.40E-01	1.00E+00	7.47E-01	1.00E+00	9.90E-01	1.00E+00	9.39E-01	1.00E+00	production of molecular mediator of immune	P
GO:0002443	158	8.89E-01	1.00E+00	9.96E-01	1.00E+00	5.86E-01	1.00E+00	9.84E-01	1.00E+00	8.14E-01	1.00E+00	9.90E-01	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	leukocyte mediated immunity	P
GO:0002444	12	3.20E-02	1.00E+00	1.03E-01	1.00E+00	5.96E-02	1.00E+00	1.92E-01	1.00E+00	7.78E-02	1.00E+00	1.48E-01	1.00E+00	9.81E-02	1.00E+00	1.38E-01	1.00E+00	myeloid leukocyte mediated immunity	P
GO:0002449	148	9.86E-01	1.00E+00	9.99E-01	1.00E+00	8.48E-01	1.00E+00	9.94E-01	1.00E+00	9.57E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	lymphocyte mediated immunity	P
GO:0002455	32	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	9.88E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	humoral immune response mediated by circ	P
GO:0002456	19	5.78E-01	1.00E+00	8.37E-01	1.00E+00	5.23E-01	1.00E+00	9.95E-01	1.00E+00	4.59E-01	1.00E+00	8.01E-01	1.00E+00	9.37E-01	1.00E+00	5.00E-01	1.00E+00	T cell mediated immunity	P
GO:0002460	147	9.27E-01	1.00E+00	9.99E-01	1.00E+00	5.56E-01	1.00E+00	9.96E-01	1.00E+00	8.77E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	adaptive immune response (sensu Gnathos	P
GO:0002474	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation of pep	P
GO:0002483	12	9.15E-01	1.00E+00	7.40E-01	1.00E+00	8.89E-01	1.00E+00	9.72E-01	1.00E+00	7.45E-01	1.00E+00	4.84E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	antigen processing and presentation of end	P
GO:0002504	41	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation of pep	P

GO:0002520	266	7.85E-01	1.00E+00	9.81E-01	1.00E+00	3.30E-01	1.00E+00	9.20E-01	1.00E+00	8.48E-01	1.00E+00	9.38E-01	1.00E+00	9.40E-01	1.00E+00	9.99E-01	1.00E+00	immune system development	P
GO:0002521	139	8.90E-01	1.00E+00	9.99E-01	1.00E+00	3.22E-01	1.00E+00	9.97E-01	1.00E+00	9.47E-01	1.00E+00	9.94E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	leukocyte differentiation	P
GO:0002524	48	9.91E-01	1.00E+00	9.98E-01	1.00E+00	8.34E-01	1.00E+00	8.99E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.53E-01	1.00E+00	9.93E-01	1.00E+00	hypersensitivity	P
GO:0002526	125	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	acute inflammatory response	P
GO:0002541	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	activation of plasma proteins during acute i	P
GO:0002562	26	3.16E-01	1.00E+00	2.08E-01	1.00E+00	5.29E-01	1.00E+00	4.98E-01	1.00E+00	1.67E-01	1.00E+00	1.51E-01	1.00E+00	9.03E-01	1.00E+00	4.96E-01	1.00E+00	somatic diversification of immune receptors	P
GO:0002573	47	8.03E-01	1.00E+00	9.45E-01	1.00E+00	4.27E-01	1.00E+00	9.45E-01	1.00E+00	9.03E-01	1.00E+00	8.79E-01	1.00E+00	8.73E-01	1.00E+00	9.94E-01	1.00E+00	myeloid leukocyte differentiation	P
GO:0002682	126	9.58E-01	1.00E+00	9.96E-01	1.00E+00	4.96E-01	1.00E+00	9.98E-01	1.00E+00	9.51E-01	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of immune system process	P
GO:0002683	15	2.43E-01	1.00E+00	7.79E-01	1.00E+00	7.67E-02	1.00E+00	9.06E-01	1.00E+00	3.96E-01	1.00E+00	7.26E-01	1.00E+00	8.59E-01	1.00E+00	6.96E-01	1.00E+00	negative regulation of immune system proc	P
GO:0002684	108	9.92E-01	1.00E+00	9.93E-01	1.00E+00	8.97E-01	1.00E+00	9.95E-01	1.00E+00	9.72E-01	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of immune system proce	P
GO:0002697	19	9.90E-01	1.00E+00	9.94E-01	1.00E+00	7.68E-01	1.00E+00	9.72E-01	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	9.15E-01	1.00E+00	9.21E-01	1.00E+00	regulation of immune effector process	P
GO:0002699	16	9.71E-01	1.00E+00	9.52E-01	1.00E+00	9.69E-01	1.00E+00	8.90E-01	1.00E+00	9.58E-01	1.00E+00	9.72E-01	1.00E+00	7.43E-01	1.00E+00	7.82E-01	1.00E+00	positive regulation of immune effector proce	P
GO:0002703	18	9.86E-01	1.00E+00	9.92E-01	1.00E+00	7.45E-01	1.00E+00	9.70E-01	1.00E+00	9.93E-01	1.00E+00	9.96E-01	1.00E+00	9.19E-01	1.00E+00	8.97E-01	1.00E+00	regulation of leukocyte mediated immunity	P
GO:0002705	15	9.58E-01	1.00E+00	9.40E-01	1.00E+00	9.58E-01	1.00E+00	8.81E-01	1.00E+00	9.40E-01	1.00E+00	9.66E-01	1.00E+00	7.48E-01	1.00E+00	7.33E-01	1.00E+00	positive regulation of leukocyte mediated im	P
GO:0002706	18	9.86E-01	1.00E+00	9.92E-01	1.00E+00	7.45E-01	1.00E+00	9.70E-01	1.00E+00	9.93E-01	1.00E+00	9.96E-01	1.00E+00	9.19E-01	1.00E+00	8.97E-01	1.00E+00	regulation of lymphocyte mediated immunit	P
GO:0002708	15	9.58E-01	1.00E+00	9.40E-01	1.00E+00	9.58E-01	1.00E+00	8.81E-01	1.00E+00	9.40E-01	1.00E+00	9.66E-01	1.00E+00	7.48E-01	1.00E+00	7.33E-01	1.00E+00	positive regulation of lymphocyte mediated	P
GO:0002757	41	2.96E-01	1.00E+00	5.38E-01	1.00E+00	3.62E-02	5.87E-01	7.53E-01	1.00E+00	3.65E-01	1.00E+00	3.84E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	immune response-activating signal transdu	P
GO:0002761	24	9.50E-01	1.00E+00	9.63E-01	1.00E+00	6.36E-01	1.00E+00	9.69E-01	1.00E+00	9.89E-01	1.00E+00	9.05E-01	1.00E+00	5.68E-01	1.00E+00	9.98E-01	1.00E+00	regulation of myeloid leukocyte differentiatio	P
GO:0002762	13	6.57E-01	1.00E+00	7.64E-01	1.00E+00	4.01E-01	1.00E+00	7.30E-01	1.00E+00	8.40E-01	1.00E+00	6.16E-01	1.00E+00	3.74E-01	1.00E+00	9.60E-01	1.00E+00	negative regulation of myeloid leukocyte dif	P
GO:0002764	42	2.93E-01	1.00E+00	5.58E-01	1.00E+00	4.54E-02	8.68E-01	7.95E-01	1.00E+00	3.28E-01	1.00E+00	4.18E-01	1.00E+00	1.00E+00	1.00E+00	8.56E-01	1.00E+00	immune response-regulating signal transdu	P
GO:0002768	39	3.38E-01	1.00E+00	6.82E-01	1.00E+00	4.78E-02	8.68E-01	8.73E-01	1.00E+00	4.06E-01	1.00E+00	5.48E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	immune response-regulating cell surface re	P
GO:0002790	37	9.99E-01	1.00E+00	9.92E-01	1.00E+00	9.75E-01	1.00E+00	4.18E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide secretion	P
GO:0002819	18	4.77E-01	1.00E+00	9.52E-01	1.00E+00	5.34E-01	1.00E+00	9.34E-01	1.00E+00	4.71E-01	1.00E+00	9.27E-01	1.00E+00	4.95E-01	1.00E+00	9.59E-01	1.00E+00	regulation of adaptive immune response	P
GO:0002821	13	3.59E-01	1.00E+00	7.16E-01	1.00E+00	6.94E-01	1.00E+00	7.44E-01	1.00E+00	3.44E-01	1.00E+00	6.41E-01	1.00E+00	2.45E-01	1.00E+00	8.96E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002822	18	4.77E-01	1.00E+00	9.52E-01	1.00E+00	5.34E-01	1.00E+00	9.34E-01	1.00E+00	4.71E-01	1.00E+00	9.27E-01	1.00E+00	4.95E-01	1.00E+00	9.59E-01	1.00E+00	regulation of adaptive immune response (se	P
GO:0002824	13	3.59E-01	1.00E+00	7.16E-01	1.00E+00	6.94E-01	1.00E+00	7.44E-01	1.00E+00	3.44E-01	1.00E+00	6.41E-01	1.00E+00	2.45E-01	1.00E+00	8.96E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0003674	15432	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.16E-07	0.00E+00	1.77E-05	2.00E-03	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	molecular_function	F
GO:0003676	3506	7.57E-01	1.00E+00	3.20E-08	1.00E-03	2.60E-03	1.80E-02	3.72E-10	0.00E+00	8.05E-01	1.00E+00	1.36E-05	2.29E-03	1.00E+00	1.00E+00	6.18E-01	1.00E+00	nucleic acid binding	F
GO:0003677	2490	9.75E-01	1.00E+00	4.33E-03	6.30E-02	7.02E-02	1.00E+00	1.61E-04	7.00E-03	9.48E-01	1.00E+00	2.01E-02	5.65E-01	1.00E+00	1.00E+00	8.47E-01	1.00E+00	DNA binding	F
GO:0003678	37	1.05E-01	1.00E+00	4.83E-03	1.15E-01	8.86E-02	1.00E+00	3.41E-02	5.42E-01	3.61E-01	1.00E+00	4.34E-02	1.00E+00	1.52E-01	1.00E+00	9.06E-02	1.00E+00	DNA helicase activity	F
GO:0003682	120	4.85E-01	1.00E+00	7.84E-03	3.40E-01	2.12E-01	1.00E+00	7.08E-03	8.10E-02	4.89E-01	1.00E+00	1.10E-02	2.12E-01	9.66E-01	1.00E+00	4.54E-01	1.00E+00	chromatin binding	F
GO:0003684	52	3.11E-04	1.10E-02	4.37E-03	6.30E-02	3.48E-03	3.50E-02	1.59E-03	1.80E-02	4.37E-03	6.24E-02	3.03E-02	1.00E+00	1.32E-01	1.00E+00	2.27E-01	1.00E+00	damaged DNA binding	F
GO:0003688	11	3.00E-01	1.00E+00	3.76E-01	1.00E+00	4.76E-01	1.00E+00	6.92E-02	1.00E+00	2.64E-01	1.00E+00	7.00E-01	1.00E+00	2.63E-01	1.00E+00	8.33E-01	1.00E+00	DNA replication origin binding	F
GO:0003690	67	9.89E-03	1.77E-01	1.36E-02	3.84E-01	7.07E-02	1.00E+00	1.71E-01	1.00E+00	6.23E-03	1.48E-01	8.82E-03	1.43E-01	7.70E-01	1.00E+00	2.55E-01	1.00E+00	double-stranded DNA binding	F
GO:0003697	45	3.38E-01	1.00E+00	1.04E-02	3.84E-01	5.11E-01	1.00E+00	7.66E-02	1.00E+00	2.31E-01	1.00E+00	1.79E-02	5.65E-01	8.12E-01	1.00E+00	1.79E-01	1.00E+00	single-stranded DNA binding	F
GO:0003700	997	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.49E-01	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transcription factor activity	F
GO:0003702	222	9.09E-01	1.00E+00	1.32E-01	1.00E+00	1.04E-01	1.00E+00	1.74E-01	1.00E+00	8.91E-01	1.00E+00	8.66E-02	1.00E+00	1.00E+00	1.00E+00	6.75E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003704	38	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.28E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	specific RNA polymerase II transcription fac	F
GO:0003705	30	8.99E-01	1.00E+00	9.76E-01	1.00E+00	4.92E-01	1.00E+00	7.63E-01	1.00E+00	8.35E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003706	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.87E-01	1.00E+00	8.39E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ligand-regulated transcription factor activity	F
GO:0003707	57	9.84E-01	1.00E+00	9.85E-01	1.00E+00	5.24E-01	1.00E+00	9.33E-01	1.00E+00	9.99E-01	1.00E+00	9.54E-01	1.00E+00	9.97E-01	1.00E+00	9.58E-01	1.00E+00	steroid hormone receptor activity	F
GO:0003708	35	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.39E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinoic acid receptor activity	F
GO:0003709	10	6.29E-02	1.00E+00	2.50E-02	1.00E+00	2.19E-02	2.63E-01	1.87E-01	1.00E+00	1.09E-01	1.00E+00	3.73E-02	1.00E+00	7.85E-01	1.00E+00	2.22E-01	1.00E+00	RNA polymerase III transcription factor activ	F
GO:0003711	20	5.07E-01	1.00E+00	6.42E-02	1.00E+00	3.50E-01	1.00E+00	1.11E-01	1.00E+00	3.97E-01	1.00E+00	1.37E-01	1.00E+00	9.90E-01	1.00E+00	6.30E-02	1.00E+00	transcriptional elongation regulator activity	F
GO:0003712	313	9.28E-01	1.00E+00	1.04E-01	1.00E+00	3.13E-01	1.00E+00	1.93E-03	2.70E-02	9.54E-01	1.00E+00	2.96E-01	1.00E+00	9.98E-01	1.00E+00	6.69E-01	1.00E+00	transcription cofactor activity	F
GO:0003713	189	7.19E-01	1.00E+00	5.18E-02	1.00E+00	5.48E-02	1.00E+00	1.96E-03	2.70E-02	9.32E-01	1.00E+00	2.55E-01	1.00E+00	9.47E-01	1.00E+00	3.01E-01	1.00E+00	transcription coactivator activity	F
GO:0003714	116	9.81E-01	1.00E+00	5.78E-01	1.00E+00	9.86E-01	1.00E+00	2.60E-01	1.00E+00	9.13E-01	1.00E+00	6.23E-01	1.00E+00	9.86E-01	1.00E+00	7.80E-01	1.00E+00	transcription corepressor activity	F
GO:0003723	710	4.38E-03	1.37E-01	1.84E-10	0.00E+00	6.19E-05	4.57E-03	2.20E-09	0.00E+00	4.56E-02	1.00E+00	1.26E-08	1.05E-04	7.58E-01	1.00E+00	8.35E-02	1.00E+00	RNA binding	F
GO:0003724	31	7.90E-01	1.00E+00	8.53E-02	1.00E+00	4.24E-01	1.00E+00	6.05E-02	1.00E+00	9.62E-01	1.00E+00	6.88E-02	1.00E+00	2.26E-01	1.00E+00	9.35E-01	1.00E+00	RNA helicase activity	F
GO:0003725	35	5.62E-01	1.00E+00	5.96E-02	1.00E+00	2.64E-01	1.00E+00	4.33E-03	6.84E-02	4.98E-01	1.00E+00	7.24E-02	1.00E+00	9.15E-01	1.00E+00	7.72E-01	1.00E+00	double-stranded RNA binding	F
GO:0003727	22	9.99E-01	1.00E+00	7.28E-01	1.00E+00	9.17E-01	1.00E+00	6.90E-01	1.00E+00	1.00E+00	1.00E+00	5.58E-01	1.00E+00	9.98E-01	1.00E+00	9.66E-01	1.00E+00	single-stranded RNA binding	F
GO:0003729	46	6.85E-01	1.00E+00	8.76E-02	1.00E+00	6.35E-01	1.00E+00	4.37E-02	1.00E+00	8.18E-01	1.00E+00	1.01E-01	1.00E+00	4.53E-01	1.00E+00	4.16E-01	1.00E+00	mRNA binding	F
GO:0003735	262	9.88E-02	1.00E+00	2.06E-01	1.00E+00	9.93E-01	1.00E+00	1.73E-01	1.00E+00	7.08E-02	1.00E+00	3.23E-01	1.00E+00	1.83E-01	1.00E+00	3.56E-01	1.00E+00	structural constituent of ribosome	F
GO:0003743	60	9.65E-04	1.60E-02	2.74E-04	8.26E-03	1.21E-03	1.25E-02	5.01E-04	7.17E-03	3.36E-02	6.55E-01	2.84E-03	6.40E-02	1.30E-01	1.00E+00	5.64E-02	1.00E+00	translation initiation factor activity	F
GO:0003746	18	9.87E-01	1.00E+00	6.51E-01	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	7.84E-01	1.00E+00	6.21E-01	1.00E+00	1.00E+00	1.00E+00	3.46E-01	1.00E+00	translation elongation factor activity	F
GO:0003755	38	9.32E-02	1.00E+00	6.79E-02	1.00E+00	9.92E-02	1.00E+00	9.85E-02	1.00E+00	3.21E-01	1.00E+00	1.09E-01	1.00E+00	1.66E-01	1.00E+00	4.60E-01	1.00E+00	peptidyl-prolyl cis-trans isomerase activity	F
GO:0003774	161	1.10E-01	1.00E+00	6.92E-01	1.00E+00	7.93E-03	1.57E-01	1.55E-01	1.00E+00	1.45E-01	1.00E+00	7.22E-01	1.00E+00	9.29E-01	1.00E+00	9.33E-01	1.00E+00	motor activity	F
GO:0003777	82	2.74E-01	1.00E+00	8.69E-02	1.00E+00	6.34E-02	1.00E+00	1.81E-02	4.10E-01	3.12E-01	1.00E+00	1.44E-01	1.00E+00	8.16E-01	1.00E+00	3.89E-01	1.00E+00	microtubule motor activity	F
GO:0003779	318	4.60E-01	1.00E+00	9.29E-01	1.00E+00	2.39E-03	1.80E-02	6.06E-01	1.00E+00	7.24E-01	1.00E+00	9.46E-01	1.00E+00	9.95E-01	1.00E+00	8.05E-01	1.00E+00	actin binding	F
GO:0003796	12	8.76E-01	1.00E+00	7.79E-01	1.00E+00	9.07E-01	1.00E+00	2.14E-01	1.00E+00	7.76E-01	1.00E+00	9.13E-01	1.00E+00	5.70E-01	1.00E+00	6.01E-01	1.00E+00	lysozyme activity	F
GO:0003823	65	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen binding	F
GO:0003824	5647	7.38E-03	1.37E-01	6.99E-04	1.90E-02	1.23E-19	0.00E+00	8.10E-16	0.00E+00	5.05E-01	1.00E+00	1.07E-01	1.00E+00	9.88E-01	1.00E+00	9.90E-01	1.00E+00	catalytic activity	F
GO:0003840	13	2.04E-01	1.00E+00	7.69E-01	1.00E+00	1.14E-01	1.00E+00	7.38E-01	1.00E+00	1.60E-01	1.00E+00	9.59E-01	1.00E+00	9.99E-01	1.00E+00	1.28E-01	1.00E+00	gamma-glutamyltransferase activity	F
GO:0003841	11	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.92E-01	1.00E+00	9.96E-01	1.00E+00	9.70E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1-acylglycerol-3-phosphate O-acyltransfera	F
GO:0003854	16	9.80E-01	1.00E+00	9.80E-01	1.00E+00	6.24E-01	1.00E+00	1.09E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3-beta-hydroxy-delta5-steroid dehydrogena	F
GO:0003887	30	6.03E-01	1.00E+00	8.13E-02	1.00E+00	3.74E-01	1.00E+00	9.70E-02	1.00E+00	6.49E-01	1.00E+00	3.46E-01	1.00E+00	6.00E-01	1.00E+00	1.53E-01	1.00E+00	DNA-directed DNA polymerase activity	F
GO:0003899	51	2.95E-02	1.00E+00	4.10E-03	6.30E-02	4.98E-02	8.68E-01	4.65E-01	1.00E+00	8.27E-02	1.00E+00	6.95E-03	1.05E-01	5.03E-01	1.00E+00	4.64E-02	8.10E-01	DNA-directed RNA polymerase activity	F
GO:0003916	22	3.02E-01	1.00E+00	3.65E-01	1.00E+00	1.68E-01	1.00E+00	1.85E-01	1.00E+00	4.76E-01	1.00E+00	4.35E-01	1.00E+00	2.12E-01	1.00E+00	9.18E-01	1.00E+00	DNA topoisomerase activity	F
GO:0003918	17	2.97E-01	1.00E+00	3.80E-01	1.00E+00	2.89E-01	1.00E+00	2.01E-01	1.00E+00	4.20E-01	1.00E+00	4.29E-01	1.00E+00	1.65E-01	1.00E+00	9.34E-01	1.00E+00	DNA topoisomerase (ATP-hydrolyzing) activ	F
GO:0003924	258	4.50E-01	1.00E+00	1.73E-01	1.00E+00	3.92E-03	3.50E-02	5.85E-02	1.00E+00	9.36E-01	1.00E+00	5.42E-01	1.00E+00	9.71E-01	1.00E+00	6.20E-01	1.00E+00	GTPase activity	F
GO:0003950	24	1.44E-01	1.00E+00	2.21E-01	1.00E+00	4.96E-02	8.68E-01	2.14E-02	4.10E-01	2.78E-01	1.00E+00	5.58E-01	1.00E+00	5.53E-01	1.00E+00	2.36E-01	1.00E+00	NAD+ ADP-ribosyltransferase activity	F
GO:0003954	44	2.98E-02	1.00E+00	1.03E-02	3.84E-01	3.70E-01	1.00E+00	4.42E-02	1.00E+00	5.60E-03	1.35E-01	1.91E-02	5.65E-01	8.71E-01	1.00E+00	1.62E-01	1.00E+00	NADH dehydrogenase activity	F
GO:0003993	16	5.42E-01	1.00E+00	1.54E-01	1.00E+00	1.97E-01	1.00E+00	3.26E-03	5.60E-02	6.98E-01	1.00E+00	3.15E-01	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	acid phosphatase activity	F
GO:0003995	16	1.31E-01	1.00E+00	8.59E-02	1.00E+00	2.87E-01	1.00E+00	7.14E-01	1.00E+00	1.41E-01	1.00E+00	5.09E-02	1.00E+00	9.86E-01	1.00E+00	3.46E-01	1.00E+00	acyl-CoA dehydrogenase activity	F
GO:0004003	24	2.11E-01	1.00E+00	9.31E-02	1.00E+00	2.82E-01	1.00E+00	1.49E-01	1.00E+00	2.80E-01	1.00E+00	1.20E-01	1.00E+00	1.69E-01	1.00E+00	2.60E-01	1.00E+00	ATP-dependent DNA helicase activity	F

GO:0004004	22	5.88E-01	1.00E+00	1.39E-01	1.00E+00	2.50E-01	1.00E+00	5.91E-02	1.00E+00	9.32E-01	1.00E+00	1.42E-01	1.00E+00	1.71E-01	1.00E+00	8.78E-01	1.00E+00	ATP-dependent RNA helicase activity	F
GO:0004012	15	7.94E-01	1.00E+00	6.54E-01	1.00E+00	2.33E-01	1.00E+00	8.73E-01	1.00E+00	9.17E-01	1.00E+00	4.85E-01	1.00E+00	9.99E-01	1.00E+00	9.25E-01	1.00E+00	phospholipid-translocating ATPase activity	F
GO:0004016	11	9.22E-01	1.00E+00	9.06E-01	1.00E+00	9.21E-01	1.00E+00	6.76E-01	1.00E+00	7.76E-01	1.00E+00	9.59E-01	1.00E+00	8.77E-01	1.00E+00	1.00E+00	1.00E+00	adenylate cyclase activity	F
GO:0004022	35	7.34E-01	1.00E+00	5.64E-01	1.00E+00	4.44E-01	1.00E+00	7.75E-01	1.00E+00	8.23E-01	1.00E+00	3.88E-01	1.00E+00	5.26E-01	1.00E+00	9.93E-01	1.00E+00	alcohol dehydrogenase activity	F
GO:0004033	15	9.21E-01	1.00E+00	4.12E-01	1.00E+00	2.58E-01	1.00E+00	1.49E-01	1.00E+00	9.82E-01	1.00E+00	5.49E-01	1.00E+00	9.91E-01	1.00E+00	4.98E-01	1.00E+00	aldo-keto reductase activity	F
GO:0004065	12	4.05E-01	1.00E+00	7.56E-01	1.00E+00	9.10E-02	1.00E+00	1.50E-01	1.00E+00	6.02E-01	1.00E+00	9.62E-01	1.00E+00	9.52E-01	1.00E+00	9.74E-01	1.00E+00	arylsulfatase activity	F
GO:0004089	21	1.13E-01	1.00E+00	5.14E-01	1.00E+00	1.63E-01	1.00E+00	8.73E-01	1.00E+00	7.36E-02	1.00E+00	2.37E-01	1.00E+00	5.42E-01	1.00E+00	1.00E+00	1.00E+00	carbonate dehydratase activity	F
GO:0004091	23	3.00E-03	4.90E-02	1.98E-01	1.00E+00	3.70E-02	5.87E-01	2.44E-01	1.00E+00	3.82E-02	1.00E+00	1.19E-01	1.00E+00	5.42E-02	1.00E+00	1.00E+00	1.00E+00	carboxylesterase activity	F
GO:0004104	13	4.77E-01	1.00E+00	8.40E-01	1.00E+00	9.57E-02	1.00E+00	6.36E-01	1.00E+00	7.77E-01	1.00E+00	8.50E-01	1.00E+00	4.79E-01	1.00E+00	7.39E-01	1.00E+00	cholinesterase activity	F
GO:0004112	25	6.63E-01	1.00E+00	9.82E-01	1.00E+00	7.78E-01	1.00E+00	9.98E-01	1.00E+00	6.27E-01	1.00E+00	9.23E-01	1.00E+00	6.04E-01	1.00E+00	9.61E-01	1.00E+00	cyclic-nucleotide phosphodiesterase activity	F
GO:0004114	24	5.91E-01	1.00E+00	9.98E-01	1.00E+00	7.19E-01	1.00E+00	9.95E-01	1.00E+00	5.56E-01	1.00E+00	9.96E-01	1.00E+00	5.69E-01	1.00E+00	9.38E-01	1.00E+00	3',5'-cyclic-nucleotide phosphodiesterase ac	F
GO:0004129	28	2.35E-01	1.00E+00	1.49E-01	1.00E+00	9.00E-01	1.00E+00	4.42E-01	1.00E+00	1.43E-01	1.00E+00	1.48E-01	1.00E+00	9.27E-01	1.00E+00	3.06E-01	1.00E+00	cytochrome-c oxidase activity	F
GO:0004143	15	9.58E-01	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	6.55E-01	1.00E+00	9.35E-01	1.00E+00	9.07E-01	1.00E+00	4.22E-01	1.00E+00	9.99E-01	1.00E+00	diacylglycerol kinase activity	F
GO:0004175	460	9.44E-01	1.00E+00	1.00E+00	1.00E+00	3.16E-01	1.00E+00	6.13E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	endopeptidase activity	F
GO:0004176	20	7.78E-01	1.00E+00	4.55E-01	1.00E+00	7.98E-01	1.00E+00	1.69E-01	1.00E+00	6.17E-01	1.00E+00	7.52E-01	1.00E+00	8.63E-01	1.00E+00	5.35E-01	1.00E+00	ATP-dependent peptidase activity	F
GO:0004177	47	3.62E-01	1.00E+00	2.70E-01	1.00E+00	3.23E-01	1.00E+00	6.93E-03	8.10E-02	2.94E-01	1.00E+00	4.39E-01	1.00E+00	9.20E-01	1.00E+00	9.94E-01	1.00E+00	aminopeptidase activity	F
GO:0004179	12	9.49E-01	1.00E+00	7.39E-01	1.00E+00	9.62E-01	1.00E+00	5.11E-01	1.00E+00	9.33E-01	1.00E+00	7.26E-01	1.00E+00	8.86E-01	1.00E+00	9.19E-01	1.00E+00	membrane alanyl aminopeptidase activity	F
GO:0004180	42	8.17E-01	1.00E+00	9.16E-01	1.00E+00	5.06E-01	1.00E+00	4.69E-01	1.00E+00	9.25E-01	1.00E+00	9.23E-01	1.00E+00	4.22E-01	1.00E+00	9.92E-01	1.00E+00	carboxypeptidase activity	F
GO:0004181	29	8.70E-01	1.00E+00	9.81E-01	1.00E+00	5.82E-01	1.00E+00	9.16E-01	1.00E+00	9.60E-01	1.00E+00	9.60E-01	1.00E+00	3.49E-01	1.00E+00	9.87E-01	1.00E+00	metallocarboxypeptidase activity	F
GO:0004182	24	8.66E-01	1.00E+00	9.62E-01	1.00E+00	5.70E-01	1.00E+00	8.90E-01	1.00E+00	9.72E-01	1.00E+00	9.09E-01	1.00E+00	2.51E-01	1.00E+00	9.82E-01	1.00E+00	carboxypeptidase A activity	F
GO:0004185	10	3.95E-01	1.00E+00	2.61E-01	1.00E+00	5.87E-01	1.00E+00	8.70E-02	1.00E+00	3.43E-01	1.00E+00	3.16E-01	1.00E+00	4.25E-01	1.00E+00	7.97E-01	1.00E+00	serine carboxypeptidase activity	F
GO:0004190	30	2.17E-01	1.00E+00	7.38E-01	1.00E+00	5.98E-01	1.00E+00	5.78E-01	1.00E+00	1.54E-01	1.00E+00	8.28E-01	1.00E+00	4.35E-01	1.00E+00	6.79E-01	1.00E+00	aspartic-type endopeptidase activity	F
GO:0004194	11	6.41E-01	1.00E+00	8.91E-01	1.00E+00	5.41E-01	1.00E+00	6.62E-01	1.00E+00	4.89E-01	1.00E+00	9.31E-01	1.00E+00	9.95E-01	1.00E+00	5.06E-01	1.00E+00	pepsin A activity	F
GO:0004197	89	3.67E-01	1.00E+00	2.28E-01	1.00E+00	5.15E-02	1.00E+00	2.45E-02	4.10E-01	6.37E-01	1.00E+00	3.36E-01	1.00E+00	5.37E-01	1.00E+00	9.85E-01	1.00E+00	cysteine-type endopeptidase activity	F
GO:0004198	16	7.45E-01	1.00E+00	7.69E-01	1.00E+00	4.63E-01	1.00E+00	7.92E-02	1.00E+00	9.61E-01	1.00E+00	9.30E-01	1.00E+00	4.48E-01	1.00E+00	9.76E-01	1.00E+00	calpain activity	F
GO:0004221	64	1.56E-01	1.00E+00	8.15E-04	2.00E-02	9.29E-03	1.57E-01	6.76E-06	8.32E-04	2.95E-01	1.00E+00	2.28E-02	7.69E-01	8.55E-01	1.00E+00	2.83E-02	2.52E-01	ubiquitin thiolesterase activity	F
GO:0004222	105	9.90E-01	1.00E+00	1.00E+00	1.00E+00	4.13E-01	1.00E+00	9.15E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	metalloendopeptidase activity	F
GO:0004252	212	9.34E-01	1.00E+00	1.00E+00	1.00E+00	5.88E-01	1.00E+00	9.01E-01	1.00E+00	9.29E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	9.84E-01	1.00E+00	serine-type endopeptidase activity	F
GO:0004289	25	7.67E-01	1.00E+00	9.99E-01	1.00E+00	7.56E-01	1.00E+00	9.99E-01	1.00E+00	6.54E-01	1.00E+00	1.00E+00	1.00E+00	6.22E-01	1.00E+00	9.97E-01	1.00E+00	subtilase activity	F
GO:0004298	23	3.53E-01	1.00E+00	6.39E-01	1.00E+00	7.10E-01	1.00E+00	1.52E-01	1.00E+00	2.35E-01	1.00E+00	6.98E-01	1.00E+00	5.98E-01	1.00E+00	9.18E-01	1.00E+00	threonine endopeptidase activity	F
GO:0004303	13	5.61E-01	1.00E+00	6.49E-01	1.00E+00	3.46E-01	1.00E+00	4.05E-01	1.00E+00	6.73E-01	1.00E+00	6.72E-01	1.00E+00	4.63E-01	1.00E+00	8.25E-01	1.00E+00	estradiol 17-beta-dehydrogenase activity	F
GO:0004364	22	8.64E-01	1.00E+00	9.95E-01	1.00E+00	8.85E-01	1.00E+00	1.47E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	3.69E-01	1.00E+00	9.95E-01	1.00E+00	glutathione transferase activity	F
GO:0004385	10	8.18E-01	1.00E+00	6.59E-01	1.00E+00	4.23E-01	1.00E+00	3.51E-02	7.12E-01	8.53E-01	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	guanylate kinase activity	F
GO:0004386	150	1.86E-01	1.00E+00	2.07E-04	8.26E-03	2.38E-02	4.97E-01	1.38E-05	2.00E-03	5.19E-01	1.00E+00	2.67E-03	6.40E-02	4.36E-01	1.00E+00	1.61E-01	1.00E+00	helicase activity	F
GO:0004402	24	1.10E-01	1.00E+00	1.47E-02	3.84E-01	1.80E-02	2.36E-01	1.92E-02	4.10E-01	2.63E-01	1.00E+00	1.76E-02	5.65E-01	4.40E-01	1.00E+00	2.15E-01	1.00E+00	histone acetyltransferase activity	F
GO:0004407	20	6.05E-02	1.00E+00	4.85E-01	1.00E+00	4.72E-02	8.68E-01	8.05E-01	1.00E+00	9.14E-02	1.00E+00	3.07E-01	1.00E+00	4.41E-01	1.00E+00	8.60E-01	1.00E+00	histone deacetylase activity	F
GO:0004428	40	1.27E-02	2.72E-01	3.41E-02	1.00E+00	1.58E-03	1.60E-02	4.15E-02	1.00E+00	5.28E-02	1.00E+00	7.85E-02	1.00E+00	1.79E-01	1.00E+00	2.03E-01	1.00E+00	inositol or phosphatidylinositol kinase activit	F
GO:0004434	27	7.92E-01	1.00E+00	1.00E+00	1.00E+00	4.65E-01	1.00E+00	9.93E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	2.68E-01	1.00E+00	1.00E+00	1.00E+00	inositol or phosphatidylinositol phosphodies	F
GO:0004435	27	7.92E-01	1.00E+00	1.00E+00	1.00E+00	4.65E-01	1.00E+00	9.93E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	2.68E-01	1.00E+00	1.00E+00	1.00E+00	phosphoinositide phospholipase C activity	F
GO:0004437	37	7.62E-01	1.00E+00	8.43E-01	1.00E+00	2.12E-01	1.00E+00	8.55E-01	1.00E+00	8.46E-01	1.00E+00	7.34E-01	1.00E+00	9.96E-01	1.00E+00	7.17E-01	1.00E+00	inositol or phosphatidylinositol phosphatase	F
GO:0004467	10	2.00E-01	1.00E+00	2.99E-01	1.00E+00	2.76E-02	4.97E-01	4.12E-01	1.00E+00	4.92E-01	1.00E+00	3.35E-01	1.00E+00	6.60E-02	1.00E+00	2.16E-01	1.00E+00	long-chain-fatty-acid-CoA ligase activity	F
GO:0004468	24	1.10E-01	1.00E+00	1.47E-02	3.84E-01	1.80E-02	2.36E-01	1.92E-02	4.10E-01	2.63E-01	1.00E+00	1.76E-02	5.65E-01	4.40E-01	1.00E+00	2.15E-01	1.00E+00	lysine N-acetyltransferase activity	F
GO:0004497	135	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	monooxygenase activity	F
GO:0004499	20	3.14E-01	1.00E+00	3.98E-01	1.00E+00	6.61E-01	1.00E+00	2.25E-01	1.00E+00	2.45E-01	1.00E+00	4.62E-01	1.00E+00	2.43E-01	1.00E+00	6.84E-01	1.00E+00	dimethylaniline monooxygenase (N-oxide-fo	F
GO:0004518	148	6.11E-02	1.00E+00	5.33E-02	1.00E+00	7.17E-03	1.57E-01	2.72E-02	4.10E-01	1.39E-01	1.00E+00	1.40E-01	1.00E+00	5.57E-01	1.00E+00	9.76E-01	1.00E+00	nuclease activity	F
GO:0004519	89	1.78E-01	1.00E+00	2.59E-01	1.00E+00	9.62E-02	1.00E+00	1.15E-01	1.00E+00	3.01E-01	1.00E+00	4.36E-01	1.00E+00	5.21E-01	1.00E+00	9.99E-01	1.00E+00	endonuclease activity	F
GO:0004520	19	1.80E-01	1.00E+00	1.69E-01	1.00E+00	2.95E-01	1.00E+00	2.51E-01	1.00E+00	3.01E-01	1.00E+00	1.56E-01	1.00E+00	8.44E-02	1.00E+00	9.72E-01	1.00E+00	endodeoxyribonuclease activity	F
GO:0004521	39	7.42E-01	1.00E+00	5.92E-01	1.00E+00	7.83E-01	1.00E+00	1.72E-01	1.00E+00	6.05E-01	1.00E+00	9.37E-01	1.00E+00	9.35E-01	1.00E+00	1.00E+00	1.00E+00	endoribonuclease activity	F
GO:0004522	13	9.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.40E-01	1.00E+00	9.90E-01	1.00E+00	6.18E-01	1.00E+00	9.88E-01	1.00E+00	pancreatic ribonuclease activity	F
GO:0004526	11	7.59E-01	1.00E+00	1.46E-01	1.00E+00	6.46E-01	1.00E+00	1.28E-01	1.00E+00	6.66E-01	1.00E+00	4.42E-01	1.00E+00	9.94E-01	1.00E+00	9.46E-01	1.00E+00	ribonuclease P activity	F
GO:0004527	52	2.48E-01	1.00E+00	8.49E-02	1.00E+00	1.57E-02	1.92E-01	2.51E-02	4.10E-01	3.50E-01	1.00E+00	1.23E-01	1.00E+00	9.39E-01	1.00E+00	9.41E-01	1.00E+00	exonuclease activity	F
GO:0004529	10	8.19E-01	1.00E+00	5.21E-01	1.00E+00	2.91E-01	1.00E+00	9.87E-01	1.00E+00	9.37E-01	1.00E+00	2.80E-01	1.00E+00	9.92E-01	1.00E+00	9.96E-01	1.00E+00	exodeoxyribonuclease activity	F
GO:0004532	12	3.34E-01	1.00E+00	9.55E-02	1.00E+00	7.33E-02	1.00E+00	1.21E-01	1.00E+00	3.88E-01	1.00E+00	7.72E-02	1.00E+00	6.90E-01	1.00E+00	9.62E-01	1.00E+00	exoribonuclease activity	F
GO:0004536	33	6.92E-02	1.00E+00	1.62E-01	1.00E+00	8.76E-02	1.00E+00	2.78E-01	1.00E+00	1.43E-01	1.00E+00	1.26E-01	1.00E+00	1.31E-01	1.00E+00	9.64E-01	1.00E+00	deoxyribonuclease activity	F
GO:0004540	59	5.88E-01	1.00E+00	3.58E-01	1.00E+00	5.67E-01	1.00E+00	1.17E-01	1.00E+00	4.83E-01	1.00E+00	6.62E-01	1.00E+00	8.67E-01	1.00E+00	9.99E-01	1.00E+00	ribonuclease activity	F
GO:0004549	13	5.59E-01	1.00E+00	1.71E-01	1.00E+00	6.68E-01	1.00E+00	1.40E-01	1.00E+00	3.75E-01	1.00E+00	5.64E-01	1.00E+00	9.55E-01	1.00E+00	9.75E-01	1.00E+00	tRNA-specific ribonuclease activity	F
GO:0004550	10	2.95E-01	1.00E+00	7.77E-01	1.00E+00	3.60E-01	1.00E+00	4.40E-01	1.00E+00	2.24E-01	1.00E+00	9.09E-01	1.00E+00	6.27E-01	1.00E+00	9.34E-01	1.00E+00	nucleoside diphosphate kinase activity	F
GO:0004553	132	2.52E-01	1.00E+00	1.26E-01	1.00E+00	1.33E-01	1.00E+00	7.08E-02	1.00E+00	5.78E-01	1.00E+00	2.19E-01	1.00E+00	2.32E-01	1.00E+00	4.49E-01	1.00E+00	hydrolase activity, hydrolyzing O-glycosyl co	F
GO:0004601	47	4.34E-01	1.00E+00	1.00E+00	1.00E+00	1.98E-01	1.00E+00	9.08E-01	1.00E+00	6.10E-01	1.00E+00	9.99E-01	1.00E+00	5.13E-01	1.00E+00	9.99E-01	1.00E+00	peroxidase activity	F
GO:0004602	10	6.17E-01	1.00E+00	1.00E+00	1.00E+00	2.34E-01	1.00E+00	5.90E-01	1.00E+00	8.13E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	glutathione peroxidase activity	F
GO:0004620	89	5.59E-01	1.00E+00	9.44E-01	1.00E+00	1.12E-01	1.00E+00	4.32E-01	1.00E+00	8.19E-01	1.00E+00	9.76E-01	1.00E+00	5.30E-01	1.00E+00	9.62E-01	1.00E+00	phospholipase activity	F
GO:0004622	11	7.05E-01	1.00E+00	5.01E-01	1.00E+00	6.62E-02	1.00E+00	5.76E-01	1.00E+00	8.65E-01	1.00E+00	4.09E-01	1.00E+00	9.55E-01	1.00E+00	7.64E-01	1.00E+00	lysophospholipase activity	F
GO:0004623	37	9.72E-01	1.00E+00	8.25E-01	1.00E+00	7.44E-01	1.00E+00	2.43E-01	1.00E+00	9.50E-01	1.00E+00	9.16E-01	1.00E+00	9.98E-01	1.00E+00	9.87E-01	1.00E+00	phospholipase A2 activity	F
GO:0004629	36	2.10E-01	1.00E+00	9.97E-01	1.00E+00	1.05E-01	1.00E+00	9.66E-01	1.00E+00	4.84E-01	1.00E+00	9.95E-01	1.00E+00	9.86E-02	1.00E+00	8.49E-01	1.00E+00	phospholipase C activity	F
GO:0004653	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	polypeptide N-acetylgalactosaminyltransfer	F
GO:0004659	13	2.65E-01	1.00E+00	5.23E-01	1.00E+00	2.01E-01	1.00E+00	1.78E-01	1.00E+00	2.41E-01	1.00E+00	4.48E-01	1.00E+00	6.87E-01	1.00E+00	1.00E+00	1.00E+00	prenyltransferase activity	F
GO:0004672	654	7.78E-01	1.00E+00	7.25E-01	1.00E+00	5.59E-03	9.30E-02	2.94E-02	5.42E-01	8.42E-01	1.00E+00	7.53E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	protein kinase activity	F
GO:0004673	13	7.13E-01	1.00E+00	9.92E-01	1.00E+00	5.06E-01	1.00E+00	9.49E-01	1.00E+00	7.73E-01	1.00E+00	9.55E-01	1.00E+00	5.62E-01	1.00E+00	9.66E-01	1.00E+00	protein histidine kinase activity	F
GO:0004674	534	2.71E-01	1.00E+00	1.16E-01	1.00E+00	2.52E-04	6.00E-03	1.90E-03	2.70E-02	4.50E-01	1.00E+00	1.23E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	protein serine/threonine kinase activity	F
GO:0004675	15	7.15E-01	1.00E+00	9.51E-01	1.00E+00	3.46E-01	1.00E+00	3.77E-01	1.00E+00	7.48E-01	1.00E+00	9.42E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor protein serine/thre	F
GO:0004680	10	4.79E-01	1.00E+00	7.47E-01	1.00E+00	1.55E-01	1.00E+00	9.36E-01	1.00E+00	6.03E-01	1.00E+00	6.60E-01	1.00E+00	7.31E-01	1.00E+00	5.00E-01	1.00E+00	casein kinase activity	F
GO:0004683	28	5.67E-01	1.00E+00	9.65E-01	1.00E+00	5.24E-01	1.00E+00	6.55E-01	1.00E+00	5.29E-01	1.00E+00	9.02E-01	1.00E+00	8.23E-01	1.00E+00	1.00E+00	1.00E+00	calmodulin regulated protein kinase activity	F
GO:0004689	20	7.89E-01	1.00E+00	9.88E-01	1.00E+00	7.94E-01	1.00E+00	6.53E-01	1.00E+00	7.69E-01	1.00E+00	9.60E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	phosphorylase kinase activity	F
GO:0004693	28	2.12E-01	1.00E+00	1.27E-01	1.00E+00	6.71E-02	1.00E+00	1.91E-02	4.10E-01	2.51E-01	1.00E+00	2.85E-01	1.00E+00	7.49E-01	1.00E+00	7.24E-01	1.00E+00	cyclin-dependent protein kinase activity	F
GO:0004697	15	1.00E-01	1.00E+00	2.02E-01	1.00E+00	8.80E-02	1.00E+00	1.94E-01	1.00E+00	1.05E-01	1.00E+00	2.00E-01	1.00E+00	5.16E-01	1.00E+00	3.98E-01	1.00E+00	protein kinase C activity	F

GO:0004702	58	7.28E-01	1.00E+00	6.19E-01	1.00E+00	2.65E-01	1.00E+00	3.52E-01	1.00E+00	8.23E-01	1.00E+00	6.30E-01	1.00E+00	8.45E-01	1.00E+00	8.49E-01	1.00E+00	receptor signaling protein serine/threonine k	F
GO:0004707	19	8.05E-01	1.00E+00	5.20E-01	1.00E+00	6.31E-01	1.00E+00	5.31E-01	1.00E+00	8.80E-01	1.00E+00	5.50E-01	1.00E+00	5.05E-01	1.00E+00	4.15E-01	1.00E+00	MAP kinase activity	F
GO:0004708	13	7.93E-01	1.00E+00	8.62E-01	1.00E+00	7.06E-01	1.00E+00	9.87E-01	1.00E+00	5.91E-01	1.00E+00	6.92E-01	1.00E+00	8.96E-01	1.00E+00	9.98E-01	1.00E+00	MAP kinase kinase activity	F
GO:0004709	18	6.44E-01	1.00E+00	7.41E-01	1.00E+00	4.10E-01	1.00E+00	5.55E-01	1.00E+00	6.20E-01	1.00E+00	7.95E-01	1.00E+00	9.88E-01	1.00E+00	7.11E-01	1.00E+00	MAP kinase kinase kinase activity	F
GO:0004712	14	8.64E-01	1.00E+00	9.05E-01	1.00E+00	7.84E-01	1.00E+00	9.94E-01	1.00E+00	6.52E-01	1.00E+00	7.49E-01	1.00E+00	9.31E-01	1.00E+00	9.99E-01	1.00E+00	protein threonine/tyrosine kinase activity	F
GO:0004713	550	7.57E-01	1.00E+00	8.29E-01	1.00E+00	3.79E-02	5.87E-01	1.27E-01	1.00E+00	7.68E-01	1.00E+00	8.27E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	protein-tyrosine kinase activity	F
GO:0004714	124	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	transmembrane receptor protein tyrosine ki	F
GO:0004715	39	2.36E-01	1.00E+00	1.93E-01	1.00E+00	2.43E-01	1.00E+00	8.97E-02	1.00E+00	1.42E-01	1.00E+00	2.04E-01	1.00E+00	9.74E-01	1.00E+00	8.02E-01	1.00E+00	non-membrane spanning protein tyrosine ki	F
GO:0004716	12	2.13E-01	1.00E+00	2.03E-01	1.00E+00	4.71E-02	8.68E-01	1.21E-01	1.00E+00	2.90E-01	1.00E+00	2.05E-01	1.00E+00	9.88E-01	1.00E+00	5.50E-01	1.00E+00	receptor signaling protein tyrosine kinase a	F
GO:0004721	169	6.89E-01	1.00E+00	1.55E-01	1.00E+00	3.59E-02	5.87E-01	2.44E-02	4.10E-01	9.22E-01	1.00E+00	3.56E-01	1.00E+00	9.81E-01	1.00E+00	5.18E-01	1.00E+00	phosphoprotein phosphatase activity	F
GO:0004722	42	1.62E-01	1.00E+00	1.93E-01	1.00E+00	2.69E-01	1.00E+00	1.08E-01	1.00E+00	3.07E-01	1.00E+00	3.04E-01	1.00E+00	2.03E-01	1.00E+00	6.92E-01	1.00E+00	protein serine/threonine phosphatase activit	F
GO:0004725	114	8.56E-01	1.00E+00	6.87E-01	1.00E+00	8.45E-02	1.00E+00	1.79E-01	1.00E+00	9.68E-01	1.00E+00	8.71E-01	1.00E+00	9.99E-01	1.00E+00	5.74E-01	1.00E+00	protein tyrosine phosphatase activity	F
GO:0004745	10	4.19E-01	1.00E+00	2.72E-01	1.00E+00	2.50E-01	1.00E+00	1.76E-01	1.00E+00	5.52E-01	1.00E+00	2.09E-01	1.00E+00	7.11E-01	1.00E+00	8.57E-01	1.00E+00	retinol dehydrogenase activity	F
GO:0004765	10	1.43E-01	1.00E+00	5.88E-01	1.00E+00	9.88E-03	1.57E-01	1.08E-01	1.00E+00	7.61E-01	1.00E+00	9.39E-01	1.00E+00	8.48E-01	1.00E+00	9.22E-01	1.00E+00	shikimate kinase activity	F
GO:0004806	17	7.51E-01	1.00E+00	7.71E-01	1.00E+00	8.12E-01	1.00E+00	9.15E-01	1.00E+00	7.50E-01	1.00E+00	9.14E-01	1.00E+00	3.85E-01	1.00E+00	5.54E-02	1.00E+00	triacylglycerol lipase activity	F
GO:0004812	76	2.06E-03	4.90E-02	3.76E-03	6.30E-02	1.16E-02	1.57E-01	1.98E-01	1.00E+00	3.82E-03	6.24E-02	6.59E-03	1.05E-01	1.26E-01	1.00E+00	2.50E-02	2.52E-01	aminoacyl-tRNA ligase activity	F
GO:0004835	14	7.61E-02	1.00E+00	4.97E-02	1.00E+00	1.54E-01	1.00E+00	1.48E-02	2.81E-01	5.42E-02	1.00E+00	9.37E-02	1.00E+00	2.10E-01	1.00E+00	2.80E-01	1.00E+00	tubulin-tyrosine ligase activity	F
GO:0004842	158	3.55E-02	1.00E+00	1.36E-03	3.90E-02	7.66E-04	1.25E-02	1.23E-05	2.00E-03	1.78E-01	1.00E+00	2.27E-02	7.69E-01	3.26E-01	1.00E+00	1.13E-01	1.00E+00	ubiquitin-protein ligase activity	F
GO:0004843	67	1.86E-01	1.00E+00	9.02E-04	2.00E-02	8.42E-03	1.57E-01	8.69E-06	9.66E-04	3.26E-01	1.00E+00	1.97E-02	5.65E-01	8.99E-01	1.00E+00	3.13E-02	3.18E-01	ubiquitin-specific protease activity	F
GO:0004857	298	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	enzyme inhibitor activity	F
GO:0004859	17	9.45E-01	1.00E+00	9.29E-01	1.00E+00	6.96E-01	1.00E+00	9.99E-01	1.00E+00	9.02E-01	1.00E+00	6.53E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	phospholipase inhibitor activity	F
GO:0004860	29	8.47E-01	1.00E+00	9.64E-01	1.00E+00	3.83E-01	1.00E+00	8.72E-01	1.00E+00	8.15E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	7.69E-01	1.00E+00	protein kinase inhibitor activity	F
GO:0004864	28	6.54E-01	1.00E+00	9.73E-01	1.00E+00	2.40E-01	1.00E+00	6.50E-01	1.00E+00	6.44E-01	1.00E+00	9.95E-01	1.00E+00	9.59E-01	1.00E+00	9.71E-01	1.00E+00	protein phosphatase inhibitor activity	F
GO:0004866	168	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endopeptidase inhibitor activity	F
GO:0004867	114	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	serine-type endopeptidase inhibitor activity	F
GO:0004869	30	1.00E+00	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.29E-01	1.00E+00	9.01E-01	1.00E+00	9.99E-01	1.00E+00	cysteine protease inhibitor activity	F
GO:0004871	2390	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	signal transducer activity	F
GO:0004872	1905	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	receptor activity	F
GO:0004879	182	1.00E+00	1.00E+00	9.98E-01	1.00E+00	3.71E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ligand-dependent nuclear receptor activity	F
GO:0004886	20	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinoid-X receptor activity	F
GO:0004887	21	5.19E-01	1.00E+00	6.17E-01	1.00E+00	1.39E-01	1.00E+00	5.44E-01	1.00E+00	7.64E-01	1.00E+00	6.44E-01	1.00E+00	9.03E-01	1.00E+00	4.30E-01	1.00E+00	thyroid hormone receptor activity	F
GO:0004888	1286	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor activity	F
GO:0004889	18	2.25E-01	1.00E+00	6.45E-01	1.00E+00	2.87E-01	1.00E+00	8.70E-01	1.00E+00	2.70E-01	1.00E+00	6.32E-01	1.00E+00	2.14E-01	1.00E+00	2.52E-01	1.00E+00	nicotinic acetylcholine-activated cation-sele	F
GO:0004890	32	9.22E-01	1.00E+00	1.00E+00	1.00E+00	6.10E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	GABA-A receptor activity	F
GO:0004896	84	8.29E-01	1.00E+00	9.95E-01	1.00E+00	8.01E-01	1.00E+00	9.84E-01	1.00E+00	6.65E-01	1.00E+00	9.50E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0004907	62	9.59E-01	1.00E+00	9.92E-01	1.00E+00	9.85E-01	1.00E+00	9.82E-01	1.00E+00	8.84E-01	1.00E+00	9.46E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	interleukin receptor activity	F
GO:0004908	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	interleukin-1 receptor activity	F
GO:0004930	780	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor activity	F
GO:0004935	33	9.98E-01	1.00E+00	8.47E-01	1.00E+00	5.69E-01	1.00E+00	2.69E-01	1.00E+00	1.00E+00	1.00E+00	9.31E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	adrenoceptor activity	F
GO:0004936	13	9.28E-01	1.00E+00	9.15E-01	1.00E+00	7.27E-01	1.00E+00	7.29E-01	1.00E+00	9.83E-01	1.00E+00	8.61E-01	1.00E+00	4.18E-01	1.00E+00	9.99E-01	1.00E+00	alpha-adrenergic receptor activity	F
GO:0004942	12	1.85E-01	1.00E+00	5.02E-02	1.00E+00	6.17E-01	1.00E+00	1.22E-01	1.00E+00	1.22E-01	1.00E+00	1.33E-01	1.00E+00	8.36E-01	1.00E+00	8.67E-01	1.00E+00	anaphylatoxin receptor activity	F
GO:0004945	60	9.88E-01	1.00E+00	9.90E-01	1.00E+00	9.84E-01	1.00E+00	5.59E-01	1.00E+00	9.43E-01	1.00E+00	9.73E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	angiotensin type II receptor activity	F
GO:0004946	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.44E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	1.00E+00	1.00E+00	bombesin receptor activity	F
GO:0004947	31	5.97E-01	1.00E+00	1.78E-01	1.00E+00	9.85E-01	1.00E+00	1.14E-01	1.00E+00	4.65E-01	1.00E+00	1.69E-01	1.00E+00	7.98E-01	1.00E+00	1.00E+00	1.00E+00	bradykinin receptor activity	F
GO:0004949	13	7.52E-01	1.00E+00	5.77E-01	1.00E+00	9.57E-01	1.00E+00	7.46E-01	1.00E+00	5.18E-01	1.00E+00	3.36E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cannabinoid receptor activity	F
GO:0004950	56	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	7.11E-01	1.00E+00	9.94E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	chemokine receptor activity	F
GO:0004952	65	9.96E-01	1.00E+00	9.86E-01	1.00E+00	9.14E-01	1.00E+00	9.55E-01	1.00E+00	9.98E-01	1.00E+00	9.56E-01	1.00E+00	9.29E-01	1.00E+00	1.00E+00	1.00E+00	dopamine receptor activity	F
GO:0004953	17	8.31E-01	1.00E+00	1.00E+00	1.00E+00	4.00E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	icosanoid receptor activity	F
GO:0004954	17	8.31E-01	1.00E+00	1.00E+00	1.00E+00	4.00E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	prostanoid receptor activity	F
GO:0004955	17	8.31E-01	1.00E+00	1.00E+00	1.00E+00	4.00E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	prostaglandin receptor activity	F
GO:0004957	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	prostaglandin E receptor activity	F
GO:0004965	28	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.58E-01	1.00E+00	9.92E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	GABA-B receptor activity	F
GO:0004966	39	8.57E-01	1.00E+00	8.83E-01	1.00E+00	3.01E-01	1.00E+00	8.35E-01	1.00E+00	9.54E-01	1.00E+00	7.71E-01	1.00E+00	8.31E-01	1.00E+00	1.00E+00	1.00E+00	galanin receptor activity	F
GO:0004969	58	3.45E-01	1.00E+00	5.66E-01	1.00E+00	6.59E-01	1.00E+00	3.15E-01	1.00E+00	1.55E-01	1.00E+00	5.31E-01	1.00E+00	8.38E-01	1.00E+00	8.88E-01	1.00E+00	histamine receptor activity	F
GO:0004970	18	9.51E-01	1.00E+00	9.99E-01	1.00E+00	5.12E-01	1.00E+00	9.94E-01	1.00E+00	9.80E-01	1.00E+00	9.96E-01	1.00E+00	9.31E-01	1.00E+00	9.99E-01	1.00E+00	ionotropic glutamate receptor activity	F
GO:0004974	21	1.00E+00	1.00E+00	3.35E-01	1.00E+00	9.39E-01	1.00E+00	2.42E-01	1.00E+00	1.00E+00	1.00E+00	5.04E-01	1.00E+00	9.91E-01	1.00E+00	9.91E-01	1.00E+00	leukotriene receptor activity	F
GO:0004977	57	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	melanocortin receptor activity	F
GO:0004981	16	9.21E-01	1.00E+00	8.25E-01	1.00E+00	6.18E-01	1.00E+00	3.12E-01	1.00E+00	7.88E-01	1.00E+00	8.00E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	muscarinic acetylcholine receptor activity	F
GO:0004982	22	7.42E-01	1.00E+00	5.27E-01	1.00E+00	9.42E-01	1.00E+00	2.19E-01	1.00E+00	5.90E-01	1.00E+00	6.71E-01	1.00E+00	8.39E-01	1.00E+00	1.00E+00	1.00E+00	N-formyl peptide receptor activity	F
GO:0004983	78	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuropeptide Y receptor activity	F
GO:0004984	103	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	olfactory receptor activity	F
GO:0004985	13	9.95E-01	1.00E+00	9.83E-01	1.00E+00	8.83E-01	1.00E+00	5.83E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	opioid receptor activity	F
GO:0004992	17	9.96E-01	1.00E+00	8.18E-01	1.00E+00	9.59E-01	1.00E+00	5.10E-01	1.00E+00	9.83E-01	1.00E+00	8.01E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	platelet activating factor receptor activity	F
GO:0004993	10	9.56E-01	1.00E+00	4.99E-01	1.00E+00	3.14E-01	1.00E+00	3.01E-01	1.00E+00	9.84E-01	1.00E+00	4.88E-01	1.00E+00	9.98E-01	1.00E+00	9.51E-01	1.00E+00	serotonin receptor activity	F
GO:0004994	18	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.97E-01	1.00E+00	7.86E-01	1.00E+00	9.99E-01	1.00E+00	7.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	somatostatin receptor activity	F
GO:0005000	13	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.26E-01	1.00E+00	8.55E-01	1.00E+00	9.96E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	8.36E-01	1.00E+00	vasopressin receptor activity	F
GO:0005001	18	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.26E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor protein tyrosine ph	F
GO:0005003	17	9.93E-01	1.00E+00	8.66E-01	1.00E+00	6.59E-01	1.00E+00	5.66E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	4.13E-01	1.00E+00	ephrin receptor activity	F
GO:0005021	71	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	vascular endothelial growth factor receptor	F
GO:0005024	15	7.15E-01	1.00E+00	9.51E-01	1.00E+00	3.46E-01	1.00E+00	3.77E-01	1.00E+00	7.48E-01	1.00E+00	9.42E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	transforming growth factor beta receptor ac	F
GO:0005035	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.11E-01	1.00E+00	3.85E-01	1.00E+00	death receptor activity	F
GO:0005041	12	7.46E-01	1.00E+00	2.87E-01	1.00E+00	5.29E-01	1.00E+00	7.32E-01	1.00E+00	6.87E-01	1.00E+00	1.53E-01	1.00E+00	9.91E-01	1.00E+00	6.89E-01	1.00E+00	low-density lipoprotein receptor activity	F
GO:0005044	42	9.76E-01	1.00E+00	1.00E+00	1.00E+00	5.62E-01	1.00E+00	7.69E-01	1.00E+00	9.29E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	scavenger receptor activity	F
GO:0005048	20	6.95E-02	1.00E+00	3.49E-01	1.00E+00	4.45E-02	7.24E-01	5.38E-01	1.00E+00	1.09E-01	1.00E+00	1.98E-01	1.00E+00	1.96E-01	1.00E+00	9.94E-01	1.00E+00	signal sequence binding	F
GO:0005057	170	9.89E-01	1.00E+00	9.61E-01	1.00E+00	4.87E-01	1.00E+00	6.12E-01	1.00E+00	9.89E-01	1.00E+00	9.41E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	receptor signaling protein activity	F

GO:0005066	11	8.71E-01	1.00E+00	7.91E-01	1.00E+00	5.09E-01	1.00E+00	2.25E-01	1.00E+00	8.19E-01	1.00E+00	8.03E-01	1.00E+00	6.21E-01	1.00E+00	9.92E-01	1.00E+00	transmembrane receptor protein tyrosine ki	F
GO:0005070	45	2.95E-01	1.00E+00	4.28E-01	1.00E+00	3.24E-02	5.87E-01	1.55E-01	1.00E+00	4.13E-01	1.00E+00	5.60E-01	1.00E+00	9.91E-01	1.00E+00	5.22E-01	1.00E+00	SH3/SH2 adaptor activity	F
GO:0005080	10	8.79E-01	1.00E+00	9.33E-01	1.00E+00	3.26E-01	1.00E+00	9.25E-01	1.00E+00	8.94E-01	1.00E+00	9.02E-01	1.00E+00	9.99E-01	1.00E+00	4.87E-01	1.00E+00	protein kinase C binding	F
GO:0005083	263	9.87E-01	1.00E+00	9.97E-01	1.00E+00	2.63E-01	1.00E+00	5.36E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	small GTPase regulator activity	F
GO:0005085	152	7.76E-01	1.00E+00	9.62E-01	1.00E+00	1.75E-01	1.00E+00	9.53E-02	1.00E+00	8.70E-01	1.00E+00	9.87E-01	1.00E+00	9.02E-01	1.00E+00	1.00E+00	1.00E+00	guanyl-nucleotide exchange factor activity	F
GO:0005086	17	8.16E-01	1.00E+00	8.92E-01	1.00E+00	3.63E-01	1.00E+00	3.36E-01	1.00E+00	9.27E-01	1.00E+00	9.72E-01	1.00E+00	8.42E-01	1.00E+00	6.97E-01	1.00E+00	ARF guanyl-nucleotide exchange factor act	F
GO:0005088	91	9.95E-01	1.00E+00	9.83E-01	1.00E+00	7.11E-01	1.00E+00	5.57E-01	1.00E+00	9.95E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	Ras guanyl-nucleotide exchange factor acti	F
GO:0005089	77	9.97E-01	1.00E+00	9.72E-01	1.00E+00	6.36E-01	1.00E+00	3.10E-01	1.00E+00	9.98E-01	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	Rho guanyl-nucleotide exchange factor acti	F
GO:0005095	10	3.90E-01	1.00E+00	7.31E-01	1.00E+00	8.25E-01	1.00E+00	9.95E-01	1.00E+00	2.07E-01	1.00E+00	6.38E-01	1.00E+00	6.42E-01	1.00E+00	7.76E-01	1.00E+00	GTPase inhibitor activity	F
GO:0005096	254	9.59E-01	1.00E+00	9.96E-01	1.00E+00	1.56E-01	1.00E+00	6.02E-01	1.00E+00	9.90E-01	1.00E+00	9.96E-01	1.00E+00	9.92E-01	1.00E+00	9.97E-01	1.00E+00	GTPase activator activity	F
GO:0005097	59	9.92E-01	1.00E+00	9.98E-01	1.00E+00	7.88E-01	1.00E+00	8.97E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.43E-01	1.00E+00	Rab GTPase activator activity	F
GO:0005099	97	9.90E-01	1.00E+00	9.85E-01	1.00E+00	5.20E-01	1.00E+00	7.38E-01	1.00E+00	9.97E-01	1.00E+00	9.86E-01	1.00E+00	9.91E-01	1.00E+00	9.64E-01	1.00E+00	Ras GTPase activator activity	F
GO:0005100	25	7.63E-01	1.00E+00	4.39E-01	1.00E+00	2.03E-01	1.00E+00	4.93E-01	1.00E+00	9.13E-01	1.00E+00	2.87E-01	1.00E+00	9.25E-01	1.00E+00	8.03E-01	1.00E+00	Rho GTPase activator activity	F
GO:0005102	914	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	receptor binding	F
GO:0005104	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.36E-01	1.00E+00	fibroblast growth factor receptor binding	F
GO:0005125	252	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.54E-01	1.00E+00	1.00E+00	1.00E+00	cytokine activity	F
GO:0005126	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0005149	16	1.00E+00	1.00E+00	8.58E-01	1.00E+00	7.72E-01	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	7.79E-01	1.00E+00	1.00E+00	1.00E+00	4.92E-01	1.00E+00	interleukin-1 receptor binding	F
GO:0005154	11	9.65E-01	1.00E+00	9.82E-01	1.00E+00	9.64E-01	1.00E+00	9.66E-01	1.00E+00	9.46E-01	1.00E+00	9.91E-01	1.00E+00	6.67E-01	1.00E+00	6.31E-01	1.00E+00	epidermal growth factor receptor binding	F
GO:0005158	22	8.71E-01	1.00E+00	8.77E-01	1.00E+00	1.00E+00	1.00E+00	4.70E-01	1.00E+00	7.62E-01	1.00E+00	9.92E-01	1.00E+00	5.99E-01	1.00E+00	6.03E-01	1.00E+00	insulin receptor binding	F
GO:0005159	13	9.83E-01	1.00E+00	9.47E-01	1.00E+00	8.39E-01	1.00E+00	8.37E-01	1.00E+00	9.84E-01	1.00E+00	9.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	insulin-like growth factor receptor binding	F
GO:0005160	12	4.34E-01	1.00E+00	6.64E-01	1.00E+00	7.86E-01	1.00E+00	6.60E-01	1.00E+00	2.75E-01	1.00E+00	5.81E-01	1.00E+00	9.97E-01	1.00E+00	9.93E-01	1.00E+00	transforming growth factor beta receptor bir	F
GO:0005164	41	1.00E+00	1.00E+00	9.26E-01	1.00E+00	9.97E-01	1.00E+00	9.12E-01	1.00E+00	1.00E+00	1.00E+00	8.46E-01	1.00E+00	1.00E+00	1.00E+00	8.38E-01	1.00E+00	tumor necrosis factor receptor binding	F
GO:0005178	49	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.27E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	integrin binding	F
GO:0005179	172	1.00E+00	1.00E+00	9.97E-01	1.00E+00	8.38E-01	1.00E+00	6.70E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	hormone activity	F
GO:0005184	27	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	8.50E-01	1.00E+00	9.88E-01	1.00E+00	neuropeptide hormone activity	F
GO:0005198	928	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	9.99E-01	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	7.35E-01	1.00E+00	9.71E-01	1.00E+00	structural molecule activity	F
GO:0005199	77	7.52E-01	1.00E+00	8.09E-01	1.00E+00	3.58E-01	1.00E+00	4.11E-01	1.00E+00	8.55E-01	1.00E+00	7.25E-01	1.00E+00	7.47E-01	1.00E+00	9.98E-01	1.00E+00	structural constituent of cell wall	F
GO:0005200	78	6.05E-01	1.00E+00	9.87E-01	1.00E+00	4.21E-01	1.00E+00	9.53E-01	1.00E+00	5.59E-01	1.00E+00	9.81E-01	1.00E+00	9.13E-01	1.00E+00	9.30E-01	1.00E+00	structural constituent of cytoskeleton	F
GO:0005201	101	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	extracellular matrix structural constituent	F
GO:0005212	17	5.10E-01	1.00E+00	7.64E-01	1.00E+00	4.46E-01	1.00E+00	9.99E-01	1.00E+00	3.89E-01	1.00E+00	3.40E-01	1.00E+00	9.64E-01	1.00E+00	9.88E-01	1.00E+00	structural constituent of eye lens	F
GO:0005215	1531	9.92E-01	1.00E+00	9.95E-01	1.00E+00	1.24E-02	1.92E-01	3.37E-01	1.00E+00	9.96E-01	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transporter activity	F
GO:0005216	483	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.08E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ion channel activity	F
GO:0005217	13	9.19E-01	1.00E+00	1.00E+00	1.00E+00	5.55E-01	1.00E+00	9.56E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	intracellular ligand-gated ion channel activit	F
GO:0005230	74	8.35E-01	1.00E+00	1.00E+00	1.00E+00	4.81E-01	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	9.99E-01	1.00E+00	7.96E-01	1.00E+00	9.11E-01	1.00E+00	extracellular ligand-gated ion channel activi	F
GO:0005231	48	5.81E-01	1.00E+00	9.64E-01	1.00E+00	3.53E-01	1.00E+00	9.92E-01	1.00E+00	6.51E-01	1.00E+00	9.38E-01	1.00E+00	7.02E-01	1.00E+00	5.93E-01	1.00E+00	excitatory extracellular ligand-gated ion cha	F
GO:0005234	19	9.35E-01	1.00E+00	9.98E-01	1.00E+00	4.31E-01	1.00E+00	9.30E-01	1.00E+00	9.76E-01	1.00E+00	9.97E-01	1.00E+00	9.60E-01	1.00E+00	9.98E-01	1.00E+00	glutamate-gated ion channel activity	F
GO:0005242	21	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.98E-01	1.00E+00	3.63E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.98E-01	1.00E+00	9.31E-01	1.00E+00	inward rectifier potassium channel activity	F
GO:0005244	300	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	voltage-gated ion channel activity	F
GO:0005245	52	5.33E-01	1.00E+00	8.37E-01	1.00E+00	1.09E-01	1.00E+00	8.33E-01	1.00E+00	3.73E-01	1.00E+00	7.36E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	voltage-gated calcium channel activity	F
GO:0005246	15	9.99E-01	1.00E+00	1.00E+00	1.00E+00	2.54E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.57E-01	1.00E+00	calcium channel regulator activity	F
GO:0005247	28	9.46E-01	1.00E+00	6.75E-01	1.00E+00	3.66E-01	1.00E+00	6.27E-01	1.00E+00	9.93E-01	1.00E+00	5.33E-01	1.00E+00	9.57E-01	1.00E+00	9.39E-01	1.00E+00	voltage-gated chloride channel activity	F
GO:0005248	17	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.27E-01	1.00E+00	9.88E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	voltage-gated sodium channel activity	F
GO:0005249	211	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	voltage-gated potassium channel activity	F
GO:0005251	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	delayed rectifier potassium channel activity	F
GO:0005253	78	1.00E+00	1.00E+00	9.98E-01	1.00E+00	7.15E-01	1.00E+00	8.60E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	anion channel activity	F
GO:0005254	73	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.72E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chloride channel activity	F
GO:0005261	362	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.28E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cation channel activity	F
GO:0005262	100	9.59E-01	1.00E+00	8.93E-01	1.00E+00	5.25E-01	1.00E+00	8.56E-01	1.00E+00	8.37E-01	1.00E+00	8.37E-01	1.00E+00	1.00E+00	1.00E+00	8.05E-01	1.00E+00	calcium channel activity	F
GO:0005267	229	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	potassium channel activity	F
GO:0005272	34	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.45E-01	1.00E+00	9.49E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	4.73E-01	1.00E+00	sodium channel activity	F
GO:0005275	67	8.26E-01	1.00E+00	9.74E-01	1.00E+00	6.93E-01	1.00E+00	8.22E-01	1.00E+00	7.02E-01	1.00E+00	9.43E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	amine transporter activity	F
GO:0005279	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	amino acid-polyamine transporter activity	F
GO:0005283	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.98E-01	1.00E+00	sodium:amino acid symporter activity	F
GO:0005310	60	9.91E-01	1.00E+00	8.70E-01	1.00E+00	7.73E-01	1.00E+00	3.58E-01	1.00E+00	9.97E-01	1.00E+00	8.06E-01	1.00E+00	7.98E-01	1.00E+00	1.00E+00	1.00E+00	dicarboxylic acid transporter activity	F
GO:0005313	10	9.98E-01	1.00E+00	9.98E-01	1.00E+00	7.76E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	L-glutamate transporter activity	F
GO:0005319	85	4.40E-01	1.00E+00	9.41E-01	1.00E+00	4.70E-02	8.68E-01	9.41E-01	1.00E+00	6.04E-01	1.00E+00	9.18E-01	1.00E+00	9.58E-01	1.00E+00	7.54E-01	1.00E+00	lipid transporter activity	F
GO:0005326	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.46E-01	1.00E+00	neurotransmitter transporter activity	F
GO:0005328	23	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.49E-01	1.00E+00	neurotransmitter:sodium symporter activity	F
GO:0005337	17	3.57E-02	1.00E+00	6.15E-01	1.00E+00	9.90E-03	1.57E-01	4.59E-02	1.00E+00	4.19E-01	1.00E+00	8.10E-01	1.00E+00	9.98E-01	1.00E+00	9.06E-01	1.00E+00	nucleoside transporter activity	F
GO:0005342	124	9.86E-01	1.00E+00	9.86E-01	1.00E+00	8.25E-01	1.00E+00	6.15E-01	1.00E+00	9.73E-01	1.00E+00	9.60E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	organic acid transporter activity	F
GO:0005343	75	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.75E-01	1.00E+00	5.18E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	organic acid:sodium symporter activity	F
GO:0005344	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen transporter activity	F
GO:0005351	44	2.93E-01	1.00E+00	4.46E-01	1.00E+00	2.99E-01	1.00E+00	8.03E-02	1.00E+00	2.83E-01	1.00E+00	6.35E-01	1.00E+00	8.31E-01	1.00E+00	7.78E-01	1.00E+00	sugar porter activity	F
GO:0005355	15	2.41E-01	1.00E+00	5.60E-01	1.00E+00	5.49E-01	1.00E+00	6.06E-01	1.00E+00	2.17E-01	1.00E+00	5.47E-01	1.00E+00	7.54E-01	1.00E+00	7.63E-01	1.00E+00	glucose transporter activity	F
GO:0005372	11	1.00E+00	1.00E+00	7.65E-01	1.00E+00	9.93E-01	1.00E+00	8.46E-01	1.00E+00	9.98E-01	1.00E+00	4.93E-01	1.00E+00	9.88E-01	1.00E+00	9.96E-01	1.00E+00	water transporter activity	F
GO:0005375	11	5.57E-01	1.00E+00	3.76E-01	1.00E+00	2.71E-01	1.00E+00	1.08E-01	1.00E+00	8.11E-01	1.00E+00	4.03E-01	1.00E+00	3.38E-01	1.00E+00	9.77E-01	1.00E+00	copper ion transporter activity	F
GO:0005385	12	7.33E-01	1.00E+00	1.49E-01	1.00E+00	8.93E-01	1.00E+00	5.41E-01	1.00E+00	5.47E-01	1.00E+00	9.18E-02	1.00E+00	9.96E-01	1.00E+00	7.65E-01	1.00E+00	zinc ion transporter activity	F
GO:0005386	401	9.79E-01	1.00E+00	9.51E-01	1.00E+00	2.96E-01	1.00E+00	3.32E-01	1.00E+00	9.93E-01	1.00E+00	8.99E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	carrier activity	F
GO:0005391	10	6.25E-01	1.00E+00	9.96E-01	1.00E+00	2.02E-01	1.00E+00	9.23E-01	1.00E+00	7.85E-01	1.00E+00	9.86E-01	1.00E+00	8.67E-01	1.00E+00	9.93E-01	1.00E+00	sodium:potassium-exchanging ATPase acti	F
GO:0005416	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	cation:amino acid symporter activity	F
GO:0005451	14	9.02E-01	1.00E+00	3.31E-01	1.00E+00	9.87E-01	1.00E+00	4.69E-01	1.00E+00	7.08E-01	1.00E+00	2.54E-01	1.00E+00	8.07E-01	1.00E+00	4.95E-01	1.00E+00	monovalent cation:proton antiporter activity	F
GO:0005452	18	8.15E-01	1.00E+00	9.98E-01	1.00E+00	3.27E-01	1.00E+00	9.89E-01	1.00E+00	9.80E-01	1.00E+00	9.72E-01	1.00E+00	3.30E-01	1.00E+00	9.90E-01	1.00E+00	inorganic anion exchanger activity	F
GO:0005478	29	2.54E-02	1.00E+00	1.45E-02	3.84E-01	2.12E-03	1.80E-02	1.50E-02	2.81E-01	5.10E-02	1.00E+00	2.97E-02	1.00E+00	6.30E-01	1.00E+00	6.02E-01	1.00E+00	intracellular transporter activity	F
GO:0005484	20	2.74E-01	1.00E+00	1.25E-01	1.00E+00	9.96E-02	1.00E+00	2.79E-01	1.00E+00	2.67E-01	1.00E+00	1.12E-01	1.00E+00	8.38E-01	1.00E+00	7.63E-01	1.00E+00	SNAP receptor activity	F

GO:0005488	12627	1.00E+00	1.00E+00	8.52E-01	1.00E+00	1.22E-08	0.00E+00	7.49E-07	0.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	binding	F
GO:0005496	85	1.00E+00	1.00E+00	9.83E-01	1.00E+00	4.56E-01	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	steroid binding	F
GO:0005501	17	6.32E-01	1.00E+00	9.06E-01	1.00E+00	8.81E-01	1.00E+00	9.98E-01	1.00E+00	2.82E-01	1.00E+00	6.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinoid binding	F
GO:0005504	25	1.10E-01	1.00E+00	4.54E-02	1.00E+00	2.31E-01	1.00E+00	1.26E-01	1.00E+00	5.36E-02	1.00E+00	3.14E-02	1.00E+00	7.42E-01	1.00E+00	8.58E-01	1.00E+00	fatty acid binding	F
GO:0005506	319	6.22E-01	1.00E+00	9.99E-01	1.00E+00	2.42E-01	1.00E+00	7.32E-01	1.00E+00	9.30E-01	1.00E+00	9.99E-01	1.00E+00	3.96E-01	1.00E+00	1.00E+00	1.00E+00	iron ion binding	F
GO:0005507	80	9.83E-01	1.00E+00	1.00E+00	1.00E+00	8.44E-01	1.00E+00	8.76E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	9.55E-01	1.00E+00	copper ion binding	F
GO:0005509	1014	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.57E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	calcium ion binding	F
GO:0005515	7459	9.98E-01	1.00E+00	5.50E-01	1.00E+00	1.02E-06	8.48E-04	2.40E-06	0.00E+00	1.00E+00	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	protein binding	F
GO:0005516	147	7.68E-01	1.00E+00	9.24E-01	1.00E+00	1.69E-01	1.00E+00	9.18E-01	1.00E+00	9.02E-01	1.00E+00	8.38E-01	1.00E+00	8.88E-01	1.00E+00	9.91E-01	1.00E+00	calmodulin binding	F
GO:0005518	18	8.40E-01	1.00E+00	9.99E-01	1.00E+00	1.62E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.71E-01	1.00E+00	5.87E-01	1.00E+00	1.00E+00	1.00E+00	collagen binding	F
GO:0005520	25	9.99E-01	1.00E+00	9.94E-01	1.00E+00	9.68E-01	1.00E+00	6.46E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.96E-01	1.00E+00	insulin-like growth factor binding	F
GO:0005523	13	6.17E-01	1.00E+00	9.49E-01	1.00E+00	6.86E-01	1.00E+00	2.98E-01	1.00E+00	5.94E-01	1.00E+00	9.99E-01	1.00E+00	5.85E-01	1.00E+00	4.98E-01	1.00E+00	tropomyosin binding	F
GO:0005524	1571	2.69E-04	1.10E-02	2.54E-06	1.41E-03	7.34E-10	0.00E+00	1.49E-07	0.00E+00	1.69E-02	3.81E-01	7.86E-05	2.29E-03	8.69E-01	1.00E+00	7.41E-01	1.00E+00	ATP binding	F
GO:0005525	398	1.13E-01	1.00E+00	1.20E-01	1.00E+00	5.42E-04	1.25E-02	3.21E-02	5.42E-01	5.82E-01	1.00E+00	3.94E-01	1.00E+00	8.71E-01	1.00E+00	7.72E-01	1.00E+00	GTP binding	F
GO:0005529	195	1.00E+00	1.00E+00	9.72E-01	1.00E+00	8.43E-01	1.00E+00	7.82E-01	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	3.83E-01	1.00E+00	sugar binding	F
GO:0005537	13	9.75E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	3.27E-01	1.00E+00	2.97E-01	1.00E+00	mannose binding	F
GO:0005539	107	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.05E-01	1.00E+00	1.00E+00	1.00E+00	9.44E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	glycosaminoglycan binding	F
GO:0005540	17	1.55E-01	1.00E+00	9.73E-01	1.00E+00	2.01E-01	1.00E+00	9.07E-01	1.00E+00	2.19E-01	1.00E+00	9.39E-01	1.00E+00	2.77E-01	1.00E+00	9.75E-01	1.00E+00	hyaluronic acid binding	F
GO:0005542	13	9.69E-01	1.00E+00	3.73E-01	1.00E+00	2.51E-01	1.00E+00	5.55E-01	1.00E+00	9.82E-01	1.00E+00	4.91E-01	1.00E+00	1.00E+00	1.00E+00	2.71E-01	1.00E+00	folic acid binding	F
GO:0005543	149	2.61E-01	1.00E+00	2.97E-02	1.00E+00	2.13E-03	1.80E-02	1.92E-03	2.70E-02	4.30E-01	1.00E+00	4.48E-02	1.00E+00	9.88E-01	1.00E+00	8.78E-01	1.00E+00	phospholipid binding	F
GO:0005544	24	7.77E-01	1.00E+00	9.89E-01	1.00E+00	1.49E-01	1.00E+00	9.74E-01	1.00E+00	8.91E-01	1.00E+00	9.36E-01	1.00E+00	9.90E-01	1.00E+00	9.94E-01	1.00E+00	calcium-dependent phospholipid binding	F
GO:0005545	16	1.88E-01	1.00E+00	1.68E-01	1.00E+00	5.49E-02	1.00E+00	3.95E-02	1.00E+00	2.22E-01	1.00E+00	2.67E-01	1.00E+00	6.95E-01	1.00E+00	2.55E-01	1.00E+00	phosphatidylinositol binding	F
GO:0005548	30	7.30E-01	1.00E+00	6.81E-01	1.00E+00	2.20E-01	1.00E+00	8.42E-01	1.00E+00	8.92E-01	1.00E+00	3.56E-01	1.00E+00	8.63E-01	1.00E+00	9.78E-01	1.00E+00	phospholipid transporter activity	F
GO:0005575	15522	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-04	1.25E-02	1.98E-04	7.00E-03	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cellular_component	C
GO:0005576	2042	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular region	C
GO:0005578	343	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular matrix (sensu Metazoa)	C
GO:0005581	37	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	collagen	C
GO:0005604	74	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.46E-01	1.00E+00	basement membrane	C
GO:0005605	29	9.99E-01	1.00E+00	9.83E-01	1.00E+00	5.30E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.85E-01	1.00E+00	2.89E-01	1.00E+00	basal lamina	C
GO:0005615	515	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular space	C
GO:0005622	10581	1.85E-01	1.00E+00	1.18E-09	1.00E-03	1.40E-15	0.00E+00	1.89E-21	0.00E+00	7.70E-01	1.00E+00	1.72E-04	2.29E-03	1.00E+00	1.00E+00	8.53E-01	1.00E+00	intracellular	C
GO:0005623	14225	1.00E+00	1.00E+00	9.52E-01	1.00E+00	1.23E-05	9.71E-04	1.44E-07	0.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell	C
GO:0005624	652	9.98E-01	1.00E+00	9.74E-01	1.00E+00	6.10E-01	1.00E+00	9.04E-02	1.00E+00	9.98E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	membrane fraction	C
GO:0005625	227	9.96E-01	1.00E+00	8.42E-01	1.00E+00	6.92E-01	1.00E+00	6.51E-01	1.00E+00	9.97E-01	1.00E+00	8.15E-01	1.00E+00	9.99E-01	1.00E+00	9.18E-01	1.00E+00	soluble fraction	C
GO:0005626	23	1.89E-01	1.00E+00	3.67E-01	1.00E+00	2.62E-01	1.00E+00	4.58E-01	1.00E+00	3.31E-01	1.00E+00	3.19E-01	1.00E+00	1.94E-01	1.00E+00	4.49E-01	1.00E+00	insoluble fraction	C
GO:0005634	4748	2.28E-01	1.00E+00	4.94E-19	0.00E+00	1.54E-07	0.00E+00	1.38E-20	0.00E+00	6.33E-01	1.00E+00	7.92E-12	1.05E-04	9.98E-01	1.00E+00	1.15E-01	1.00E+00	nucleus	C
GO:0005635	201	3.44E-03	1.37E-01	4.75E-06	1.41E-03	2.50E-06	8.48E-04	6.92E-06	8.32E-04	1.13E-02	3.01E-01	1.35E-04	2.29E-03	9.22E-01	1.00E+00	3.67E-02	5.54E-01	nuclear envelope	C
GO:0005637	21	7.82E-01	1.00E+00	1.83E-01	1.00E+00	3.50E-01	1.00E+00	5.87E-01	1.00E+00	8.62E-01	1.00E+00	2.27E-01	1.00E+00	8.25E-01	1.00E+00	1.86E-01	1.00E+00	nuclear inner membrane	C
GO:0005640	15	3.23E-01	1.00E+00	4.99E-01	1.00E+00	1.00E-01	1.00E+00	5.10E-01	1.00E+00	5.32E-01	1.00E+00	9.71E-01	1.00E+00	3.99E-01	1.00E+00	1.55E-01	1.00E+00	nuclear outer membrane	C
GO:0005643	70	3.82E-05	5.00E-03	1.61E-09	1.00E-03	2.55E-06	8.48E-04	6.19E-07	0.00E+00	2.72E-04	4.00E-03	9.39E-08	1.05E-04	8.53E-02	1.00E+00	2.26E-04	5.00E-04	nuclear pore	C
GO:0005654	736	7.07E-05	5.00E-03	9.47E-11	0.00E+00	1.97E-08	0.00E+00	1.82E-08	0.00E+00	3.65E-03	6.24E-02	5.47E-08	1.05E-04	8.06E-01	1.00E+00	2.62E-02	2.52E-01	nucleoplasm	C
GO:0005657	30	5.28E-02	1.00E+00	1.50E-02	3.84E-01	2.05E-03	1.80E-02	4.57E-03	6.84E-02	6.54E-02	1.00E+00	4.63E-02	1.00E+00	8.94E-01	1.00E+00	2.73E-01	1.00E+00	replication fork	C
GO:0005665	14	3.39E-01	1.00E+00	1.31E-01	1.00E+00	1.83E-01	1.00E+00	7.51E-01	1.00E+00	6.83E-01	1.00E+00	6.75E-02	1.00E+00	6.17E-01	1.00E+00	6.83E-01	1.00E+00	DNA-directed RNA polymerase II, core com	C
GO:0005667	221	3.21E-01	1.00E+00	1.38E-01	1.00E+00	8.00E-03	1.57E-01	6.70E-02	1.00E+00	4.23E-01	1.00E+00	1.45E-01	1.00E+00	9.97E-01	1.00E+00	9.16E-01	1.00E+00	transcription factor complex	C
GO:0005669	24	1.79E-02	5.62E-01	3.68E-03	6.30E-02	5.85E-03	9.30E-02	1.48E-01	1.00E+00	4.73E-02	1.00E+00	1.36E-03	1.70E-02	8.87E-01	1.00E+00	3.98E-01	1.00E+00	transcription factor TFIID complex	C
GO:0005680	12	6.94E-02	1.00E+00	2.62E-02	1.00E+00	4.15E-02	5.87E-01	2.32E-02	4.10E-01	8.24E-02	1.00E+00	3.77E-02	1.00E+00	8.92E-01	1.00E+00	6.57E-01	1.00E+00	anaphase-promoting complex	C
GO:0005681	135	2.00E-03	4.90E-02	1.16E-04	4.00E-03	4.32E-04	1.25E-02	3.29E-04	7.00E-03	3.42E-02	6.55E-01	6.31E-04	1.02E-02	8.63E-02	1.00E+00	1.33E-01	1.00E+00	spliceosome complex	C
GO:0005684	10	4.82E-04	1.60E-02	1.45E-02	3.84E-01	4.12E-04	1.25E-02	6.68E-02	1.00E+00	1.30E-02	3.01E-01	2.23E-02	7.69E-01	5.17E-02	1.00E+00	8.67E-02	1.00E+00	major (U2-dependent) spliceosome	C
GO:0005689	11	4.70E-02	1.00E+00	1.82E-03	3.90E-02	4.98E-03	9.30E-02	1.67E-02	4.10E-01	6.15E-02	1.00E+00	1.13E-02	2.12E-01	8.13E-01	1.00E+00	5.96E-02	1.00E+00	minor (U12-dependent) spliceosome compl	C
GO:0005694	435	1.34E-02	2.72E-01	2.32E-04	8.26E-03	9.65E-04	1.25E-02	2.90E-04	7.00E-03	3.16E-02	6.55E-01	1.15E-03	1.02E-02	8.65E-01	1.00E+00	3.24E-01	1.00E+00	chromosome	C
GO:0005720	24	6.71E-01	1.00E+00	1.65E-01	1.00E+00	2.88E-01	1.00E+00	4.58E-01	1.00E+00	6.83E-01	1.00E+00	1.92E-01	1.00E+00	9.95E-01	1.00E+00	8.13E-02	1.00E+00	nuclear heterochromatin	C
GO:0005730	174	2.84E-02	1.00E+00	2.82E-04	8.26E-03	2.73E-01	1.00E+00	4.82E-03	6.84E-02	3.44E-02	6.55E-01	5.43E-03	7.40E-02	1.94E-01	1.00E+00	2.92E-01	1.00E+00	nucleolus	C
GO:0005732	15	4.03E-01	1.00E+00	1.45E-01	1.00E+00	2.56E-01	1.00E+00	1.50E-01	1.00E+00	4.30E-01	1.00E+00	2.95E-01	1.00E+00	9.70E-01	1.00E+00	6.68E-01	1.00E+00	small nucleolar ribonucleoprotein complex	C
GO:0005737	6633	1.38E-02	2.72E-01	6.03E-05	4.00E-03	3.59E-15	0.00E+00	1.42E-16	0.00E+00	3.44E-01	1.00E+00	3.20E-02	1.00E+00	9.94E-01	1.00E+00	9.25E-01	1.00E+00	cytoplasm	C
GO:0005739	951	1.47E-09	1.25E-04	5.69E-10	1.00E-03	1.34E-08	0.00E+00	1.29E-08	0.00E+00	3.13E-06	5.00E-04	1.75E-07	2.22E-04	6.58E-02	1.00E+00	2.10E-01	1.00E+00	mitochondrion	C
GO:0005740	390	3.99E-04	1.60E-02	8.10E-05	4.00E-03	5.89E-05	4.57E-03	4.76E-04	7.17E-03	1.55E-02	3.01E-01	3.71E-04	1.02E-02	1.48E-01	1.00E+00	2.71E-01	1.00E+00	mitochondrial envelope	C
GO:0005741	73	2.83E-01	1.00E+00	3.11E-02	1.00E+00	2.43E-01	1.00E+00	7.22E-02	1.00E+00	6.61E-01	1.00E+00	5.01E-02	1.00E+00	5.10E-02	1.00E+00	3.18E-01	1.00E+00	mitochondrial outer membrane	C
GO:0005743	284	3.90E-04	1.60E-02	7.36E-04	1.90E-02	8.91E-04	1.25E-02	9.74E-04	1.11E-02	2.95E-03	5.00E-02	2.37E-03	5.10E-02	1.84E-01	1.00E+00	4.01E-01	1.00E+00	mitochondrial inner membrane	C
GO:0005744	12	2.22E-01	1.00E+00	4.44E-02	1.00E+00	1.63E-01	1.00E+00	1.26E-02	1.57E-01	5.87E-01	1.00E+00	1.13E-01	1.00E+00	2.09E-01	1.00E+00	3.89E-01	1.00E+00	mitochondrial inner membrane presequenc	C
GO:0005746	64	3.09E-02	1.00E+00	1.40E-02	3.84E-01	3.80E-01	1.00E+00	4.89E-02	1.00E+00	3.01E-02	6.55E-01	4.55E-02	1.00E+00	1.36E-01	1.00E+00	1.15E-01	1.00E+00	mitochondrial electron transport chain	C
GO:0005747	37	3.71E-03	1.37E-01	1.49E-03	3.90E-02	2.30E-01	1.00E+00	2.60E-02	4.10E-01	6.35E-04	4.90E-03	2.10E-03	5.10E-02	5.65E-01	1.00E+00	9.97E-02	1.00E+00	respiratory chain complex I (sensu Eukaryo	C
GO:0005753	16	1.40E-02	2.72E-01	1.93E-01	1.00E+00	3.90E-02	5.87E-01	3.66E-01	1.00E+00	1.07E-01	1.00E+00	1.72E-01	1.00E+00	2.54E-01	1.00E+00	4.65E-01	1.00E+00	proton-transporting ATP synthase complex	C
GO:0005758	28	7.95E-01	1.00E+00	3.86E-01	1.00E+00	3.79E-01	1.00E+00	6.88E-02	1.00E+00	9.37E-01	1.00E+00	5.04E-01	1.00E+00	7.89E-01	1.00E+00	8.27E-01	1.00E+00	mitochondrial intermembrane space	C
GO:0005759	195	2.12E-03	4.90E-02	1.06E-03	2.00E-02	9.60E-02	1.00E+00	2.75E-03	5.60E-02	2.36E-03	4.30E-02	1.01E-02	2.12E-01	2.77E-01	1.00E+00	6.44E-01	1.00E+00	mitochondrial matrix	C
GO:0005761	50	1.09E-01	1.00E+00	2.79E-01	1.00E+00	9.73E-01	1.00E+00	1.14E-01	1.00E+00	1.91E-02	3.81E-01	4.39E-01	1.00E+00	7.50E-01	1.00E+00	7.29E-01	1.00E+00	mitochondrial ribosome	C
GO:0005762	17	8.38E-01	1.00E+00	6.91E-01	1.00E+00	9.97E-01	1.00E+00	3.45E-01	1.00E+00	3.76E-01	1.00E+00	6.68E-01	1.00E+00	1.00E+00	1.00E+00	8.86E-01	1.00E+00	mitochondrial large ribosomal subunit	C
GO:0005763	20	2.25E-02	1.00E+00	5.77E-01	1.00E+00	9.96E-01	1.00E+00	3.84E-01	1.00E+00	8.70E-03	2.02E-01	7.64E-01	1.00E+00	1.80E-01	1.00E+00	3.40E-01	1.00E+00	mitochondrial small ribosomal subunit	C
GO:0005764	213	2.20E-01	1.00E+00	8.04E-02	1.00E+00	4.54E-02	8.68E-01	9.39E-03	1.12E-01	3.08E-01	1.00E+00	1.28E-01	1.00E+00	7.37E-01	1.00E+00	7.55E-01	1.00E+00	lysosome	C
GO:0005765	62	1.12E-01	1.00E+00	9.24E-02	1.00E+00	7.61E-02	1.00E+00	1.24E-02	1.57E-01	6.99E-02	1.00E+00	1.25E-01	1.00E+00	9.91E-01	1.00E+00	8.07E-01	1.00E+00	lysosomal membrane	C
GO:0005768	233	2.57E-01	1.00E+00	1.63E-01	1.00E+00	2.19E-02	2.63E-01	4.52E-03	6.84E-02	2.69E-01	1.00E+00	3.18E-01	1.00E+00	9.99E-01	1.00E+00	6.39E-01	1.00E+00	endosome	C
GO:0005769	65	4.43E-02	1.00E+00	1.68E-03	3.90E-02	3.12E-02	5.65E-01	5.41E-03	8.10E-02	6.85E-02	1.00E+00	1.41E-02	5.65E-01	6.75E-01	1.00E+00	1.69E-02	1.77E-01	early endosome	C
GO:0005770	60	1.29E-01	1.00E+00	1.25E-01	1.00E+00	1.75E-01	1.00E+00	1.65E-02	4.10E-01	5.85E-02	1.00E+00	1.64E-01	1.00E+00	1.00E+00	1.00E+00	7.49E-01	1.00E+00	late endosome	C
GO:0005773	236	2.33E-01	1.00E+00	4.84E-02	1.00E+00	1.11E-01	1.00E+00	3.80E-03	6.84E-02	2.35E-01	1.00E+00	7.41E-02	1.00E+00	7.69E-01	1.00E+00	8.45E-01	1.00E+00	vacuole	C
GO:0005774	73	2.31E-01	1.00E+00	1.20E-01	1.00E+00	1.78E-01	1.00E+00	5.70E-03	8.10E-02	1.27E-01	1.00E+00	1.77E-01	1.00E+00	9.98E-01	1.00E+00	9.19E-01	1.00E+00	vacuolar membrane	C
GO:0005776	10	2.76E-02	1.00E+00	9.05E-03	3.84E-01	5.65E-01	1.00E+00	8.90E-02	1.00E+00	3.12E-02	6.55E-01	7.83E-04	1.02E-02	2.56E-01	1.00E+00	3.80E-01	1.00E+00	autophagic vacuole	C

GO:0005777	98	5.33E-03	1.37E-01	7.61E-02	1.00E+00	8.51E-03	1.57E-01	3.07E-03	5.60E-02	4.87E-02	1.00E+00	2.53E-01	1.00E+00	4.22E-01	1.00E+00	7.32E-01	1.00E+00	peroxisome	C
GO:0005778	42	3.11E-02	1.00E+00	3.47E-01	1.00E+00	9.70E-02	1.00E+00	8.05E-02	1.00E+00	7.29E-02	1.00E+00	5.60E-01	1.00E+00	4.37E-01	1.00E+00	4.44E-01	1.00E+00	peroxisomal membrane	C
GO:0005779	12	1.21E-01	1.00E+00	5.75E-01	1.00E+00	1.18E-01	1.00E+00	7.26E-01	1.00E+00	1.88E-01	1.00E+00	4.40E-01	1.00E+00	7.75E-01	1.00E+00	5.68E-01	1.00E+00	integral to peroxisomal membrane	C
GO:0005783	863	4.38E-01	1.00E+00	1.53E-01	1.00E+00	1.53E-03	1.60E-02	5.42E-04	7.17E-03	5.82E-01	1.00E+00	4.51E-01	1.00E+00	9.99E-01	1.00E+00	8.83E-01	1.00E+00	endoplasmic reticulum	C
GO:0005788	69	6.35E-02	1.00E+00	6.43E-02	1.00E+00	6.23E-03	9.30E-02	1.15E-01	1.00E+00	1.62E-01	1.00E+00	5.35E-02	1.00E+00	2.43E-01	1.00E+00	5.39E-01	1.00E+00	endoplasmic reticulum lumen	C
GO:0005789	506	5.92E-01	1.00E+00	3.02E-01	1.00E+00	1.89E-03	1.80E-02	3.12E-03	5.60E-02	7.88E-01	1.00E+00	6.91E-01	1.00E+00	9.99E-01	1.00E+00	8.32E-01	1.00E+00	endoplasmic reticulum membrane	C
GO:0005790	10	6.40E-01	1.00E+00	8.47E-01	1.00E+00	2.95E-01	1.00E+00	3.67E-01	1.00E+00	8.69E-01	1.00E+00	8.42E-01	1.00E+00	6.67E-01	1.00E+00	1.00E+00	1.00E+00	smooth endoplasmic reticulum	C
GO:0005791	17	4.08E-01	1.00E+00	3.71E-01	1.00E+00	4.52E-01	1.00E+00	5.66E-01	1.00E+00	2.80E-01	1.00E+00	3.59E-01	1.00E+00	8.85E-01	1.00E+00	4.24E-01	1.00E+00	rough endoplasmic reticulum	C
GO:0005792	182	9.98E-01	1.00E+00	9.44E-01	1.00E+00	6.66E-01	1.00E+00	1.99E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	microsome	C
GO:0005793	34	2.29E-02	1.00E+00	5.18E-02	1.00E+00	1.41E-02	1.92E-01	6.76E-03	8.10E-02	1.80E-02	3.81E-01	1.96E-01	1.00E+00	9.86E-01	1.00E+00	4.40E-01	1.00E+00	ER-Golgi intermediate compartment	C
GO:0005794	688	4.21E-01	1.00E+00	1.83E-02	9.24E-01	1.23E-06	8.48E-04	1.64E-05	2.00E-03	8.35E-01	1.00E+00	1.30E-01	1.00E+00	1.00E+00	1.00E+00	8.78E-01	1.00E+00	Golgi apparatus	C
GO:0005795	19	3.18E-01	1.00E+00	1.11E-01	1.00E+00	7.58E-02	1.00E+00	2.28E-02	4.10E-01	3.86E-01	1.00E+00	1.57E-01	1.00E+00	1.00E+00	1.00E+00	9.08E-01	1.00E+00	Golgi stack	C
GO:0005798	53	4.85E-02	1.00E+00	1.88E-02	9.24E-01	1.27E-02	1.92E-01	1.85E-02	4.10E-01	6.15E-02	1.00E+00	7.09E-02	1.00E+00	8.57E-01	1.00E+00	7.07E-02	1.00E+00	Golgi-associated vesicle	C
GO:0005801	14	2.58E-01	1.00E+00	2.93E-02	1.00E+00	1.40E-01	1.00E+00	1.14E-01	1.00E+00	3.44E-01	1.00E+00	7.86E-02	1.00E+00	5.28E-01	1.00E+00	1.02E-03	9.50E-03	Golgi cis face	C
GO:0005802	27	2.85E-01	1.00E+00	3.49E-02	1.00E+00	1.74E-02	2.36E-01	1.17E-02	1.27E-01	3.95E-01	1.00E+00	8.04E-02	1.00E+00	9.99E-01	1.00E+00	8.48E-01	1.00E+00	Golgi trans face	C
GO:0005811	13	2.44E-01	1.00E+00	2.05E-02	9.24E-01	1.97E-01	1.00E+00	8.41E-02	1.00E+00	2.65E-01	1.00E+00	1.11E-01	1.00E+00	2.47E-01	1.00E+00	7.55E-02	1.00E+00	lipid particle	C
GO:0005813	141	1.03E-01	1.00E+00	2.82E-03	5.10E-02	3.49E-02	5.87E-01	2.34E-03	2.70E-02	3.25E-01	1.00E+00	1.50E-02	5.65E-01	4.42E-01	1.00E+00	9.89E-02	1.00E+00	centrosome	C
GO:0005814	10	1.68E-01	1.00E+00	2.40E-02	1.00E+00	5.75E-02	1.00E+00	8.79E-02	1.00E+00	4.94E-01	1.00E+00	3.92E-02	1.00E+00	5.60E-02	1.00E+00	6.24E-02	1.00E+00	centriole	C
GO:0005815	162	1.53E-01	1.00E+00	1.30E-02	3.84E-01	3.07E-02	5.65E-01	5.56E-03	8.10E-02	4.72E-01	1.00E+00	4.72E-02	1.00E+00	4.16E-01	1.00E+00	2.03E-01	1.00E+00	microtubule organizing center	C
GO:0005819	89	1.27E-01	1.00E+00	6.47E-04	1.90E-02	5.19E-02	1.00E+00	1.24E-02	1.57E-01	1.44E-01	1.00E+00	1.17E-03	1.02E-02	8.74E-01	1.00E+00	2.84E-02	2.52E-01	spindle	C
GO:0005829	973	1.60E-02	3.10E-01	2.15E-06	1.41E-03	1.32E-05	9.71E-04	9.76E-10	0.00E+00	3.46E-01	1.00E+00	1.24E-04	2.29E-03	7.11E-01	1.00E+00	5.14E-01	1.00E+00	cytosol	C
GO:0005833	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hemoglobin complex	C
GO:0005834	27	9.50E-01	1.00E+00	8.49E-01	1.00E+00	9.87E-01	1.00E+00	9.92E-01	1.00E+00	8.99E-01	1.00E+00	6.96E-01	1.00E+00	7.10E-01	1.00E+00	6.29E-01	1.00E+00	heterotrimeric G-protein complex	C
GO:0005839	23	3.37E-01	1.00E+00	6.42E-01	1.00E+00	6.70E-01	1.00E+00	1.68E-01	1.00E+00	2.25E-01	1.00E+00	7.04E-01	1.00E+00	6.11E-01	1.00E+00	9.00E-01	1.00E+00	proteasome core complex (sensu Eukaryot	C
GO:0005840	296	8.24E-02	1.00E+00	1.12E-01	1.00E+00	9.84E-01	1.00E+00	1.60E-01	1.00E+00	6.39E-02	1.00E+00	1.73E-01	1.00E+00	1.93E-01	1.00E+00	3.38E-01	1.00E+00	ribosome	C
GO:0005844	12	5.12E-01	1.00E+00	7.18E-01	1.00E+00	1.48E-01	1.00E+00	3.73E-01	1.00E+00	7.08E-01	1.00E+00	7.00E-01	1.00E+00	4.74E-01	1.00E+00	9.97E-01	1.00E+00	polysome	C
GO:0005852	12	2.01E-02	1.00E+00	4.38E-03	6.30E-02	8.65E-02	1.00E+00	5.91E-02	1.00E+00	6.53E-02	1.00E+00	9.48E-03	1.43E-01	3.56E-02	9.62E-01	2.16E-02	1.77E-01	eukaryotic translation initiation factor 3 com	C
GO:0005856	1142	7.90E-01	1.00E+00	8.11E-01	1.00E+00	5.64E-04	1.25E-02	3.10E-01	1.00E+00	9.77E-01	1.00E+00	7.89E-01	1.00E+00	9.97E-01	1.00E+00	9.72E-01	1.00E+00	cytoskeleton	C
GO:0005858	13	5.05E-01	1.00E+00	3.45E-01	1.00E+00	2.80E-01	1.00E+00	2.44E-01	1.00E+00	4.39E-01	1.00E+00	3.90E-01	1.00E+00	9.95E-01	1.00E+00	3.95E-01	1.00E+00	axonemal dynein complex	C
GO:0005863	18	3.34E-01	1.00E+00	9.89E-01	1.00E+00	3.12E-01	1.00E+00	8.64E-01	1.00E+00	3.49E-01	1.00E+00	9.72E-01	1.00E+00	6.71E-01	1.00E+00	9.99E-01	1.00E+00	striated muscle thick filament	C
GO:0005865	13	7.28E-01	1.00E+00	9.71E-01	1.00E+00	4.03E-01	1.00E+00	8.59E-01	1.00E+00	8.46E-01	1.00E+00	9.72E-01	1.00E+00	9.05E-01	1.00E+00	9.99E-01	1.00E+00	striated muscle thin filament	C
GO:0005871	18	9.28E-03	1.77E-01	9.66E-03	3.84E-01	4.18E-02	5.87E-01	2.45E-02	4.10E-01	3.83E-03	6.24E-02	8.04E-03	1.05E-01	5.85E-01	1.00E+00	3.25E-01	1.00E+00	kinesin complex	C
GO:0005874	255	1.29E-02	2.72E-01	1.04E-02	3.84E-01	1.69E-05	9.71E-04	5.01E-04	7.17E-03	8.33E-02	1.00E+00	2.25E-02	7.69E-01	7.34E-01	1.00E+00	4.99E-01	1.00E+00	microtubule	C
GO:0005875	117	9.75E-02	1.00E+00	6.80E-02	1.00E+00	3.35E-03	3.50E-02	6.84E-03	8.10E-02	1.51E-01	1.00E+00	1.12E-01	1.00E+00	9.03E-01	1.00E+00	5.47E-01	1.00E+00	microtubule associated complex	C
GO:0005876	19	1.69E-03	4.90E-02	3.67E-03	6.30E-02	1.57E-03	1.60E-02	3.53E-03	5.60E-02	7.91E-03	2.02E-01	3.24E-02	1.00E+00	4.92E-01	1.00E+00	4.37E-02	8.10E-01	spindle microtubule	C
GO:0005882	106	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	intermediate filament	C
GO:0005884	30	2.48E-01	1.00E+00	5.98E-01	1.00E+00	8.78E-02	1.00E+00	2.24E-01	1.00E+00	2.64E-01	1.00E+00	6.85E-01	1.00E+00	8.63E-01	1.00E+00	5.68E-01	1.00E+00	actin filament	C
GO:0005886	2991	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	plasma membrane	C
GO:0005887	1190	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	integral to plasma membrane	C
GO:0005891	32	8.57E-01	1.00E+00	9.76E-01	1.00E+00	1.71E-01	1.00E+00	9.77E-01	1.00E+00	8.57E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	voltage-gated calcium channel complex	C
GO:0005892	14	3.22E-01	1.00E+00	6.87E-01	1.00E+00	1.99E-01	1.00E+00	8.67E-01	1.00E+00	5.67E-01	1.00E+00	5.91E-01	1.00E+00	9.42E-02	1.00E+00	5.35E-01	1.00E+00	nicotinic acetylcholine-gated receptor-chan	C
GO:0005901	36	1.59E-01	1.00E+00	8.37E-01	1.00E+00	1.93E-01	1.00E+00	2.14E-01	1.00E+00	1.40E-01	1.00E+00	9.44E-01	1.00E+00	8.59E-01	1.00E+00	7.46E-01	1.00E+00	caveola	C
GO:0005902	16	9.91E-01	1.00E+00	9.24E-01	1.00E+00	3.83E-01	1.00E+00	4.38E-01	1.00E+00	9.97E-01	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	microvillus	C
GO:0005903	27	9.51E-01	1.00E+00	9.91E-01	1.00E+00	9.83E-01	1.00E+00	8.64E-01	1.00E+00	8.34E-01	1.00E+00	9.77E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	brush border	C
GO:0005905	38	1.35E-01	1.00E+00	1.50E-01	1.00E+00	1.50E-02	1.92E-01	1.07E-02	1.23E-01	1.61E-01	1.00E+00	2.75E-01	1.00E+00	9.98E-01	1.00E+00	7.02E-01	1.00E+00	coated pit	C
GO:0005911	169	8.87E-01	1.00E+00	9.66E-01	1.00E+00	5.82E-01	1.00E+00	8.35E-01	1.00E+00	9.05E-01	1.00E+00	9.13E-01	1.00E+00	9.22E-01	1.00E+00	9.73E-01	1.00E+00	intercellular junction	C
GO:0005912	71	6.46E-01	1.00E+00	8.10E-01	1.00E+00	1.58E-01	1.00E+00	9.38E-02	1.00E+00	6.38E-01	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	adherens junction	C
GO:0005913	25	9.94E-01	1.00E+00	5.92E-01	1.00E+00	6.13E-01	1.00E+00	2.39E-01	1.00E+00	9.99E-01	1.00E+00	6.53E-01	1.00E+00	1.00E+00	1.00E+00	7.25E-01	1.00E+00	cell-cell adherens junction	C
GO:0005921	28	9.65E-01	1.00E+00	7.32E-01	1.00E+00	8.98E-01	1.00E+00	8.57E-01	1.00E+00	9.96E-01	1.00E+00	8.02E-01	1.00E+00	5.00E-01	1.00E+00	1.98E-01	1.00E+00	gap junction	C
GO:0005922	22	8.74E-01	1.00E+00	7.23E-01	1.00E+00	8.12E-01	1.00E+00	8.48E-01	1.00E+00	9.77E-01	1.00E+00	8.41E-01	1.00E+00	3.71E-01	1.00E+00	1.68E-01	1.00E+00	connexon complex	C
GO:0005923	82	1.36E-01	1.00E+00	5.20E-01	1.00E+00	1.30E-01	1.00E+00	3.27E-01	1.00E+00	1.08E-01	1.00E+00	3.49E-01	1.00E+00	6.88E-01	1.00E+00	9.96E-01	1.00E+00	tight junction	C
GO:0005924	44	3.62E-01	1.00E+00	8.49E-01	1.00E+00	1.18E-01	1.00E+00	3.89E-01	1.00E+00	2.92E-01	1.00E+00	8.35E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	cell-substrate adherens junction	C
GO:0005925	40	6.56E-01	1.00E+00	7.89E-01	1.00E+00	3.47E-01	1.00E+00	4.04E-01	1.00E+00	5.30E-01	1.00E+00	7.66E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	focal adhesion	C
GO:0005929	85	8.04E-01	1.00E+00	3.21E-01	1.00E+00	2.40E-01	1.00E+00	7.38E-02	1.00E+00	8.27E-01	1.00E+00	4.29E-01	1.00E+00	9.86E-01	1.00E+00	6.90E-01	1.00E+00	cilium	C
GO:0005930	22	6.26E-01	1.00E+00	4.12E-01	1.00E+00	2.66E-01	1.00E+00	3.23E-01	1.00E+00	6.65E-01	1.00E+00	3.73E-01	1.00E+00	9.58E-01	1.00E+00	8.14E-01	1.00E+00	axoneme	C
GO:0005932	13	8.28E-01	1.00E+00	8.80E-01	1.00E+00	4.95E-02	8.68E-01	2.83E-01	1.00E+00	9.83E-01	1.00E+00	9.23E-01	1.00E+00	9.64E-01	1.00E+00	7.82E-01	1.00E+00	basal body	C
GO:0005938	81	4.34E-01	1.00E+00	6.68E-01	1.00E+00	4.00E-02	5.87E-01	5.43E-01	1.00E+00	5.75E-01	1.00E+00	8.30E-01	1.00E+00	9.51E-01	1.00E+00	2.87E-01	1.00E+00	cell cortex	C
GO:0005941	51	9.79E-01	1.00E+00	8.02E-01	1.00E+00	9.36E-01	1.00E+00	3.77E-01	1.00E+00	9.82E-01	1.00E+00	8.73E-01	1.00E+00	9.69E-01	1.00E+00	8.83E-01	1.00E+00	unlocalized protein complex	C
GO:0005942	18	6.40E-02	1.00E+00	5.25E-02	1.00E+00	1.75E-02	2.36E-01	3.50E-01	1.00E+00	8.46E-02	1.00E+00	5.91E-02	1.00E+00	5.15E-01	1.00E+00	1.13E-01	1.00E+00	phosphoinositide 3-kinase complex	C
GO:0005952	24	9.56E-01	1.00E+00	9.04E-01	1.00E+00	9.23E-01	1.00E+00	8.94E-01	1.00E+00	9.64E-01	1.00E+00	9.42E-01	1.00E+00	8.81E-01	1.00E+00	5.76E-01	1.00E+00	cAMP-dependent protein kinase complex	C
GO:0005964	19	7.32E-01	1.00E+00	9.80E-01	1.00E+00	7.13E-01	1.00E+00	6.26E-01	1.00E+00	7.07E-01	1.00E+00	9.40E-01	1.00E+00	9.18E-01	1.00E+00	1.00E+00	1.00E+00	phosphorylase kinase complex	C
GO:0005975	548	2.34E-01	1.00E+00	4.60E-02	1.00E+00	9.12E-03	1.57E-01	2.23E-03	2.70E-02	4.33E-01	1.00E+00	1.02E-01	1.00E+00	9.10E-01	1.00E+00	9.50E-01	1.00E+00	carbohydrate metabolism	P
GO:0005976	88	8.72E-01	1.00E+00	9.92E-01	1.00E+00	2.29E-01	1.00E+00	7.95E-01	1.00E+00	9.22E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	polysaccharide metabolism	P
GO:0005977	55	7.10E-01	1.00E+00	9.99E-01	1.00E+00	1.05E-01	1.00E+00	9.88E-01	1.00E+00	8.80E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	glycogen metabolism	P
GO:0005978	30	6.64E-01	1.00E+00	1.00E+00	1.00E+00	1.89E-01	1.00E+00	9.64E-01	1.00E+00	8.40E-01	1.00E+00	9.98E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	glycogen biosynthesis	P
GO:0005996	181	8.32E-02	1.00E+00	5.34E-02	1.00E+00	9.09E-03	1.57E-01	6.39E-02	1.00E+00	1.38E-01	1.00E+00	6.90E-02	1.00E+00	8.78E-01	1.00E+00	4.55E-01	1.00E+00	monosaccharide metabolism	P
GO:0006000	13	4.68E-01	1.00E+00	4.42E-01	1.00E+00	6.48E-01	1.00E+00	3.69E-01	1.00E+00	5.25E-01	1.00E+00	6.73E-01	1.00E+00	2.76E-01	1.00E+00	1.11E-01	1.00E+00	fructose metabolism	P
GO:0006004	14	7.12E-01	1.00E+00	1.04E-01	1.00E+00	8.75E-01	1.00E+00	1.39E-01	1.00E+00	6.09E-01	1.00E+00	1.46E-01	1.00E+00	6.81E-01	1.00E+00	1.40E-01	1.00E+00	fucose metabolism	P
GO:0006006	129	4.27E-02	1.00E+00	1.30E-01	1.00E+00	1.30E-02	1.92E-01	2.32E-01	1.00E+00	5.88E-02	1.00E+00	1.41E-01	1.00E+00	7.80E-01	1.00E+00	4.30E-01	1.00E+00	glucose metabolism	P
GO:0006007	72	1.08E-02	1.77E-01	2.39E-02	1.00E+00	2.29E-03	1.80E-02	1.28E-01	1.00E+00	3.17E-02	6.55E-01	4.17E-02	1.00E+00	6.49E-01	1.00E+00	1.07E-01	1.00E+00	glucose catabolism	P
GO:0006022	45	3.59E-01	1.00E+00	6.01E-01	1.00E+00	2.37E-01	1.00E+00	4.83E-01	1.00E+00	4.00E-01	1.00E+00	6.07E-01	1.00E+00	5.30E-01	1.00E+00	6.08E-01	1.00E+00	aminoglycan metabolism	P
GO:0006023	20	3.35E-01	1.00E+00	3.43E-01	1.00E+00	2.42E-01	1.00E+00	6.20E-01	1.00E+00	2.85E-01	1.00E+00	2.91E-01	1.00E+00	8.37E-01	1.00E+00	4.34E-01	1.00E+00	aminoglycan biosynthesis	P
GO:0006024	20	3.35E-01	1.00E+00	3.43E-01	1.00E+00	2.42E-01	1.00E+00	6.20E-01	1.00E+00	2.85E-01	1.00E+00	2.91E-01	1.00E+00	8.37E-01	1.00E+00	4.34E-01	1.00E+00	glycosaminoglycan biosynthesis	P
GO:0006029	33	9.84E-01	1.00E+00	9.63E-01	1.00E+00	7.67E-01	1.00E+00	5.29E-01	1.00E+00	9.86E-01	1.00E+00	9.16E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	proteoglycan metabolism	P
GO:0006030	10	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.88E-01	1.00E+00	9.97E-01	1.00E+00	chitin metabolism	P

GO:0006040	33	7.23E-01	1.00E+00	1.74E-01	1.00E+00	9.35E-01	1.00E+00	5.01E-01	1.00E+00	5.59E-01	1.00E+00	1.25E-01	1.00E+00	6.33E-01	1.00E+00	4.30E-01	1.00E+00	amino sugar metabolism	P
GO:0006041	27	8.49E-01	1.00E+00	2.18E-01	1.00E+00	9.71E-01	1.00E+00	3.64E-01	1.00E+00	6.56E-01	1.00E+00	1.67E-01	1.00E+00	8.80E-01	1.00E+00	5.50E-01	1.00E+00	glucosamine metabolism	P
GO:0006044	27	8.49E-01	1.00E+00	2.18E-01	1.00E+00	9.71E-01	1.00E+00	3.64E-01	1.00E+00	6.56E-01	1.00E+00	1.67E-01	1.00E+00	8.80E-01	1.00E+00	5.50E-01	1.00E+00	N-acetylglucosamine metabolism	P
GO:0006066	397	6.34E-01	1.00E+00	1.50E-01	1.00E+00	1.03E-02	1.57E-01	2.60E-02	4.10E-01	8.52E-01	1.00E+00	2.10E-01	1.00E+00	9.85E-01	1.00E+00	9.14E-01	1.00E+00	alcohol metabolism	P
GO:0006071	36	8.35E-01	1.00E+00	5.25E-01	1.00E+00	6.72E-01	1.00E+00	2.71E-01	1.00E+00	9.12E-01	1.00E+00	4.58E-01	1.00E+00	6.19E-01	1.00E+00	9.86E-01	1.00E+00	glycerol metabolism	P
GO:0006072	19	9.54E-01	1.00E+00	7.26E-01	1.00E+00	9.02E-01	1.00E+00	3.70E-01	1.00E+00	9.89E-01	1.00E+00	8.84E-01	1.00E+00	3.86E-01	1.00E+00	7.62E-01	1.00E+00	glycerol-3-phosphate metabolism	P
GO:0006073	56	7.42E-01	1.00E+00	1.00E+00	1.00E+00	1.23E-01	1.00E+00	9.90E-01	1.00E+00	8.97E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	glucan metabolism	P
GO:0006081	18	5.96E-01	1.00E+00	5.81E-01	1.00E+00	1.21E-01	1.00E+00	2.86E-01	1.00E+00	7.59E-01	1.00E+00	4.87E-01	1.00E+00	8.05E-01	1.00E+00	9.97E-01	1.00E+00	aldehyde metabolism	P
GO:0006082	679	1.88E-01	1.00E+00	2.31E-01	1.00E+00	1.22E-04	4.57E-03	1.35E-01	1.00E+00	4.66E-01	1.00E+00	1.87E-01	1.00E+00	9.96E-01	1.00E+00	9.04E-01	1.00E+00	organic acid metabolism	P
GO:0006084	28	2.19E-01	1.00E+00	7.43E-02	1.00E+00	3.46E-02	5.87E-01	5.52E-01	1.00E+00	3.54E-01	1.00E+00	2.14E-02	7.69E-01	9.64E-01	1.00E+00	7.34E-01	1.00E+00	acetyl-CoA metabolism	P
GO:0006090	29	8.02E-01	1.00E+00	7.25E-01	1.00E+00	4.26E-01	1.00E+00	6.49E-01	1.00E+00	6.72E-01	1.00E+00	6.49E-01	1.00E+00	1.00E+00	1.00E+00	7.56E-01	1.00E+00	pyruvate metabolism	P
GO:0006091	318	7.40E-03	1.37E-01	4.53E-02	1.00E+00	1.77E-03	1.60E-02	7.52E-02	1.00E+00	1.41E-02	3.01E-01	6.76E-02	1.00E+00	8.86E-01	1.00E+00	5.27E-01	1.00E+00	generation of precursor metabolites and en	P
GO:0006092	122	1.08E-02	1.77E-01	2.03E-02	9.24E-01	2.23E-03	1.80E-02	8.82E-02	1.00E+00	1.53E-02	3.01E-01	1.95E-02	5.65E-01	9.62E-01	1.00E+00	3.20E-01	1.00E+00	main pathways of carbohydrate metabolism	P
GO:0006094	26	6.56E-01	1.00E+00	6.72E-01	1.00E+00	3.09E-01	1.00E+00	5.69E-01	1.00E+00	5.38E-01	1.00E+00	5.95E-01	1.00E+00	9.99E-01	1.00E+00	7.68E-01	1.00E+00	gluconeogenesis	P
GO:0006096	61	9.53E-02	1.00E+00	1.36E-01	1.00E+00	3.45E-02	5.87E-01	4.09E-01	1.00E+00	9.17E-02	1.00E+00	1.10E-01	1.00E+00	9.66E-01	1.00E+00	4.10E-01	1.00E+00	glycolysis	P
GO:0006098	10	5.25E-02	1.00E+00	6.91E-02	1.00E+00	2.23E-02	2.63E-01	4.99E-02	1.00E+00	1.55E-01	1.00E+00	2.32E-01	1.00E+00	1.54E-01	1.00E+00	5.88E-02	1.00E+00	pentose-phosphate shunt	P
GO:0006099	24	2.09E-01	1.00E+00	6.59E-02	1.00E+00	4.70E-02	8.68E-01	5.07E-01	1.00E+00	3.37E-01	1.00E+00	1.86E-02	5.65E-01	9.13E-01	1.00E+00	7.97E-01	1.00E+00	tricarboxylic acid cycle	P
GO:0006100	22	3.92E-01	1.00E+00	3.65E-01	1.00E+00	1.85E-01	1.00E+00	3.39E-01	1.00E+00	3.90E-01	1.00E+00	2.69E-01	1.00E+00	9.60E-01	1.00E+00	9.15E-01	1.00E+00	tricarboxylic acid cycle intermediate metabc	P
GO:0006109	18	1.69E-01	1.00E+00	5.44E-01	1.00E+00	1.10E-01	1.00E+00	1.65E-01	1.00E+00	7.24E-02	1.00E+00	5.58E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	regulation of carbohydrate metabolism	P
GO:0006110	10	1.48E-01	1.00E+00	2.21E-01	1.00E+00	2.64E-01	1.00E+00	1.75E-01	1.00E+00	2.47E-02	6.55E-01	2.34E-01	1.00E+00	1.00E+00	1.00E+00	5.52E-01	1.00E+00	regulation of glycolysis	P
GO:0006112	62	6.77E-01	1.00E+00	9.81E-01	1.00E+00	9.14E-02	1.00E+00	3.95E-01	1.00E+00	8.41E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	energy reserve metabolism	P
GO:0006118	58	7.62E-03	1.37E-01	6.20E-03	1.50E-01	3.08E-01	1.00E+00	6.17E-02	1.00E+00	1.88E-03	4.30E-02	1.64E-02	5.65E-01	2.21E-01	1.00E+00	6.05E-02	1.00E+00	electron transport	P
GO:0006119	75	4.73E-05	5.00E-03	3.87E-03	6.30E-02	3.13E-02	5.65E-01	3.84E-02	1.00E+00	2.25E-04	4.00E-03	7.46E-03	1.05E-01	5.25E-02	1.00E+00	1.36E-01	1.00E+00	oxidative phosphorylation	P
GO:0006120	38	1.00E-02	1.77E-01	4.84E-03	1.15E-01	2.79E-01	1.00E+00	6.79E-02	1.00E+00	1.91E-03	4.30E-02	4.36E-03	7.40E-02	5.69E-01	1.00E+00	1.39E-01	1.00E+00	mitochondrial electron transport, NADH to u	P
GO:0006139	3977	1.30E-01	1.00E+00	2.60E-14	0.00E+00	3.50E-09	0.00E+00	2.42E-16	0.00E+00	4.42E-01	1.00E+00	5.66E-09	1.05E-04	1.00E+00	1.00E+00	2.46E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	P
GO:0006140	15	7.45E-01	1.00E+00	8.85E-01	1.00E+00	3.33E-01	1.00E+00	8.99E-01	1.00E+00	7.51E-01	1.00E+00	7.54E-01	1.00E+00	9.31E-01	1.00E+00	9.99E-01	1.00E+00	regulation of nucleotide metabolism	P
GO:0006144	10	4.50E-01	1.00E+00	3.02E-02	1.00E+00	6.00E-01	1.00E+00	5.60E-02	1.00E+00	3.40E-01	1.00E+00	2.50E-02	7.69E-01	4.73E-01	1.00E+00	1.32E-01	1.00E+00	purine base metabolism	P
GO:0006163	78	2.62E-02	1.00E+00	8.50E-02	1.00E+00	1.84E-02	2.36E-01	6.08E-02	1.00E+00	6.37E-02	1.00E+00	1.12E-01	1.00E+00	5.67E-01	1.00E+00	7.46E-01	1.00E+00	purine nucleotide metabolism	P
GO:0006164	63	6.28E-02	1.00E+00	1.69E-01	1.00E+00	4.30E-02	7.24E-01	1.54E-01	1.00E+00	1.56E-01	1.00E+00	1.58E-01	1.00E+00	3.03E-01	1.00E+00	7.27E-01	1.00E+00	purine nucleotide biosynthesis	P
GO:0006171	19	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	cAMP biosynthesis	P
GO:0006182	13	9.88E-01	1.00E+00	1.00E+00	1.00E+00	4.55E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	cGMP biosynthesis	P
GO:0006183	10	2.95E-01	1.00E+00	7.77E-01	1.00E+00	3.60E-01	1.00E+00	4.40E-01	1.00E+00	2.24E-01	1.00E+00	9.09E-01	1.00E+00	6.27E-01	1.00E+00	9.34E-01	1.00E+00	GTP biosynthesis	P
GO:0006206	10	7.15E-03	1.37E-01	3.51E-01	1.00E+00	2.53E-02	4.97E-01	9.82E-02	1.00E+00	1.80E-01	1.00E+00	4.77E-01	1.00E+00	1.15E-01	1.00E+00	8.05E-01	1.00E+00	pyrimidine base metabolism	P
GO:0006213	13	7.70E-01	1.00E+00	5.76E-01	1.00E+00	1.77E-01	1.00E+00	2.18E-01	1.00E+00	1.00E+00	1.00E+00	7.60E-01	1.00E+00	7.86E-01	1.00E+00	9.16E-01	1.00E+00	pyrimidine nucleoside metabolism	P
GO:0006220	31	3.53E-01	1.00E+00	5.09E-01	1.00E+00	9.53E-02	1.00E+00	1.21E-01	1.00E+00	6.80E-01	1.00E+00	7.87E-01	1.00E+00	7.85E-01	1.00E+00	5.97E-01	1.00E+00	pyrimidine nucleotide metabolism	P
GO:0006221	22	2.73E-01	1.00E+00	2.88E-01	1.00E+00	1.87E-01	1.00E+00	6.66E-02	1.00E+00	3.80E-01	1.00E+00	5.25E-01	1.00E+00	4.62E-01	1.00E+00	7.20E-01	1.00E+00	pyrimidine nucleotide biosynthesis	P
GO:0006228	10	2.95E-01	1.00E+00	7.77E-01	1.00E+00	3.60E-01	1.00E+00	4.40E-01	1.00E+00	2.24E-01	1.00E+00	9.09E-01	1.00E+00	6.27E-01	1.00E+00	9.34E-01	1.00E+00	UTP biosynthesis	P
GO:0006241	11	3.10E-01	1.00E+00	7.53E-01	1.00E+00	3.54E-01	1.00E+00	3.31E-01	1.00E+00	2.73E-01	1.00E+00	9.12E-01	1.00E+00	6.29E-01	1.00E+00	9.66E-01	1.00E+00	CTP biosynthesis	P
GO:0006259	824	4.08E-05	5.00E-03	1.28E-10	0.00E+00	3.67E-10	0.00E+00	2.82E-09	0.00E+00	2.08E-03	4.30E-02	1.84E-07	2.22E-04	9.95E-01	1.00E+00	1.93E-02	1.77E-01	DNA metabolism	P
GO:0006260	220	8.14E-07	1.25E-04	2.71E-07	1.00E-03	8.25E-08	0.00E+00	1.23E-05	2.00E-03	2.97E-04	4.00E-03	2.58E-05	2.29E-03	6.67E-01	1.00E+00	4.87E-02	8.10E-01	DNA replication	P
GO:0006261	118	3.09E-05	5.00E-03	6.86E-05	4.00E-03	9.93E-05	4.57E-03	1.77E-02	4.10E-01	1.11E-03	4.30E-02	2.04E-04	2.90E-03	4.74E-01	1.00E+00	7.15E-02	1.00E+00	DNA-dependent DNA replication	P
GO:0006265	24	1.92E-01	1.00E+00	2.32E-01	1.00E+00	1.37E-01	1.00E+00	1.53E-01	1.00E+00	3.51E-01	1.00E+00	2.33E-01	1.00E+00	1.45E-01	1.00E+00	9.47E-01	1.00E+00	DNA topological change	P
GO:0006268	12	1.79E-01	1.00E+00	6.00E-02	1.00E+00	8.98E-02	1.00E+00	5.83E-01	1.00E+00	6.99E-01	1.00E+00	1.96E-01	1.00E+00	1.38E-01	1.00E+00	1.00E-01	1.00E+00	DNA unwinding during replication	P
GO:0006270	26	2.40E-01	1.00E+00	4.81E-02	1.00E+00	1.70E-01	1.00E+00	1.22E-01	1.00E+00	3.78E-01	1.00E+00	7.09E-02	1.00E+00	2.00E-01	1.00E+00	1.11E-01	1.00E+00	DNA replication initiation	P
GO:0006275	46	1.39E-01	1.00E+00	2.73E-01	1.00E+00	6.82E-02	1.00E+00	5.77E-02	1.00E+00	2.26E-01	1.00E+00	5.19E-01	1.00E+00	5.12E-01	1.00E+00	4.50E-01	1.00E+00	regulation of DNA replication	P
GO:0006281	298	2.46E-03	4.90E-02	9.72E-07	1.00E-03	8.74E-05	4.57E-03	3.95E-06	8.32E-04	1.36E-02	3.01E-01	6.37E-05	2.29E-03	9.70E-01	1.00E+00	5.28E-02	8.10E-01	DNA repair	P
GO:0006284	27	9.35E-02	1.00E+00	8.81E-02	1.00E+00	1.01E-01	1.00E+00	3.05E-02	5.42E-01	8.36E-02	1.00E+00	1.13E-01	1.00E+00	5.79E-01	1.00E+00	9.98E-01	1.00E+00	base-excision repair	P
GO:0006289	58	2.30E-02	1.00E+00	1.75E-02	9.24E-01	8.47E-02	1.00E+00	5.41E-02	1.00E+00	2.60E-02	6.55E-01	8.57E-02	1.00E+00	2.75E-01	1.00E+00	1.39E-01	1.00E+00	nucleotide-excision repair	P
GO:0006297	17	6.63E-02	1.00E+00	6.51E-04	1.90E-02	2.60E-02	4.97E-01	6.55E-02	1.00E+00	1.21E-01	1.00E+00	8.35E-03	1.05E-01	3.10E-01	1.00E+00	8.46E-02	1.00E+00	nucleotide-excision repair, DNA gap filling	P
GO:0006298	30	2.10E-07	1.25E-04	1.98E-06	1.41E-03	7.84E-03	1.57E-01	1.46E-01	1.00E+00	1.08E-05	5.00E-04	5.19E-08	1.05E-04	6.62E-01	1.00E+00	1.52E-01	1.00E+00	mismatch repair	P
GO:0006302	40	3.62E-01	1.00E+00	1.17E-02	3.84E-01	6.06E-01	1.00E+00	3.23E-02	5.42E-01	3.50E-01	1.00E+00	2.76E-02	1.00E+00	2.64E-01	1.00E+00	1.05E-01	1.00E+00	double-strand break repair	P
GO:0006303	10	6.40E-01	1.00E+00	1.19E-01	1.00E+00	7.65E-01	1.00E+00	1.31E-01	1.00E+00	5.59E-01	1.00E+00	1.39E-01	1.00E+00	7.30E-01	1.00E+00	1.90E-01	1.00E+00	double-strand break repair via nonhomologc	P
GO:0006304	30	6.17E-01	1.00E+00	1.71E-01	1.00E+00	3.54E-01	1.00E+00	1.14E-01	1.00E+00	4.73E-01	1.00E+00	2.07E-01	1.00E+00	9.64E-01	1.00E+00	6.76E-01	1.00E+00	DNA modification	P
GO:0006305	20	6.98E-01	1.00E+00	1.54E-01	1.00E+00	4.56E-01	1.00E+00	3.90E-02	1.00E+00	5.03E-01	1.00E+00	2.84E-01	1.00E+00	9.79E-01	1.00E+00	2.93E-01	1.00E+00	DNA alkylation	P
GO:0006306	20	6.98E-01	1.00E+00	1.54E-01	1.00E+00	4.56E-01	1.00E+00	3.90E-02	1.00E+00	5.03E-01	1.00E+00	2.84E-01	1.00E+00	9.79E-01	1.00E+00	2.93E-01	1.00E+00	DNA methylation	P
GO:0006308	23	9.29E-02	1.00E+00	5.10E-02	1.00E+00	3.95E-02	5.87E-01	9.77E-02	1.00E+00	2.64E-01	1.00E+00	7.40E-02	1.00E+00	1.06E-01	1.00E+00	2.77E-01	1.00E+00	DNA catabolism	P
GO:0006309	15	3.45E-01	1.00E+00	2.14E-01	1.00E+00	4.23E-01	1.00E+00	2.65E-01	1.00E+00	4.72E-01	1.00E+00	3.65E-01	1.00E+00	2.10E-01	1.00E+00	1.90E-01	1.00E+00	DNA fragmentation during apoptosis	P
GO:0006310	111	2.20E-01	1.00E+00	2.31E-04	8.26E-03	3.65E-01	1.00E+00	3.82E-03	6.84E-02	6.73E-02	1.00E+00	1.00E-03	1.02E-02	9.93E-01	1.00E+00	5.80E-02	1.00E+00	DNA recombination	P
GO:0006323	335	2.34E-02	1.00E+00	1.04E-04	4.00E-03	1.61E-04	4.57E-03	5.48E-04	7.17E-03	6.58E-02	1.00E+00	3.75E-04	1.02E-02	9.89E-01	1.00E+00	2.52E-01	1.00E+00	DNA packaging	P
GO:0006325	331	1.83E-02	5.62E-01	8.95E-05	4.00E-03	1.40E-04	4.57E-03	7.89E-04	1.03E-02	5.56E-02	1.00E+00	3.19E-04	1.02E-02	9.85E-01	1.00E+00	2.09E-01	1.00E+00	establishment and/or maintenance of chrom	P
GO:0006333	158	2.01E-01	1.00E+00	2.78E-01	1.00E+00	2.17E-01	1.00E+00	3.29E-01	1.00E+00	1.57E-01	1.00E+00	1.68E-01	1.00E+00	9.56E-01	1.00E+00	9.87E-01	1.00E+00	chromatin assembly or disassembly	P
GO:0006334	104	4.24E-01	1.00E+00	6.64E-01	1.00E+00	5.62E-01	1.00E+00	5.87E-01	1.00E+00	2.97E-01	1.00E+00	5.08E-01	1.00E+00	9.70E-01	1.00E+00	9.98E-01	1.00E+00	nucleosome assembly	P
GO:0006338	56	6.04E-03	1.37E-01	9.22E-05	4.00E-03	1.50E-02	1.92E-01	6.69E-03	8.10E-02	9.01E-03	2.02E-01	1.66E-04	2.29E-03	7.15E-01	1.00E+00	1.17E-01	1.00E+00	chromatin remodeling	P
GO:0006342	14	6.00E-02	1.00E+00	9.01E-02	1.00E+00	1.31E-01	1.00E+00	2.13E-01	1.00E+00	5.47E-02	1.00E+00	3.86E-02	1.00E+00	4.70E-01	1.00E+00	8.09E-01	1.00E+00	chromatin silencing	P
GO:0006350	2702	9.87E-01	1.00E+00	2.31E-05	2.21E-03	2.69E-02	4.97E-01	6.41E-08	0.00E+00	9.89E-01	1.00E+00	1.18E-03	1.02E-02	1.00E+00	1.00E+00	5.61E-01	1.00E+00	transcription	P
GO:0006351	2502	9.90E-01	1.00E+00	2.24E-05	2.21E-03	2.96E-02	5.65E-01	2.99E-07	0.00E+00	9.94E-01	1.00E+00	8.73E-04	1.02E-02	1.00E+00	1.00E+00	5.35E-01	1.00E+00	transcription, DNA-dependent	P
GO:0006352	100	1.84E-03	4.90E-02	2.14E-06	1.41E-03	1.06E-03	1.25E-02	9.85E-03	1.23E-01	1.98E-02	3.81E-01	2.00E-06	1.67E-03	1.28E-01	1.00E+00	7.68E-02	1.00E+00	transcription initiation	P
GO:0006354	52	7.72E-03	1.37E-01	2.01E-05	2.21E-03	1.80E-02	2.36E-01	1.39E-02	2.81E-01	4.70E-02	1.00E+00	2.37E-04	7.00E-03	4.89E-01	1.00E+00	5.40E-03	6.60E-02	RNA elongation	P
GO:0006355	2438	9.94E-01	1.00E+00	1.15E-04	4.00E-03	3.69E-02	5.87E-01	2.13E-07	0.00E+00	9.96E-01	1.00E+00	3.61E-03	7.40E-02	1.00E+00	1.00E+00	6.32E-01	1.00E+00	regulation of transcription, DNA-dependent	P
GO:0006357	542	1.00E+00	1.00E+00	9.80E-01	1.00E+00	5.77E-01	1.00E+00	7.73E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	regulation of transcription from RNA polyme	P
GO:0006360	11	2.75E-01	1.00E+00	8.53E-02	1.00E+00	5.86E-02	1.00E+00	4.64E-01	1.00E+00	6.41E-01	1.00E+00	1.89E-01	1.00E+00	9.99E-01	1.00E+00	3.01E-01	1.00E+00	transcription from RNA polymerase I promo	P
GO:0006364	68	8.57E-02	1.00E+00	1.03E-01	1.00E+00	2.17E-02	2.63E-01	4.46E-02	1.00E+00	1.64E-01	1.00E+00	2.21E-01	1.00E+00	4.52E-01	1.00E+00	9.21E-01	1.00E+00	rRNA processing	P
GO:0006366	706	9.98E-01	1.00E+00	7.38E-01	1.00E+00	2.56E-01	1.00E+00	3.76E-01	1.00E+00	9.97E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	8.00E-01	1.00E+00	transcription from RNA polymerase II promc	P
GO:0006367	70	6.24E-04	1.60E-02	2.08E-05	2.21E-03	1.41E-03	1.60E-02	1.75E-02	4.10E-01	9.93E-03	2.02E-01	2.14E-05	2.29E-03	1.78E-01	1.00E+00	4.98E-02	8.10E-01	transcription initiation from RNA polymerase	P
GO:0006368	49	9.54E-03	1.77E-01	3.07E-05	3.00E-03	1.93E-02	2.36E-01	1.05E-02	1.23E-01	6.67E-02	1.00E+00	4.08E-04	1.02E-02	4.28E-01	1.00E+00	7.10E-03	6.60E-02	RNA elongation from RNA polymerase II pr	P

GO:0006376	17	7.45E-01	1.00E+00	7.41E-01	1.00E+00	2.87E-01	1.00E+00	3.07E-01	1.00E+00	7.78E-01	1.00E+00	8.11E-01	1.00E+00	9.07E-01	1.00E+00	9.89E-01	1.00E+00	mRNA splice site selection	P
GO:0006383	28	2.57E-02	1.00E+00	3.50E-03	6.30E-02	1.50E-02	1.92E-01	6.29E-01	1.00E+00	1.31E-01	1.00E+00	6.43E-03	1.05E-01	6.30E-01	1.00E+00	6.34E-02	1.00E+00	transcription from RNA polymerase III prom	P
GO:0006396	491	4.47E-06	2.60E-03	3.52E-13	0.00E+00	5.25E-08	0.00E+00	1.40E-08	0.00E+00	2.44E-03	4.30E-02	4.83E-09	1.05E-04	8.80E-02	1.00E+00	1.39E-02	1.38E-01	RNA processing	P
GO:0006397	301	5.88E-05	5.00E-03	5.61E-09	1.00E-03	3.82E-05	4.57E-03	3.14E-07	0.00E+00	7.97E-03	2.02E-01	7.17E-07	2.22E-04	7.05E-02	1.00E+00	1.56E-02	1.38E-01	mRNA processing	P
GO:0006399	137	8.35E-03	1.56E-01	6.58E-04	1.90E-02	4.52E-02	8.68E-01	4.12E-02	1.00E+00	3.45E-03	6.24E-02	3.89E-03	7.40E-02	4.66E-01	1.00E+00	9.01E-02	1.00E+00	tRNA metabolism	P
GO:0006400	12	2.47E-01	1.00E+00	7.44E-02	1.00E+00	3.18E-01	1.00E+00	5.14E-01	1.00E+00	1.09E-01	1.00E+00	8.88E-02	1.00E+00	8.05E-01	1.00E+00	9.19E-02	1.00E+00	tRNA modification	P
GO:0006401	48	1.90E-01	1.00E+00	9.98E-02	1.00E+00	2.05E-02	2.36E-01	8.56E-03	1.12E-01	3.80E-01	1.00E+00	2.26E-01	1.00E+00	4.09E-01	1.00E+00	6.01E-01	1.00E+00	RNA catabolism	P
GO:0006402	31	1.92E-01	1.00E+00	4.74E-02	1.00E+00	1.17E-01	1.00E+00	9.50E-03	1.12E-01	3.67E-01	1.00E+00	7.65E-02	1.00E+00	1.00E-01	1.00E+00	4.65E-01	1.00E+00	mRNA catabolism	P
GO:0006403	93	1.15E-02	2.72E-01	1.55E-05	2.21E-03	9.67E-04	1.25E-02	4.36E-06	8.32E-04	3.81E-02	1.00E+00	1.16E-04	2.29E-03	4.46E-01	1.00E+00	6.60E-02	1.00E+00	RNA localization	P
GO:0006405	36	1.40E-01	1.00E+00	6.68E-02	1.00E+00	2.17E-02	2.63E-01	1.47E-02	2.81E-01	2.50E-01	1.00E+00	1.13E-01	1.00E+00	6.76E-01	1.00E+00	8.48E-01	1.00E+00	RNA export from nucleus	P
GO:0006406	28	2.05E-01	1.00E+00	1.97E-01	1.00E+00	9.61E-03	1.57E-01	5.60E-02	1.00E+00	4.99E-01	1.00E+00	2.39E-01	1.00E+00	4.65E-01	1.00E+00	7.38E-01	1.00E+00	mRNA export from nucleus	P
GO:0006412	772	1.74E-02	5.62E-01	2.26E-03	5.10E-02	1.51E-01	1.00E+00	2.14E-03	2.70E-02	3.17E-02	6.55E-01	1.13E-02	2.12E-01	4.14E-01	1.00E+00	2.68E-01	1.00E+00	protein biosynthesis	P
GO:0006413	67	6.21E-02	1.00E+00	1.12E-02	3.84E-01	1.07E-02	1.57E-01	3.53E-03	5.60E-02	3.85E-01	1.00E+00	3.72E-02	1.00E+00	6.45E-01	1.00E+00	1.83E-01	1.00E+00	translational initiation	P
GO:0006414	107	7.49E-01	1.00E+00	4.40E-02	1.00E+00	7.23E-01	1.00E+00	4.08E-01	1.00E+00	8.31E-01	1.00E+00	2.42E-02	7.69E-01	6.92E-01	1.00E+00	4.18E-01	1.00E+00	translational elongation	P
GO:0006415	10	3.89E-02	1.00E+00	8.11E-02	1.00E+00	9.10E-02	1.00E+00	1.75E-01	1.00E+00	5.51E-02	1.00E+00	1.12E-01	1.00E+00	3.24E-01	1.00E+00	1.06E-01	1.00E+00	translational termination	P
GO:0006417	182	4.25E-01	1.00E+00	1.41E-01	1.00E+00	1.06E-01	1.00E+00	6.98E-02	1.00E+00	5.69E-01	1.00E+00	1.23E-01	1.00E+00	9.33E-01	1.00E+00	8.77E-01	1.00E+00	regulation of protein biosynthesis	P
GO:0006418	75	3.76E-03	1.37E-01	3.98E-03	6.30E-02	2.71E-02	4.97E-01	1.90E-01	1.00E+00	5.46E-03	1.35E-01	7.13E-03	1.05E-01	1.08E-01	1.00E+00	2.80E-02	2.52E-01	tRNA aminoacylation for protein translation	P
GO:0006445	60	2.77E-01	1.00E+00	3.44E-02	1.00E+00	5.25E-01	1.00E+00	4.15E-03	6.84E-02	3.38E-01	1.00E+00	6.82E-02	1.00E+00	5.56E-01	1.00E+00	2.38E-01	1.00E+00	regulation of translation	P
GO:0006446	44	2.75E-01	1.00E+00	5.38E-02	1.00E+00	2.02E-01	1.00E+00	1.26E-02	1.57E-01	3.65E-01	1.00E+00	8.03E-02	1.00E+00	9.39E-01	1.00E+00	6.13E-01	1.00E+00	regulation of translational initiation	P
GO:0006457	195	4.37E-03	1.37E-01	1.83E-03	3.90E-02	2.02E-02	2.36E-01	5.90E-02	1.00E+00	4.58E-02	1.00E+00	3.01E-03	6.40E-02	8.78E-02	1.00E+00	2.56E-01	1.00E+00	protein folding	P
GO:0006461	397	6.12E-01	1.00E+00	3.79E-02	1.00E+00	6.15E-02	1.00E+00	1.35E-02	2.81E-01	7.50E-01	1.00E+00	5.15E-02	1.00E+00	8.94E-01	1.00E+00	7.82E-01	1.00E+00	protein complex assembly	P
GO:0006464	1868	2.44E-02	1.00E+00	5.15E-05	4.00E-03	3.38E-08	0.00E+00	1.69E-11	0.00E+00	2.44E-01	1.00E+00	1.02E-02	2.12E-01	1.00E+00	1.00E+00	5.56E-01	1.00E+00	protein modification	P
GO:0006468	717	7.74E-01	1.00E+00	8.43E-01	1.00E+00	5.74E-03	9.30E-02	1.27E-01	1.00E+00	8.31E-01	1.00E+00	7.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	protein amino acid phosphorylation	P
GO:0006469	62	9.91E-01	1.00E+00	9.71E-01	1.00E+00	4.77E-01	1.00E+00	6.35E-01	1.00E+00	9.80E-01	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	negative regulation of protein kinase activity	P
GO:0006470	145	6.78E-01	1.00E+00	1.87E-01	1.00E+00	3.36E-02	5.87E-01	2.60E-02	4.10E-01	9.21E-01	1.00E+00	5.13E-01	1.00E+00	9.48E-01	1.00E+00	2.48E-01	1.00E+00	protein amino acid dephosphorylation	P
GO:0006471	20	2.60E-02	1.00E+00	4.23E-01	1.00E+00	8.67E-02	1.00E+00	3.67E-01	1.00E+00	5.31E-02	1.00E+00	3.64E-01	1.00E+00	6.01E-01	1.00E+00	8.86E-01	1.00E+00	protein amino acid ADP-ribosylation	P
GO:0006473	23	1.34E-01	1.00E+00	4.00E-02	1.00E+00	3.86E-02	5.87E-01	3.43E-02	5.42E-01	1.68E-01	1.00E+00	8.45E-02	1.00E+00	8.15E-01	1.00E+00	3.08E-01	1.00E+00	protein amino acid acetylation	P
GO:0006476	20	3.09E-02	1.00E+00	2.97E-01	1.00E+00	1.48E-02	1.92E-01	5.18E-01	1.00E+00	6.91E-02	1.00E+00	1.63E-01	1.00E+00	5.26E-01	1.00E+00	9.76E-01	1.00E+00	protein amino acid deacetylation	P
GO:0006479	28	7.83E-02	1.00E+00	2.62E-02	1.00E+00	5.68E-02	1.00E+00	8.81E-03	1.12E-01	1.67E-01	1.00E+00	1.37E-01	1.00E+00	2.45E-01	1.00E+00	1.55E-02	1.38E-01	protein amino acid methylation	P
GO:0006486	116	5.82E-01	1.00E+00	1.53E-01	1.00E+00	1.10E-01	1.00E+00	6.14E-02	1.00E+00	7.48E-01	1.00E+00	1.93E-01	1.00E+00	8.55E-01	1.00E+00	8.16E-01	1.00E+00	protein amino acid glycosylation	P
GO:0006487	41	3.33E-01	1.00E+00	3.98E-01	1.00E+00	4.85E-01	1.00E+00	1.52E-01	1.00E+00	2.93E-01	1.00E+00	5.11E-01	1.00E+00	4.63E-01	1.00E+00	5.75E-01	1.00E+00	protein amino acid N-linked glycosylation	P
GO:0006493	23	6.17E-01	1.00E+00	5.73E-01	1.00E+00	1.80E-01	1.00E+00	5.10E-01	1.00E+00	9.48E-01	1.00E+00	5.61E-01	1.00E+00	5.55E-01	1.00E+00	9.38E-01	1.00E+00	protein amino acid O-linked glycosylation	P
GO:0006497	50	6.23E-01	1.00E+00	2.05E-01	1.00E+00	3.53E-01	1.00E+00	1.24E-01	1.00E+00	4.83E-01	1.00E+00	3.45E-01	1.00E+00	9.68E-01	1.00E+00	5.07E-01	1.00E+00	protein amino acid lipidation	P
GO:0006505	33	4.92E-01	1.00E+00	2.67E-01	1.00E+00	5.30E-01	1.00E+00	1.90E-01	1.00E+00	3.11E-01	1.00E+00	4.73E-01	1.00E+00	9.12E-01	1.00E+00	4.00E-01	1.00E+00	GPI anchor metabolism	P
GO:0006506	30	5.81E-01	1.00E+00	2.21E-01	1.00E+00	4.36E-01	1.00E+00	1.85E-01	1.00E+00	4.72E-01	1.00E+00	4.16E-01	1.00E+00	9.02E-01	1.00E+00	3.39E-01	1.00E+00	GPI anchor biosynthesis	P
GO:0006508	840	7.15E-01	1.00E+00	8.50E-01	1.00E+00	2.79E-02	4.97E-01	7.96E-03	8.10E-02	9.59E-01	1.00E+00	9.60E-01	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	proteolysis	P
GO:0006509	12	7.10E-01	1.00E+00	6.60E-01	1.00E+00	1.15E-01	1.00E+00	7.96E-01	1.00E+00	8.48E-01	1.00E+00	5.98E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	membrane protein ectodomain proteolysis	P
GO:0006511	218	4.96E-03	1.37E-01	1.11E-05	1.41E-03	2.33E-02	4.97E-01	1.80E-08	0.00E+00	4.33E-02	1.00E+00	8.72E-04	1.02E-02	5.60E-01	1.00E+00	4.98E-02	8.10E-01	ubiquitin-dependent protein catabolism	P
GO:0006512	579	5.04E-04	1.60E-02	2.41E-09	1.00E-03	1.66E-04	4.57E-03	2.46E-14	0.00E+00	4.70E-02	1.00E+00	1.22E-05	2.29E-03	4.66E-01	1.00E+00	4.58E-03	6.60E-02	ubiquitin cycle	P
GO:0006515	18	6.95E-01	1.00E+00	3.71E-01	1.00E+00	8.95E-01	1.00E+00	1.83E-01	1.00E+00	5.06E-01	1.00E+00	4.33E-01	1.00E+00	8.18E-01	1.00E+00	6.68E-01	1.00E+00	misfolded or incompletely synthesized prote	P
GO:0006516	17	1.80E-01	1.00E+00	3.42E-01	1.00E+00	1.16E-01	1.00E+00	5.15E-01	1.00E+00	2.34E-01	1.00E+00	2.80E-01	1.00E+00	3.60E-01	1.00E+00	4.98E-01	1.00E+00	glycoprotein catabolism	P
GO:0006518	25	3.81E-01	1.00E+00	8.38E-01	1.00E+00	9.89E-01	1.00E+00	9.56E-01	1.00E+00	1.48E-01	1.00E+00	6.44E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	peptide metabolism	P
GO:0006519	482	3.25E-01	1.00E+00	3.79E-01	1.00E+00	2.22E-03	1.80E-02	2.97E-01	1.00E+00	5.52E-01	1.00E+00	2.76E-01	1.00E+00	9.90E-01	1.00E+00	9.48E-01	1.00E+00	amino acid and derivative metabolism	P
GO:0006520	399	3.57E-01	1.00E+00	3.90E-01	1.00E+00	1.29E-02	1.92E-01	4.78E-01	1.00E+00	5.30E-01	1.00E+00	2.66E-01	1.00E+00	9.86E-01	1.00E+00	8.82E-01	1.00E+00	amino acid metabolism	P
GO:0006521	92	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.52E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of amino acid metabolism	P
GO:0006525	15	8.96E-01	1.00E+00	9.98E-01	1.00E+00	6.90E-01	1.00E+00	9.90E-01	1.00E+00	8.49E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	arginine metabolism	P
GO:0006536	13	1.59E-01	1.00E+00	9.14E-01	1.00E+00	1.41E-01	1.00E+00	6.95E-01	1.00E+00	1.44E-01	1.00E+00	9.35E-01	1.00E+00	8.71E-01	1.00E+00	9.84E-01	1.00E+00	glutamate metabolism	P
GO:0006541	18	1.90E-01	1.00E+00	2.90E-01	1.00E+00	1.12E-01	1.00E+00	3.91E-01	1.00E+00	3.46E-01	1.00E+00	2.27E-01	1.00E+00	3.35E-01	1.00E+00	7.85E-01	1.00E+00	glutamine metabolism	P
GO:0006544	13	2.51E-01	1.00E+00	2.87E-01	1.00E+00	5.21E-01	1.00E+00	2.76E-01	1.00E+00	4.55E-01	1.00E+00	2.61E-01	1.00E+00	2.14E-01	1.00E+00	5.96E-01	1.00E+00	glycine metabolism	P
GO:0006547	12	9.58E-01	1.00E+00	9.38E-01	1.00E+00	4.65E-01	1.00E+00	3.47E-01	1.00E+00	9.11E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	histidine metabolism	P
GO:0006555	10	3.83E-01	1.00E+00	7.56E-01	1.00E+00	1.29E-01	1.00E+00	3.32E-01	1.00E+00	6.76E-01	1.00E+00	8.52E-01	1.00E+00	4.15E-01	1.00E+00	9.57E-01	1.00E+00	methionine metabolism	P
GO:0006558	10	3.70E-01	1.00E+00	7.57E-01	1.00E+00	1.80E-01	1.00E+00	8.49E-01	1.00E+00	4.57E-01	1.00E+00	8.37E-01	1.00E+00	7.93E-01	1.00E+00	3.74E-01	1.00E+00	L-phenylalanine metabolism	P
GO:0006559	10	3.70E-01	1.00E+00	7.57E-01	1.00E+00	1.80E-01	1.00E+00	8.49E-01	1.00E+00	4.57E-01	1.00E+00	8.37E-01	1.00E+00	7.93E-01	1.00E+00	3.74E-01	1.00E+00	L-phenylalanine catabolism	P
GO:0006560	11	3.51E-01	1.00E+00	5.98E-01	1.00E+00	2.64E-01	1.00E+00	2.87E-01	1.00E+00	5.53E-01	1.00E+00	4.76E-01	1.00E+00	2.44E-01	1.00E+00	1.00E+00	1.00E+00	proline metabolism	P
GO:0006570	14	3.77E-01	1.00E+00	8.79E-01	1.00E+00	1.15E-01	1.00E+00	9.16E-01	1.00E+00	4.35E-01	1.00E+00	8.66E-01	1.00E+00	9.12E-01	1.00E+00	5.22E-01	1.00E+00	tyrosine metabolism	P
GO:0006575	146	6.29E-01	1.00E+00	4.26E-01	1.00E+00	6.37E-02	1.00E+00	2.42E-01	1.00E+00	7.44E-01	1.00E+00	3.07E-01	1.00E+00	9.61E-01	1.00E+00	9.91E-01	1.00E+00	amino acid derivative metabolism	P
GO:0006576	77	7.41E-01	1.00E+00	8.25E-01	1.00E+00	3.49E-01	1.00E+00	4.32E-01	1.00E+00	6.95E-01	1.00E+00	7.26E-01	1.00E+00	9.18E-01	1.00E+00	9.86E-01	1.00E+00	biogenic amine metabolism	P
GO:0006582	10	3.04E-01	1.00E+00	8.51E-01	1.00E+00	1.24E-01	1.00E+00	4.53E-01	1.00E+00	4.04E-01	1.00E+00	8.15E-01	1.00E+00	6.72E-01	1.00E+00	9.91E-01	1.00E+00	melanin metabolism	P
GO:0006584	32	9.90E-01	1.00E+00	8.86E-01	1.00E+00	5.95E-01	1.00E+00	2.85E-01	1.00E+00	9.92E-01	1.00E+00	8.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	catecholamine metabolism	P
GO:0006586	11	1.30E-01	1.00E+00	1.59E-01	1.00E+00	4.53E-01	1.00E+00	5.92E-01	1.00E+00	9.58E-02	1.00E+00	1.66E-01	1.00E+00	1.89E-01	1.00E+00	2.14E-01	1.00E+00	indolalkylamine metabolism	P
GO:0006595	15	1.50E-01	1.00E+00	1.18E-01	1.00E+00	1.31E-01	1.00E+00	5.20E-01	1.00E+00	1.41E-01	1.00E+00	7.22E-02	1.00E+00	3.90E-01	1.00E+00	4.65E-01	1.00E+00	polyamine metabolism	P
GO:0006596	10	1.73E-01	1.00E+00	1.52E-01	1.00E+00	8.91E-02	1.00E+00	8.19E-01	1.00E+00	2.28E-01	1.00E+00	3.12E-02	1.00E+00	2.82E-01	1.00E+00	1.00E+00	1.00E+00	polyamine biosynthesis	P
GO:0006605	220	1.73E-02	5.62E-01	5.17E-04	1.90E-02	3.91E-03	3.50E-02	2.96E-05	3.91E-03	4.82E-02	1.00E+00	5.58E-03	7.40E-02	3.95E-01	1.00E+00	1.43E-01	1.00E+00	protein targeting	P
GO:0006606	104	8.96E-02	1.00E+00	1.44E-02	3.84E-01	5.62E-02	1.00E+00	5.63E-03	8.10E-02	9.69E-02	1.00E+00	2.40E-02	7.69E-01	5.26E-01	1.00E+00	4.91E-01	1.00E+00	protein import into nucleus	P
GO:0006607	14	1.20E-01	1.00E+00	1.55E-01	1.00E+00	2.89E-02	5.65E-01	2.32E-01	1.00E+00	2.35E-01	1.00E+00	2.03E-01	1.00E+00	1.94E-01	1.00E+00	2.50E-01	1.00E+00	NLS-bearing substrate import into nucleus	P
GO:0006611	20	1.41E-01	1.00E+00	3.68E-02	1.00E+00	1.02E-01	1.00E+00	7.11E-02	1.00E+00	1.83E-01	1.00E+00	8.29E-02	1.00E+00	5.35E-01	1.00E+00	1.43E-01	1.00E+00	protein export from nucleus	P
GO:0006612	30	4.40E-01	1.00E+00	1.23E-01	1.00E+00	3.72E-01	1.00E+00	4.40E-02	1.00E+00	5.34E-01	1.00E+00	2.81E-01	1.00E+00	8.20E-01	1.00E+00	2.17E-01	1.00E+00	protein targeting to membrane	P
GO:0006613	17	5.44E-01	1.00E+00	3.31E-01	1.00E+00	6.25E-01	1.00E+00	6.42E-02	1.00E+00	5.47E-01	1.00E+00	5.97E-01	1.00E+00	8.97E-01	1.00E+00	4.97E-01	1.00E+00	cotranslational protein targeting to membra	P
GO:0006614	11	9.15E-01	1.00E+00	3.71E-01	1.00E+00	9.69E-01	1.00E+00	1.94E-01	1.00E+00	8.54E-01	1.00E+00	5.27E-01	1.00E+00	9.13E-01	1.00E+00	4.07E-01	1.00E+00	SRP-dependent cotranslational protein targ	P
GO:0006625	13	4.09E-01	1.00E+00	8.97E-01	1.00E+00	1.20E-01	1.00E+00	3.19E-01	1.00E+00	5.63E-01	1.00E+00	9.92E-01	1.00E+00	8.37E-01	1.00E+00	3.98E-01	1.00E+00	protein targeting to peroxisome	P
GO:0006626	20	3.24E-01	1.00E+00	3.09E-01	1.00E+00	4.15E-01	1.00E+00	4.86E-02	1.00E+00	4.66E-01	1.00E+00	4.70E-01	1.00E+00	1.89E-01	1.00E+00	9.82E-01	1.00E+00	protein targeting to mitochondrion	P
GO:0006629	830	7.80E-01	1.00E+00	8.42E-01	1.00E+00	8.09E-03	1.57E-01	8.04E-02	1.00E+00	9.35E-01	1.00E+00	8.93E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	lipid metabolism	P
GO:0006631	191	2.33E-01	1.00E+00	2.34E-01	1.00E+00	6.98E-02	1.00E+00	5.79E-02	1.00E+00	2.89E-01	1.00E+00	2.58E-01	1.00E+00	7.96E-01	1.00E+00	9.78E-01	1.00E+00	fatty acid metabolism	P
GO:0006633	78	5.71E-01	1.00E+00	4.37E-01	1.00E+00	3.70E-01	1.00E+00	1.59E-01	1.00E+00	5.23E-01	1.00E+00	5.96E-01	1.00E+00	9.53E-01	1.00E+00	8.72E-01	1.00E+00	fatty acid biosynthesis	P
GO:0006635	22	6.04E-02	1.00E+00	1.16E-01	1.00E+00	1.48E-01	1.00E+00	1.95E-01	1.00E+00	8.48E-02	1.00E+00	1.51E-01	1.00E+00	1.99E-01	1.00E+00	2.68E-01	1.00E+00	fatty acid beta-oxidation	P

GO:0006637	11	1.21E-01	1.00E+00	1.52E-02	3.84E-01	6.83E-01	1.00E+00	6.94E-02	1.00E+00	1.10E-01	1.00E+00	3.67E-02	1.00E+00	1.52E-01	1.00E+00	1.00E+00	1.00E+00	acyl-CoA metabolism	P
GO:0006638	37	7.79E-01	1.00E+00	9.45E-01	1.00E+00	4.90E-01	1.00E+00	9.15E-01	1.00E+00	6.83E-01	1.00E+00	9.41E-01	1.00E+00	9.89E-01	1.00E+00	8.15E-01	1.00E+00	neutral lipid metabolism	P
GO:0006639	37	7.79E-01	1.00E+00	9.45E-01	1.00E+00	4.90E-01	1.00E+00	9.15E-01	1.00E+00	6.83E-01	1.00E+00	9.41E-01	1.00E+00	9.89E-01	1.00E+00	8.15E-01	1.00E+00	acylglycerol metabolism	P
GO:0006641	32	7.50E-01	1.00E+00	8.93E-01	1.00E+00	4.21E-01	1.00E+00	8.71E-01	1.00E+00	6.62E-01	1.00E+00	8.69E-01	1.00E+00	9.97E-01	1.00E+00	8.56E-01	1.00E+00	triacylglycerol metabolism	P
GO:0006643	239	5.77E-01	1.00E+00	2.55E-01	1.00E+00	3.30E-02	5.87E-01	5.14E-02	1.00E+00	6.32E-01	1.00E+00	4.15E-01	1.00E+00	9.95E-01	1.00E+00	9.09E-01	1.00E+00	membrane lipid metabolism	P
GO:0006644	180	6.77E-01	1.00E+00	4.85E-01	1.00E+00	1.73E-01	1.00E+00	1.05E-01	1.00E+00	6.88E-01	1.00E+00	7.32E-01	1.00E+00	9.91E-01	1.00E+00	9.07E-01	1.00E+00	phospholipid metabolism	P
GO:0006650	93	2.35E-01	1.00E+00	1.01E-01	1.00E+00	1.89E-01	1.00E+00	5.57E-02	1.00E+00	2.04E-01	1.00E+00	2.74E-01	1.00E+00	7.35E-01	1.00E+00	3.86E-01	1.00E+00	glycerophospholipid metabolism	P
GO:0006656	10	5.07E-01	1.00E+00	3.19E-01	1.00E+00	9.18E-01	1.00E+00	2.04E-01	1.00E+00	3.52E-01	1.00E+00	3.39E-01	1.00E+00	9.92E-01	1.00E+00	9.77E-01	1.00E+00	phosphatidylcholine biosynthesis	P
GO:0006662	39	7.84E-01	1.00E+00	8.70E-01	1.00E+00	5.32E-01	1.00E+00	8.59E-01	1.00E+00	6.78E-01	1.00E+00	8.30E-01	1.00E+00	9.83E-01	1.00E+00	8.71E-01	1.00E+00	glycerol ether metabolism	P
GO:0006664	27	5.70E-01	1.00E+00	7.00E-02	1.00E+00	2.14E-01	1.00E+00	2.13E-01	1.00E+00	3.58E-01	1.00E+00	3.94E-02	1.00E+00	1.00E+00	1.00E+00	6.84E-01	1.00E+00	glycolipid metabolism	P
GO:0006665	65	1.72E-01	1.00E+00	2.37E-02	1.00E+00	2.49E-03	1.80E-02	3.91E-02	1.00E+00	3.06E-01	1.00E+00	2.79E-02	1.00E+00	9.41E-01	1.00E+00	4.13E-01	1.00E+00	sphingolipid metabolism	P
GO:0006672	33	7.23E-02	1.00E+00	1.94E-02	9.24E-01	6.03E-04	1.25E-02	2.92E-02	5.42E-01	1.19E-01	1.00E+00	3.04E-02	1.00E+00	9.65E-01	1.00E+00	8.97E-02	1.00E+00	ceramide metabolism	P
GO:0006684	11	3.60E-01	1.00E+00	9.12E-02	1.00E+00	5.45E-02	1.00E+00	2.16E-02	4.10E-01	5.48E-01	1.00E+00	2.17E-01	1.00E+00	8.90E-01	1.00E+00	6.14E-01	1.00E+00	sphingomyelin metabolism	P
GO:0006687	18	4.71E-01	1.00E+00	1.30E-01	1.00E+00	1.68E-01	1.00E+00	2.76E-01	1.00E+00	3.23E-01	1.00E+00	1.00E-01	1.00E+00	1.00E+00	1.00E+00	4.80E-01	1.00E+00	glycosphingolipid metabolism	P
GO:0006690	42	8.75E-01	1.00E+00	4.67E-01	1.00E+00	9.48E-01	1.00E+00	8.19E-01	1.00E+00	7.01E-01	1.00E+00	2.67E-01	1.00E+00	9.34E-01	1.00E+00	6.47E-01	1.00E+00	icosanoid metabolism	P
GO:0006691	23	8.21E-01	1.00E+00	5.73E-01	1.00E+00	8.41E-01	1.00E+00	8.42E-01	1.00E+00	7.64E-01	1.00E+00	5.02E-01	1.00E+00	6.53E-01	1.00E+00	4.84E-01	1.00E+00	leukotriene metabolism	P
GO:0006692	17	6.82E-01	1.00E+00	3.29E-01	1.00E+00	7.78E-01	1.00E+00	5.77E-01	1.00E+00	5.09E-01	1.00E+00	1.37E-01	1.00E+00	8.46E-01	1.00E+00	8.33E-01	1.00E+00	prostanoid metabolism	P
GO:0006693	17	6.82E-01	1.00E+00	3.29E-01	1.00E+00	7.78E-01	1.00E+00	5.77E-01	1.00E+00	5.09E-01	1.00E+00	1.37E-01	1.00E+00	8.46E-01	1.00E+00	8.33E-01	1.00E+00	prostaglandin metabolism	P
GO:0006694	101	9.95E-01	1.00E+00	9.75E-01	1.00E+00	4.22E-01	1.00E+00	1.80E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.32E-01	1.00E+00	steroid biosynthesis	P
GO:0006695	27	2.12E-01	1.00E+00	9.18E-02	1.00E+00	1.72E-01	1.00E+00	7.61E-02	1.00E+00	3.12E-01	1.00E+00	2.20E-01	1.00E+00	4.64E-01	1.00E+00	5.53E-01	1.00E+00	cholesterol biosynthesis	P
GO:0006700	14	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.22E-01	1.00E+00	7.21E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	C21-steroid hormone biosynthesis	P
GO:0006706	18	1.29E-01	1.00E+00	9.40E-02	1.00E+00	5.42E-02	1.00E+00	2.87E-01	1.00E+00	2.61E-01	1.00E+00	9.49E-02	1.00E+00	5.09E-01	1.00E+00	5.45E-01	1.00E+00	steroid catabolism	P
GO:0006707	10	1.74E-01	1.00E+00	2.91E-01	1.00E+00	7.52E-02	1.00E+00	8.19E-01	1.00E+00	4.79E-01	1.00E+00	2.76E-01	1.00E+00	9.09E-01	1.00E+00	3.81E-01	1.00E+00	cholesterol catabolism	P
GO:0006720	30	1.78E-01	1.00E+00	9.80E-01	1.00E+00	1.21E-01	1.00E+00	5.38E-01	1.00E+00	1.55E-01	1.00E+00	9.91E-01	1.00E+00	8.66E-01	1.00E+00	7.76E-01	1.00E+00	isoprenoid metabolism	P
GO:0006725	171	7.08E-01	1.00E+00	2.50E-01	1.00E+00	4.32E-02	7.24E-01	1.06E-01	1.00E+00	9.12E-01	1.00E+00	2.23E-01	1.00E+00	9.76E-01	1.00E+00	9.80E-01	1.00E+00	aromatic compound metabolism	P
GO:0006730	111	2.00E-01	1.00E+00	1.29E-02	3.84E-01	5.58E-02	1.00E+00	1.57E-03	1.80E-02	1.63E-01	1.00E+00	5.26E-02	1.00E+00	9.50E-01	1.00E+00	1.40E-01	1.00E+00	one-carbon compound metabolism	P
GO:0006732	173	1.24E-03	3.76E-02	5.38E-04	1.90E-02	1.47E-04	4.57E-03	1.02E-02	1.23E-01	2.77E-02	6.55E-01	1.90E-03	5.10E-02	2.71E-01	1.00E+00	2.03E-01	1.00E+00	coenzyme metabolism	P
GO:0006733	40	4.45E-03	1.37E-01	1.04E-02	3.84E-01	3.23E-03	3.50E-02	1.64E-02	4.10E-01	1.78E-02	3.81E-01	1.71E-02	5.65E-01	2.01E-01	1.00E+00	7.90E-02	1.00E+00	oxidoreduction coenzyme metabolism	P
GO:0006739	14	1.66E-01	1.00E+00	3.39E-01	1.00E+00	5.88E-02	1.00E+00	2.00E-01	1.00E+00	3.49E-01	1.00E+00	5.14E-01	1.00E+00	2.20E-01	1.00E+00	2.42E-01	1.00E+00	NADP metabolism	P
GO:0006740	10	5.25E-02	1.00E+00	6.91E-02	1.00E+00	2.23E-02	2.63E-01	4.99E-02	1.00E+00	1.55E-01	1.00E+00	2.32E-01	1.00E+00	1.54E-01	1.00E+00	5.88E-02	1.00E+00	NADPH regeneration	P
GO:0006749	28	1.25E-01	1.00E+00	2.02E-01	1.00E+00	9.03E-02	1.00E+00	1.44E-01	1.00E+00	2.14E-01	1.00E+00	3.71E-01	1.00E+00	3.14E-01	1.00E+00	5.70E-01	1.00E+00	glutathione metabolism	P
GO:0006750	10	3.99E-02	1.00E+00	4.81E-01	1.00E+00	3.39E-02	5.87E-01	4.30E-01	1.00E+00	5.28E-02	1.00E+00	6.73E-01	1.00E+00	4.11E-01	1.00E+00	1.71E-01	1.00E+00	glutathione biosynthesis	P
GO:0006752	61	1.47E-01	1.00E+00	1.68E-01	1.00E+00	2.88E-02	5.65E-01	3.84E-01	1.00E+00	4.40E-01	1.00E+00	1.16E-01	1.00E+00	4.79E-01	1.00E+00	6.28E-01	1.00E+00	group transfer coenzyme metabolism	P
GO:0006753	27	2.24E-02	1.00E+00	2.31E-01	1.00E+00	3.47E-02	5.87E-01	3.82E-01	1.00E+00	9.34E-02	1.00E+00	1.89E-01	1.00E+00	3.03E-01	1.00E+00	5.73E-01	1.00E+00	nucleoside phosphate metabolism	P
GO:0006754	27	2.24E-02	1.00E+00	2.31E-01	1.00E+00	3.47E-02	5.87E-01	3.82E-01	1.00E+00	9.34E-02	1.00E+00	1.89E-01	1.00E+00	3.03E-01	1.00E+00	5.73E-01	1.00E+00	ATP biosynthesis	P
GO:0006760	18	8.60E-01	1.00E+00	9.78E-02	1.00E+00	2.70E-01	1.00E+00	2.81E-01	1.00E+00	9.88E-01	1.00E+00	7.49E-02	1.00E+00	9.04E-01	1.00E+00	2.79E-01	1.00E+00	folic acid and derivative metabolism	P
GO:0006766	84	4.57E-01	1.00E+00	2.30E-01	1.00E+00	9.72E-02	1.00E+00	2.33E-01	1.00E+00	5.53E-01	1.00E+00	3.17E-01	1.00E+00	8.57E-01	1.00E+00	4.71E-01	1.00E+00	vitamin metabolism	P
GO:0006767	57	7.36E-02	1.00E+00	5.84E-02	1.00E+00	8.65E-03	1.57E-01	2.47E-02	4.10E-01	1.55E-01	1.00E+00	1.52E-01	1.00E+00	5.05E-01	1.00E+00	2.89E-01	1.00E+00	water-soluble vitamin metabolism	P
GO:0006769	28	5.99E-02	1.00E+00	1.10E-01	1.00E+00	2.39E-02	4.97E-01	1.36E-01	1.00E+00	1.18E-01	1.00E+00	1.34E-01	1.00E+00	1.69E-01	1.00E+00	1.28E-01	1.00E+00	nicotinamide metabolism	P
GO:0006775	24	9.97E-01	1.00E+00	7.48E-01	1.00E+00	9.92E-01	1.00E+00	9.73E-01	1.00E+00	9.85E-01	1.00E+00	5.85E-01	1.00E+00	9.93E-01	1.00E+00	6.41E-01	1.00E+00	fat-soluble vitamin metabolism	P
GO:0006776	19	9.81E-01	1.00E+00	9.35E-01	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	9.61E-01	1.00E+00	8.06E-01	1.00E+00	9.90E-01	1.00E+00	6.09E-01	1.00E+00	vitamin A metabolism	P
GO:0006778	28	4.29E-01	1.00E+00	2.56E-01	1.00E+00	7.64E-02	1.00E+00	6.85E-01	1.00E+00	6.62E-01	1.00E+00	2.03E-01	1.00E+00	8.80E-01	1.00E+00	4.33E-01	1.00E+00	porphyrin metabolism	P
GO:0006779	22	6.57E-01	1.00E+00	3.91E-01	1.00E+00	2.47E-01	1.00E+00	7.62E-01	1.00E+00	7.10E-01	1.00E+00	3.23E-01	1.00E+00	9.24E-01	1.00E+00	4.02E-01	1.00E+00	porphyrin biosynthesis	P
GO:0006783	15	5.59E-01	1.00E+00	3.87E-01	1.00E+00	3.59E-01	1.00E+00	6.59E-01	1.00E+00	4.52E-01	1.00E+00	3.32E-01	1.00E+00	7.98E-01	1.00E+00	4.83E-01	1.00E+00	heme biosynthesis	P
GO:0006790	88	4.38E-01	1.00E+00	2.61E-01	1.00E+00	9.07E-02	1.00E+00	5.93E-02	1.00E+00	6.04E-01	1.00E+00	3.57E-01	1.00E+00	8.44E-01	1.00E+00	9.15E-01	1.00E+00	sulfur metabolism	P
GO:0006793	1025	2.95E-01	1.00E+00	2.63E-01	1.00E+00	4.01E-05	4.57E-03	3.18E-03	5.60E-02	6.20E-01	1.00E+00	4.16E-01	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	phosphorus metabolism	P
GO:0006796	1025	2.95E-01	1.00E+00	2.63E-01	1.00E+00	4.01E-05	4.57E-03	3.18E-03	5.60E-02	6.20E-01	1.00E+00	4.16E-01	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	phosphate metabolism	P
GO:0006800	161	8.49E-01	1.00E+00	9.36E-01	1.00E+00	9.37E-02	1.00E+00	7.11E-01	1.00E+00	9.41E-01	1.00E+00	9.53E-01	1.00E+00	9.48E-01	1.00E+00	8.05E-01	1.00E+00	oxygen and reactive oxygen species metab	P
GO:0006801	23	9.74E-01	1.00E+00	7.92E-01	1.00E+00	9.94E-01	1.00E+00	4.80E-01	1.00E+00	9.89E-01	1.00E+00	7.91E-01	1.00E+00	4.59E-01	1.00E+00	7.81E-01	1.00E+00	superoxide metabolism	P
GO:0006805	30	9.01E-01	1.00E+00	8.65E-01	1.00E+00	4.82E-01	1.00E+00	7.73E-01	1.00E+00	9.87E-01	1.00E+00	7.16E-01	1.00E+00	4.91E-01	1.00E+00	1.00E+00	1.00E+00	xenobiotic metabolism	P
GO:0006807	601	1.83E-01	1.00E+00	4.48E-01	1.00E+00	1.25E-03	1.25E-02	2.33E-01	1.00E+00	3.12E-01	1.00E+00	3.50E-01	1.00E+00	9.79E-01	1.00E+00	9.66E-01	1.00E+00	nitrogen compound metabolism	P
GO:0006809	28	3.33E-01	1.00E+00	4.67E-01	1.00E+00	3.22E-01	1.00E+00	3.83E-01	1.00E+00	1.95E-01	1.00E+00	6.16E-01	1.00E+00	9.84E-01	1.00E+00	2.56E-01	1.00E+00	nitric oxide biosynthesis	P
GO:0006810	2992	6.12E-01	1.00E+00	7.28E-01	1.00E+00	9.02E-06	9.71E-04	5.46E-04	7.17E-03	8.95E-01	1.00E+00	8.59E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	transport	P
GO:0006811	970	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.16E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ion transport	P
GO:0006812	674	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.38E-01	1.00E+00	8.02E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cation transport	P
GO:0006813	283	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	potassium ion transport	P
GO:0006814	140	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.39E-01	1.00E+00	9.76E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	sodium ion transport	P
GO:0006816	165	9.95E-01	1.00E+00	9.95E-01	1.00E+00	5.73E-01	1.00E+00	7.88E-01	1.00E+00	9.80E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	calcium ion transport	P
GO:0006817	98	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	phosphate transport	P
GO:0006818	75	2.92E-02	1.00E+00	1.60E-01	1.00E+00	7.51E-03	1.57E-01	5.56E-02	1.00E+00	1.23E-01	1.00E+00	2.08E-01	1.00E+00	6.78E-01	1.00E+00	8.48E-01	1.00E+00	hydrogen transport	P
GO:0006820	231	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	anion transport	P
GO:0006821	79	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.92E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	chloride transport	P
GO:0006825	15	8.88E-01	1.00E+00	9.31E-01	1.00E+00	7.58E-01	1.00E+00	4.82E-01	1.00E+00	9.81E-01	1.00E+00	9.26E-01	1.00E+00	5.31E-01	1.00E+00	9.92E-01	1.00E+00	copper ion transport	P
GO:0006826	30	3.66E-01	1.00E+00	3.46E-01	1.00E+00	1.94E-01	1.00E+00	4.01E-01	1.00E+00	4.49E-01	1.00E+00	2.70E-01	1.00E+00	4.35E-01	1.00E+00	5.89E-01	1.00E+00	iron ion transport	P
GO:0006829	26	8.13E-01	1.00E+00	2.52E-01	1.00E+00	9.06E-01	1.00E+00	6.00E-01	1.00E+00	5.79E-01	1.00E+00	1.39E-01	1.00E+00	1.00E+00	1.00E+00	9.04E-01	1.00E+00	zinc ion transport	P
GO:0006833	11	9.92E-01	1.00E+00	8.42E-01	1.00E+00	9.93E-01	1.00E+00	9.59E-01	1.00E+00	8.95E-01	1.00E+00	5.71E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	water transport	P
GO:0006835	59	9.94E-01	1.00E+00	8.56E-01	1.00E+00	8.71E-01	1.00E+00	3.52E-01	1.00E+00	9.97E-01	1.00E+00	7.82E-01	1.00E+00	7.74E-01	1.00E+00	1.00E+00	1.00E+00	dicarboxylic acid transport	P
GO:0006836	55	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter transport	P
GO:0006839	58	5.38E-02	1.00E+00	1.82E-01	1.00E+00	2.52E-02	4.97E-01	2.01E-02	4.10E-01	2.73E-01	1.00E+00	3.12E-01	1.00E+00	7.20E-02	1.00E+00	7.99E-01	1.00E+00	mitochondrial transport	P
GO:0006857	13	9.73E-01	1.00E+00	9.92E-01	1.00E+00	7.17E-01	1.00E+00	8.85E-01	1.00E+00	9.64E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	7.28E-01	1.00E+00	oligopeptide transport	P
GO:0006865	74	7.15E-01	1.00E+00	5.80E-01	1.00E+00	3.84E-01	1.00E+00	4.86E-01	1.00E+00	6.37E-01	1.00E+00	3.95E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	amino acid transport	P
GO:0006869	114	2.97E-01	1.00E+00	3.99E-01	1.00E+00	3.64E-03	3.50E-02	5.03E-01	1.00E+00	4.57E-01	1.00E+00	4.15E-01	1.00E+00	9.90E-01	1.00E+00	4.90E-01	1.00E+00	lipid transport	P
GO:0006873	200	6.79E-01	1.00E+00	9.98E-01	1.00E+00	3.41E-02	5.87E-01	9.80E-01	1.00E+00	8.78E-01	1.00E+00	9.84E-01	1.00E+00	9.63E-01	1.00E+00	9.94E-01	1.00E+00	cell ion homeostasis	P
GO:0006874	125	8.58E-01	1.00E+00	9.91E-01	1.00E+00	1.88E-01	1.00E+00	8.25E-01	1.00E+00	9.06E-01	1.00E+00	9.80E-01	1.00E+00	9.84E-01	1.00E+00	9.83E-01	1.00E+00	calcium ion homeostasis	P
GO:0006875	175	7.66E-01	1.00E+00	9.94E-01	1.00E+00	4.08E-02	5.87E-01	9.54E-01	1.00E+00	9.25E-01	1.00E+00	9.77E-01	1.00E+00	9.72E-01	1.00E+00	9.88E-01	1.00E+00	metal ion homeostasis	P

GO:0006878	10	9.90E-01	1.00E+00	9.38E-01	1.00E+00	2.10E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	8.41E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	copper ion homeostasis	P
GO:0006879	29	2.09E-01	1.00E+00	4.11E-01	1.00E+00	8.03E-02	1.00E+00	8.70E-01	1.00E+00	4.36E-01	1.00E+00	3.73E-01	1.00E+00	1.63E-01	1.00E+00	3.38E-01	1.00E+00	iron ion homeostasis	P
GO:0006884	11	6.61E-01	1.00E+00	1.97E-01	1.00E+00	2.80E-01	1.00E+00	2.40E-01	1.00E+00	8.91E-01	1.00E+00	1.34E-01	1.00E+00	5.34E-01	1.00E+00	1.00E+00	1.00E+00	regulation of cell volume	P
GO:0006885	35	3.93E-01	1.00E+00	5.08E-01	1.00E+00	5.65E-01	1.00E+00	4.76E-01	1.00E+00	2.87E-01	1.00E+00	3.08E-01	1.00E+00	7.95E-01	1.00E+00	9.69E-01	1.00E+00	regulation of pH	P
GO:0006886	520	7.22E-04	1.60E-02	6.21E-06	1.41E-03	1.97E-06	8.48E-04	1.28E-04	7.00E-03	3.51E-03	6.24E-02	1.04E-03	1.02E-02	9.24E-01	1.00E+00	1.81E-01	1.00E+00	intracellular protein transport	P
GO:0006887	97	1.45E-01	1.00E+00	8.32E-01	1.00E+00	1.68E-01	1.00E+00	2.68E-01	1.00E+00	1.62E-01	1.00E+00	9.76E-01	1.00E+00	4.01E-01	1.00E+00	7.83E-01	1.00E+00	exocytosis	P
GO:0006888	36	6.04E-01	1.00E+00	6.25E-02	1.00E+00	1.24E-01	1.00E+00	1.87E-02	4.10E-01	9.11E-01	1.00E+00	1.38E-01	1.00E+00	3.94E-01	1.00E+00	1.17E-01	1.00E+00	ER to Golgi vesicle-mediated transport	P
GO:0006890	18	4.19E-01	1.00E+00	1.69E-01	1.00E+00	4.43E-01	1.00E+00	1.97E-01	1.00E+00	4.42E-01	1.00E+00	1.41E-01	1.00E+00	4.02E-01	1.00E+00	5.49E-01	1.00E+00	retrograde vesicle-mediated transport, Golg	P
GO:0006891	17	9.50E-02	1.00E+00	1.17E-01	1.00E+00	1.17E-01	1.00E+00	3.69E-02	1.00E+00	1.76E-01	1.00E+00	3.17E-01	1.00E+00	2.56E-01	1.00E+00	1.20E-01	1.00E+00	intra-Golgi vesicle-mediated transport	P
GO:0006892	23	2.70E-01	1.00E+00	3.44E-01	1.00E+00	5.72E-02	1.00E+00	1.69E-01	1.00E+00	4.37E-01	1.00E+00	3.83E-01	1.00E+00	4.83E-01	1.00E+00	6.87E-01	1.00E+00	post-Golgi vesicle-mediated transport	P
GO:0006895	10	1.02E-01	1.00E+00	2.17E-01	1.00E+00	7.20E-03	1.57E-01	1.22E-01	1.00E+00	2.76E-01	1.00E+00	2.57E-01	1.00E+00	7.48E-01	1.00E+00	6.38E-01	1.00E+00	Golgi to endosome transport	P
GO:0006897	215	1.15E-01	1.00E+00	3.54E-02	1.00E+00	1.60E-01	1.00E+00	4.00E-03	6.84E-02	4.65E-02	1.00E+00	1.48E-01	1.00E+00	9.99E-01	1.00E+00	1.96E-01	1.00E+00	endocytosis	P
GO:0006898	51	6.36E-01	1.00E+00	4.03E-01	1.00E+00	6.65E-01	1.00E+00	3.20E-01	1.00E+00	5.38E-01	1.00E+00	3.21E-01	1.00E+00	7.49E-01	1.00E+00	9.20E-01	1.00E+00	receptor mediated endocytosis	P
GO:0006900	12	5.09E-03	1.37E-01	2.44E-02	1.00E+00	3.31E-02	5.87E-01	1.46E-01	1.00E+00	1.16E-02	3.01E-01	1.58E-02	5.65E-01	3.92E-02	9.62E-01	2.71E-01	1.00E+00	vesicle budding	P
GO:0006901	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	vesicle coating	P
GO:0006903	21	9.57E-03	1.77E-01	1.63E-02	3.84E-01	5.85E-03	9.30E-02	7.95E-02	1.00E+00	1.90E-02	3.81E-01	8.48E-03	1.05E-01	3.41E-02	9.62E-01	1.15E-01	1.00E+00	vesicle targeting	P
GO:0006904	20	2.22E-01	1.00E+00	3.96E-01	1.00E+00	9.21E-02	1.00E+00	3.04E-01	1.00E+00	2.30E-01	1.00E+00	3.17E-01	1.00E+00	8.65E-01	1.00E+00	7.57E-01	1.00E+00	vesicle docking during exocytosis	P
GO:0006909	46	6.08E-01	1.00E+00	9.48E-01	1.00E+00	8.81E-01	1.00E+00	9.36E-01	1.00E+00	4.79E-01	1.00E+00	9.82E-01	1.00E+00	9.76E-01	1.00E+00	2.04E-01	1.00E+00	phagocytosis	P
GO:0006913	273	2.22E-02	1.00E+00	3.40E-03	6.30E-02	5.71E-04	1.25E-02	1.25E-02	1.57E-01	3.01E-02	6.55E-01	3.72E-02	1.00E+00	9.79E-01	1.00E+00	2.47E-01	1.00E+00	nucleocytoplasmic transport	P
GO:0006914	28	2.97E-01	1.00E+00	3.85E-02	1.00E+00	5.10E-01	1.00E+00	1.39E-01	1.00E+00	2.46E-01	1.00E+00	7.31E-02	1.00E+00	6.22E-01	1.00E+00	2.55E-01	1.00E+00	autophagy	P
GO:0006915	859	9.69E-01	1.00E+00	8.55E-01	1.00E+00	1.29E-02	1.92E-01	2.54E-01	1.00E+00	9.99E-01	1.00E+00	9.11E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	apoptosis	P
GO:0006916	173	9.86E-01	1.00E+00	9.45E-01	1.00E+00	3.80E-01	1.00E+00	7.63E-01	1.00E+00	9.99E-01	1.00E+00	9.66E-01	1.00E+00	9.75E-01	1.00E+00	8.98E-01	1.00E+00	anti-apoptosis	P
GO:0006917	243	5.82E-01	1.00E+00	7.90E-02	1.00E+00	2.50E-02	4.97E-01	1.36E-02	2.81E-01	9.23E-01	1.00E+00	2.19E-01	1.00E+00	7.12E-01	1.00E+00	8.12E-01	1.00E+00	induction of apoptosis	P
GO:0006919	45	1.10E-01	1.00E+00	1.25E-01	1.00E+00	4.61E-01	1.00E+00	5.36E-02	1.00E+00	9.06E-02	1.00E+00	1.56E-01	1.00E+00	2.96E-01	1.00E+00	4.59E-01	1.00E+00	caspase activation	P
GO:0006921	20	4.92E-01	1.00E+00	4.27E-01	1.00E+00	8.18E-01	1.00E+00	5.13E-01	1.00E+00	6.20E-01	1.00E+00	4.45E-01	1.00E+00	1.88E-01	1.00E+00	5.57E-01	1.00E+00	disassembly of cell structures during apopto	P
GO:0006928	497	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell motility	P
GO:0006929	12	9.89E-01	1.00E+00	9.49E-01	1.00E+00	9.97E-01	1.00E+00	9.91E-01	1.00E+00	9.95E-01	1.00E+00	7.68E-01	1.00E+00	7.92E-01	1.00E+00	1.00E+00	1.00E+00	substrate-bound cell migration	P
GO:0006935	195	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	6.07E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chemotaxis	P
GO:0006936	148	7.71E-01	1.00E+00	1.00E+00	1.00E+00	4.86E-01	1.00E+00	9.99E-01	1.00E+00	7.84E-01	1.00E+00	1.00E+00	1.00E+00	8.69E-01	1.00E+00	1.00E+00	1.00E+00	muscle contraction	P
GO:0006937	41	7.71E-01	1.00E+00	1.00E+00	1.00E+00	2.63E-01	1.00E+00	9.99E-01	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	8.23E-01	1.00E+00	1.00E+00	1.00E+00	regulation of muscle contraction	P
GO:0006939	31	9.53E-01	1.00E+00	1.00E+00	1.00E+00	6.95E-01	1.00E+00	9.51E-01	1.00E+00	9.56E-01	1.00E+00	9.96E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	smooth muscle contraction	P
GO:0006940	19	8.17E-01	1.00E+00	1.00E+00	1.00E+00	3.91E-01	1.00E+00	9.99E-01	1.00E+00	9.26E-01	1.00E+00	9.97E-01	1.00E+00	8.75E-01	1.00E+00	1.00E+00	1.00E+00	regulation of smooth muscle contraction	P
GO:0006941	39	3.68E-01	1.00E+00	1.00E+00	1.00E+00	1.45E-01	1.00E+00	9.91E-01	1.00E+00	4.70E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	striated muscle contraction	P
GO:0006942	11	5.98E-01	1.00E+00	1.00E+00	1.00E+00	2.32E-01	1.00E+00	1.00E+00	1.00E+00	7.12E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	regulation of striated muscle contraction	P
GO:0006944	42	3.39E-01	1.00E+00	5.33E-01	1.00E+00	1.86E-01	1.00E+00	1.50E-01	1.00E+00	3.50E-01	1.00E+00	7.63E-01	1.00E+00	9.24E-01	1.00E+00	6.64E-01	1.00E+00	membrane fusion	P
GO:0006950	1455	1.00E+00	1.00E+00	1.00E+00	1.00E+00	2.84E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to stress	P
GO:0006952	718	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	defense response	P
GO:0006953	30	8.67E-01	1.00E+00	1.00E+00	1.00E+00	7.18E-01	1.00E+00	1.00E+00	1.00E+00	6.76E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	acute-phase response	P
GO:0006954	381	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inflammatory response	P
GO:0006955	805	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	immune response	P
GO:0006956	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	complement activation	P
GO:0006957	17	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	complement activation, alternative pathway	P
GO:0006958	29	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	complement activation, classical pathway	P
GO:0006959	84	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	humoral immune response	P
GO:0006968	65	9.90E-01	1.00E+00	9.76E-01	1.00E+00	7.19E-01	1.00E+00	7.77E-01	1.00E+00	9.86E-01	1.00E+00	8.65E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cellular defense response	P
GO:0006970	13	2.15E-01	1.00E+00	4.84E-01	1.00E+00	1.15E-01	1.00E+00	3.68E-01	1.00E+00	1.96E-01	1.00E+00	3.15E-01	1.00E+00	9.13E-01	1.00E+00	9.66E-01	1.00E+00	response to osmotic stress	P
GO:0006974	369	2.27E-03	4.90E-02	6.47E-08	1.00E-03	3.76E-05	4.57E-03	6.75E-07	0.00E+00	1.17E-02	3.01E-01	8.20E-06	2.29E-03	9.86E-01	1.00E+00	2.94E-02	2.52E-01	response to DNA damage stimulus	P
GO:0006979	125	6.19E-01	1.00E+00	7.54E-01	1.00E+00	6.00E-02	1.00E+00	7.80E-01	1.00E+00	8.01E-01	1.00E+00	7.18E-01	1.00E+00	9.03E-01	1.00E+00	5.78E-01	1.00E+00	response to oxidative stress	P
GO:0006984	26	6.67E-01	1.00E+00	6.11E-01	1.00E+00	8.94E-01	1.00E+00	2.33E-01	1.00E+00	4.61E-01	1.00E+00	5.58E-01	1.00E+00	9.79E-01	1.00E+00	9.88E-01	1.00E+00	ER-nuclear signaling pathway	P
GO:0006986	82	9.17E-01	1.00E+00	5.48E-01	1.00E+00	4.72E-01	1.00E+00	7.22E-01	1.00E+00	9.76E-01	1.00E+00	4.09E-01	1.00E+00	8.86E-01	1.00E+00	7.00E-01	1.00E+00	response to unfolded protein	P
GO:0006996	1158	1.68E-03	4.90E-02	3.82E-04	1.10E-02	5.47E-11	0.00E+00	8.36E-06	8.32E-04	5.06E-02	1.00E+00	4.85E-03	7.40E-02	9.75E-01	1.00E+00	5.74E-01	1.00E+00	organelle organization and biogenesis	P
GO:0006997	13	6.87E-01	1.00E+00	1.02E-01	1.00E+00	5.01E-01	1.00E+00	4.52E-02	1.00E+00	5.47E-01	1.00E+00	1.03E-01	1.00E+00	1.00E+00	1.00E+00	8.80E-01	1.00E+00	nuclear organization and biogenesis	P
GO:0007001	359	1.43E-02	2.72E-01	3.77E-05	3.00E-03	1.13E-04	4.57E-03	3.39E-04	7.00E-03	4.30E-02	1.00E+00	3.13E-04	1.02E-02	9.88E-01	1.00E+00	1.02E-01	1.00E+00	chromosome organization and biogenesis (	P
GO:0007004	13	9.84E-01	1.00E+00	4.20E-01	1.00E+00	8.64E-01	1.00E+00	3.64E-01	1.00E+00	9.82E-01	1.00E+00	5.09E-01	1.00E+00	9.84E-01	1.00E+00	4.11E-01	1.00E+00	telomere maintenance via telomerase	P
GO:0007005	43	2.61E-01	1.00E+00	4.25E-01	1.00E+00	2.43E-01	1.00E+00	2.32E-01	1.00E+00	4.82E-01	1.00E+00	4.34E-01	1.00E+00	3.40E-01	1.00E+00	9.86E-01	1.00E+00	mitochondrion organization and biogenesis	P
GO:0007006	21	3.08E-01	1.00E+00	4.08E-01	1.00E+00	8.62E-01	1.00E+00	5.15E-01	1.00E+00	4.24E-01	1.00E+00	3.39E-01	1.00E+00	1.40E-01	1.00E+00	8.18E-01	1.00E+00	mitochondrial membrane organization and b	P
GO:0007009	19	1.00E+00	1.00E+00	9.51E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	7.47E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	plasma membrane organization and biogen	P
GO:0007010	540	4.01E-01	1.00E+00	6.89E-01	1.00E+00	5.87E-05	4.57E-03	1.27E-01	1.00E+00	7.84E-01	1.00E+00	8.08E-01	1.00E+00	9.67E-01	1.00E+00	8.11E-01	1.00E+00	cytoskeleton organization and biogenesis	P
GO:0007015	50	8.96E-01	1.00E+00	5.30E-01	1.00E+00	4.52E-01	1.00E+00	3.75E-01	1.00E+00	9.26E-01	1.00E+00	6.48E-01	1.00E+00	8.74E-01	1.00E+00	4.17E-01	1.00E+00	actin filament organization	P
GO:0007017	228	4.38E-01	1.00E+00	2.53E-01	1.00E+00	2.37E-03	1.80E-02	5.28E-02	1.00E+00	7.94E-01	1.00E+00	4.02E-01	1.00E+00	8.32E-01	1.00E+00	5.26E-01	1.00E+00	microtubule-based process	P
GO:0007018	115	3.60E-01	1.00E+00	4.19E-01	1.00E+00	4.76E-03	9.30E-02	5.08E-02	1.00E+00	7.37E-01	1.00E+00	6.69E-01	1.00E+00	7.21E-01	1.00E+00	5.65E-01	1.00E+00	microtubule-based movement	P
GO:0007019	17	4.66E-01	1.00E+00	1.43E-01	1.00E+00	2.61E-01	1.00E+00	1.80E-01	1.00E+00	4.79E-01	1.00E+00	1.23E-01	1.00E+00	8.47E-01	1.00E+00	5.71E-01	1.00E+00	microtubule depolymerization	P
GO:0007026	16	3.10E-01	1.00E+00	1.66E-01	1.00E+00	1.68E-01	1.00E+00	3.34E-01	1.00E+00	3.35E-01	1.00E+00	1.21E-01	1.00E+00	7.80E-01	1.00E+00	4.91E-01	1.00E+00	negative regulation of microtubule depolym	P
GO:0007028	128	8.08E-02	1.00E+00	2.38E-02	1.00E+00	8.61E-03	1.57E-01	2.83E-02	5.42E-01	1.88E-01	1.00E+00	5.47E-02	1.00E+00	6.18E-01	1.00E+00	7.35E-01	1.00E+00	cytoplasm organization and biogenesis	P
GO:0007030	13	4.71E-01	1.00E+00	1.79E-01	1.00E+00	3.30E-02	5.87E-01	1.13E-02	1.27E-01	8.62E-01	1.00E+00	5.28E-01	1.00E+00	6.40E-01	1.00E+00	3.50E-01	1.00E+00	Golgi organization and biogenesis	P
GO:0007031	22	8.20E-02	1.00E+00	6.28E-01	1.00E+00	1.31E-01	1.00E+00	1.88E-01	1.00E+00	1.48E-01	1.00E+00	7.20E-01	1.00E+00	4.94E-01	1.00E+00	7.38E-01	1.00E+00	peroxisome organization and biogenesis	P
GO:0007033	34	2.21E-01	1.00E+00	2.64E-01	1.00E+00	1.47E-02	1.92E-01	2.16E-01	1.00E+00	2.51E-01	1.00E+00	1.56E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	vacuole organization and biogenesis	P
GO:0007034	22	1.56E-01	1.00E+00	1.06E-01	1.00E+00	4.83E-02	8.68E-01	3.19E-02	5.42E-01	2.29E-01	1.00E+00	1.70E-01	1.00E+00	7.19E-01	1.00E+00	4.02E-01	1.00E+00	vacuolar transport	P
GO:0007040	32	1.42E-01	1.00E+00	1.76E-01	1.00E+00	6.74E-03	1.57E-01	2.22E-01	1.00E+00	1.81E-01	1.00E+00	9.18E-02	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	lysosome organization and biogenesis	P
GO:0007041	14	9.50E-02	1.00E+00	3.07E-01	1.00E+00	4.85E-02	8.68E-01	1.02E-01	1.00E+00	1.23E-01	1.00E+00	2.94E-01	1.00E+00	7.93E-01	1.00E+00	8.02E-01	1.00E+00	lysosomal transport	P
GO:0007043	14	7.44E-01	1.00E+00	4.59E-01	1.00E+00	7.79E-01	1.00E+00	5.96E-01	1.00E+00	6.75E-01	1.00E+00	6.04E-01	1.00E+00	6.43E-01	1.00E+00	1.32E-01	1.00E+00	intercellular junction assembly	P
GO:0007046	68	8.57E-02	1.00E+00	1.03E-01	1.00E+00	2.17E-02	2.63E-01	4.46E-02	1.00E+00	1.64E-01	1.00E+00	2.21E-01	1.00E+00	4.52E-01	1.00E+00	9.21E-01	1.00E+00	ribosome biogenesis	P
GO:0007049	844	1.45E-02	2.72E-01	5.96E-07	1.00E-03	2.80E-05	1.00E-03	8.39E-09	0.00E+00	8.14E-02	1.00E+00	4.48E-04	1.02E-02	9.51E-01	1.00E+00	2.55E-02	2.52E-01	cell cycle	P
GO:0007050	91	4.86E-01	1.00E+00	9.26E-01	1.00E+00	8.07E-02	1.00E+00	3.41E-01	1.00E+00	6.38E-01	1.00E+00	9.72E-01	1.00E+00	7.22E-01	1.00E+00	7.69E-01	1.00E+00	cell cycle arrest	P
GO:0007051	30	5.95E-02	1.00E+00	2.26E-03	5.10E-02	4.69E-02	8.68E-01	2.66E-02	4.10E-01	5.04E-02	1.00E+00	1.12E-02	2.12E-01	8.38E-01	1.00E+00	1.09E-01	1.00E+00	spindle organization and biogenesis	P

GO:0007052	12	1.19E-01	1.00E+00	2.98E-04	8.26E-03	2.02E-01	1.00E+00	2.37E-02	4.10E-01	1.07E-01	1.00E+00	2.08E-03	5.10E-02	2.46E-01	1.00E+00	2.12E-01	1.00E+00	mitotic spindle organization and biogenesis	P
GO:0007059	65	7.17E-02	1.00E+00	5.95E-03	1.50E-01	5.18E-02	1.00E+00	6.83E-02	1.00E+00	2.98E-01	1.00E+00	7.28E-03	1.05E-01	9.31E-02	1.00E+00	2.92E-01	1.00E+00	chromosome segregation	P
GO:0007062	10	6.45E-01	1.00E+00	1.35E-01	1.00E+00	8.66E-01	1.00E+00	3.83E-01	1.00E+00	7.38E-01	1.00E+00	8.13E-02	1.00E+00	2.95E-01	1.00E+00	9.49E-01	1.00E+00	sister chromatid cohesion	P
GO:0007067	218	4.15E-03	1.37E-01	2.08E-07	1.00E-03	6.87E-04	1.25E-02	3.23E-06	0.00E+00	5.26E-02	1.00E+00	9.73E-06	2.29E-03	4.01E-01	1.00E+00	5.43E-03	6.60E-02	mitosis	P
GO:0007076	15	2.13E-01	1.00E+00	2.06E-01	1.00E+00	3.08E-01	1.00E+00	9.29E-02	1.00E+00	4.36E-01	1.00E+00	4.84E-01	1.00E+00	6.96E-02	1.00E+00	1.86E-01	1.00E+00	mitotic chromosome condensation	P
GO:0007088	67	2.07E-01	1.00E+00	6.09E-02	1.00E+00	5.28E-02	1.00E+00	2.58E-01	1.00E+00	2.86E-01	1.00E+00	5.14E-02	1.00E+00	7.83E-01	1.00E+00	3.63E-01	1.00E+00	regulation of mitosis	P
GO:0007091	10	4.50E-02	1.00E+00	3.00E-02	1.00E+00	2.75E-01	1.00E+00	1.41E-01	1.00E+00	3.69E-03	6.24E-02	2.71E-02	1.00E+00	3.27E-01	1.00E+00	4.47E-01	1.00E+00	mitotic metaphase/anaphase transition	P
GO:0007093	20	4.76E-01	1.00E+00	1.87E-01	1.00E+00	2.58E-02	4.97E-01	9.50E-02	1.00E+00	8.21E-01	1.00E+00	2.05E-01	1.00E+00	6.55E-01	1.00E+00	4.23E-01	1.00E+00	mitotic checkpoint	P
GO:0007096	11	8.90E-03	1.56E-01	2.28E-03	5.10E-02	1.27E-02	1.92E-01	2.22E-02	4.10E-01	3.33E-02	6.55E-01	5.62E-03	7.40E-02	2.96E-01	1.00E+00	6.95E-02	1.00E+00	regulation of exit from mitosis	P
GO:0007098	13	1.10E-01	1.00E+00	3.54E-02	1.00E+00	3.96E-02	5.87E-01	5.23E-02	1.00E+00	2.01E-01	1.00E+00	9.15E-02	1.00E+00	5.08E-01	1.00E+00	4.30E-02	8.10E-01	centrosome cycle	P
GO:0007126	86	3.83E-01	1.00E+00	2.72E-03	5.10E-02	4.87E-01	1.00E+00	5.03E-02	1.00E+00	4.30E-01	1.00E+00	9.42E-03	1.43E-01	4.33E-01	1.00E+00	3.99E-02	8.10E-01	meiosis	P
GO:0007127	38	1.63E-01	1.00E+00	5.83E-03	1.50E-01	7.80E-01	1.00E+00	8.26E-02	1.00E+00	8.71E-02	1.00E+00	7.14E-03	1.05E-01	3.08E-01	1.00E+00	2.15E-01	1.00E+00	meiosis I	P
GO:0007131	21	4.31E-01	1.00E+00	9.62E-03	3.84E-01	8.61E-01	1.00E+00	2.58E-02	4.10E-01	2.70E-01	1.00E+00	1.46E-02	5.65E-01	7.22E-01	1.00E+00	2.65E-01	1.00E+00	meiotic recombination	P
GO:0007154	3884	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell communication	P
GO:0007155	825	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell adhesion	P
GO:0007156	100	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	homophilic cell adhesion	P
GO:0007157	46	9.97E-01	1.00E+00	9.95E-01	1.00E+00	8.46E-01	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	heterophilic cell adhesion	P
GO:0007159	26	8.52E-01	1.00E+00	8.37E-01	1.00E+00	4.22E-01	1.00E+00	6.25E-01	1.00E+00	9.13E-01	1.00E+00	8.58E-01	1.00E+00	9.57E-01	1.00E+00	7.28E-01	1.00E+00	leukocyte adhesion	P
GO:0007160	117	8.16E-01	1.00E+00	8.91E-01	1.00E+00	2.66E-01	1.00E+00	6.86E-01	1.00E+00	7.47E-01	1.00E+00	8.23E-01	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	cell-matrix adhesion	P
GO:0007162	19	4.17E-01	1.00E+00	9.84E-01	1.00E+00	3.18E-01	1.00E+00	6.41E-01	1.00E+00	4.58E-01	1.00E+00	9.79E-01	1.00E+00	4.24E-01	1.00E+00	9.99E-01	1.00E+00	negative regulation of cell adhesion	P
GO:0007163	37	8.49E-01	1.00E+00	7.02E-01	1.00E+00	4.19E-01	1.00E+00	2.10E-01	1.00E+00	8.72E-01	1.00E+00	8.94E-01	1.00E+00	8.61E-01	1.00E+00	3.21E-01	1.00E+00	establishment and/or maintenance of cell p	P
GO:0007165	3501	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	signal transduction	P
GO:0007166	1730	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell surface receptor linked signal transduct	P
GO:0007167	349	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	enzyme linked receptor protein signaling pa	P
GO:0007169	230	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.52E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor protein tyrosine ki	P
GO:0007172	16	7.68E-01	1.00E+00	6.33E-01	1.00E+00	5.03E-01	1.00E+00	6.16E-02	1.00E+00	7.14E-01	1.00E+00	7.98E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	signal complex formation	P
GO:0007173	34	1.98E-01	1.00E+00	5.03E-01	1.00E+00	3.33E-01	1.00E+00	2.17E-01	1.00E+00	1.73E-01	1.00E+00	7.15E-01	1.00E+00	4.67E-01	1.00E+00	3.62E-01	1.00E+00	epidermal growth factor receptor signaling p	P
GO:0007178	107	9.98E-01	1.00E+00	9.97E-01	1.00E+00	6.15E-01	1.00E+00	8.74E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	transmembrane receptor protein serine/thre	P
GO:0007179	64	8.93E-01	1.00E+00	8.70E-01	1.00E+00	3.04E-01	1.00E+00	8.32E-01	1.00E+00	8.89E-01	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	7.30E-01	1.00E+00	transforming growth factor beta receptor sig	P
GO:0007186	1021	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor protein signalinc	P
GO:0007187	119	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein signaling, coupled to cyclic nucle	P
GO:0007188	93	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.40E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein signaling, coupled to cAMP nucle	P
GO:0007189	41	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.61E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	9.98E-01	1.00E+00	G-protein signaling, adenylate cyclase activ	P
GO:0007190	23	9.50E-01	1.00E+00	8.58E-01	1.00E+00	9.16E-01	1.00E+00	2.94E-01	1.00E+00	9.41E-01	1.00E+00	9.86E-01	1.00E+00	6.33E-01	1.00E+00	9.51E-01	1.00E+00	adenylate cyclase activation	P
GO:0007193	21	9.63E-01	1.00E+00	9.97E-01	1.00E+00	8.58E-01	1.00E+00	8.90E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.92E-01	1.00E+00	G-protein signaling, adenylate cyclase inhib	P
GO:0007194	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of adenylate cyclase ac	P
GO:0007200	76	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	8.60E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	G-protein signaling, coupled to IP3 second	P
GO:0007202	15	5.13E-01	1.00E+00	3.70E-01	1.00E+00	4.22E-01	1.00E+00	1.69E-01	1.00E+00	4.61E-01	1.00E+00	3.88E-01	1.00E+00	7.06E-01	1.00E+00	9.52E-01	1.00E+00	phospholipase C activation	P
GO:0007204	72	6.43E-01	1.00E+00	9.74E-01	1.00E+00	5.09E-01	1.00E+00	6.83E-01	1.00E+00	5.73E-01	1.00E+00	9.27E-01	1.00E+00	8.99E-01	1.00E+00	1.00E+00	1.00E+00	elevation of cytosolic calcium ion concentra	P
GO:0007205	28	9.44E-01	1.00E+00	9.67E-01	1.00E+00	9.47E-01	1.00E+00	6.26E-01	1.00E+00	9.36E-01	1.00E+00	9.54E-01	1.00E+00	6.96E-01	1.00E+00	9.97E-01	1.00E+00	protein kinase C activation	P
GO:0007212	10	7.27E-01	1.00E+00	1.00E+00	1.00E+00	4.48E-01	1.00E+00	1.00E+00	1.00E+00	6.98E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	9.88E-01	1.00E+00	dopamine receptor signaling pathway	P
GO:0007214	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.41E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	gamma-aminobutyric acid signaling pathwa	P
GO:0007215	22	9.60E-01	1.00E+00	9.38E-01	1.00E+00	5.24E-01	1.00E+00	9.48E-01	1.00E+00	9.89E-01	1.00E+00	9.26E-01	1.00E+00	9.88E-01	1.00E+00	6.82E-01	1.00E+00	glutamate signaling pathway	P
GO:0007218	93	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuropeptide signaling pathway	P
GO:0007219	53	9.98E-01	1.00E+00	9.91E-01	1.00E+00	7.37E-01	1.00E+00	8.06E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.73E-01	1.00E+00	9.98E-01	1.00E+00	Notch signaling pathway	P
GO:0007223	21	8.98E-01	1.00E+00	9.92E-01	1.00E+00	7.35E-01	1.00E+00	6.78E-01	1.00E+00	9.35E-01	1.00E+00	1.00E+00	1.00E+00	7.48E-01	1.00E+00	8.62E-01	1.00E+00	frizzled-2 signaling pathway	P
GO:0007224	25	6.81E-01	1.00E+00	9.89E-01	1.00E+00	4.36E-01	1.00E+00	9.59E-01	1.00E+00	7.64E-01	1.00E+00	9.96E-01	1.00E+00	6.66E-01	1.00E+00	6.07E-01	1.00E+00	smoothened signaling pathway	P
GO:0007229	62	1.63E-01	1.00E+00	9.46E-01	1.00E+00	5.95E-02	1.00E+00	3.15E-01	1.00E+00	1.73E-01	1.00E+00	9.85E-01	1.00E+00	7.74E-01	1.00E+00	9.93E-01	1.00E+00	integrin-mediated signaling pathway	P
GO:0007242	1422	9.99E-01	1.00E+00	9.82E-01	1.00E+00	9.30E-02	1.00E+00	5.86E-02	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	intracellular signaling cascade	P
GO:0007243	445	9.85E-01	1.00E+00	8.39E-01	1.00E+00	3.17E-01	1.00E+00	5.15E-01	1.00E+00	9.82E-01	1.00E+00	6.30E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	protein kinase cascade	P
GO:0007249	148	6.18E-01	1.00E+00	7.61E-02	1.00E+00	3.94E-02	5.87E-01	2.24E-01	1.00E+00	7.26E-01	1.00E+00	4.11E-02	1.00E+00	9.95E-01	1.00E+00	7.94E-01	1.00E+00	I-kappaB kinase/NF-kappaB cascade	P
GO:0007250	12	5.04E-01	1.00E+00	6.77E-01	1.00E+00	2.46E-01	1.00E+00	7.63E-01	1.00E+00	8.14E-01	1.00E+00	5.49E-01	1.00E+00	2.50E-01	1.00E+00	6.18E-01	1.00E+00	activation of NF-kappaB-inducing kinase	P
GO:0007254	80	9.46E-01	1.00E+00	9.63E-01	1.00E+00	7.88E-01	1.00E+00	8.89E-01	1.00E+00	9.35E-01	1.00E+00	9.62E-01	1.00E+00	9.69E-01	1.00E+00	8.22E-01	1.00E+00	JNK cascade	P
GO:0007257	24	8.93E-01	1.00E+00	7.63E-01	1.00E+00	9.43E-01	1.00E+00	3.66E-01	1.00E+00	8.20E-01	1.00E+00	8.22E-01	1.00E+00	9.68E-01	1.00E+00	9.05E-01	1.00E+00	activation of JNK activity	P
GO:0007259	54	8.19E-01	1.00E+00	8.95E-01	1.00E+00	2.25E-01	1.00E+00	9.36E-01	1.00E+00	8.75E-01	1.00E+00	6.92E-01	1.00E+00	9.73E-01	1.00E+00	9.99E-01	1.00E+00	JAK-STAT cascade	P
GO:0007260	25	9.89E-01	1.00E+00	8.44E-01	1.00E+00	3.60E-01	1.00E+00	8.21E-01	1.00E+00	9.99E-01	1.00E+00	6.34E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tyrosine phosphorylation of STAT protein	P
GO:0007263	13	9.70E-01	1.00E+00	1.00E+00	1.00E+00	7.38E-01	1.00E+00	9.41E-01	1.00E+00	8.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	nitric oxide mediated signal transduction	P
GO:0007264	452	3.36E-01	1.00E+00	2.06E-01	1.00E+00	5.69E-03	9.30E-02	2.00E-02	4.10E-01	4.99E-01	1.00E+00	7.14E-01	1.00E+00	9.74E-01	1.00E+00	8.66E-01	1.00E+00	small GTPase mediated signal transduction	P
GO:0007265	68	2.23E-01	1.00E+00	2.26E-01	1.00E+00	3.64E-02	5.87E-01	1.52E-02	2.81E-01	4.28E-01	1.00E+00	4.19E-01	1.00E+00	8.69E-01	1.00E+00	6.74E-01	1.00E+00	Ras protein signal transduction	P
GO:0007266	109	8.41E-01	1.00E+00	8.05E-01	1.00E+00	2.74E-01	1.00E+00	1.38E-01	1.00E+00	8.49E-01	1.00E+00	8.88E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	Rho protein signal transduction	P
GO:0007267	625	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell-cell signaling	P
GO:0007268	301	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synaptic transmission	P
GO:0007269	60	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	4.45E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter secretion	P
GO:0007270	47	8.62E-01	1.00E+00	9.58E-01	1.00E+00	2.19E-01	1.00E+00	8.80E-01	1.00E+00	9.90E-01	1.00E+00	9.53E-01	1.00E+00	5.47E-01	1.00E+00	9.60E-01	1.00E+00	nerve-nerve synaptic transmission	P
GO:0007271	19	6.93E-01	1.00E+00	7.06E-01	1.00E+00	1.46E-01	1.00E+00	8.11E-01	1.00E+00	9.71E-01	1.00E+00	6.66E-01	1.00E+00	3.06E-01	1.00E+00	6.99E-01	1.00E+00	synaptic transmission, cholinergic	P
GO:0007272	36	4.50E-01	1.00E+00	8.02E-01	1.00E+00	1.02E-01	1.00E+00	3.89E-01	1.00E+00	7.14E-01	1.00E+00	7.41E-01	1.00E+00	8.47E-01	1.00E+00	9.15E-01	1.00E+00	ensheathment of neurons	P
GO:0007274	13	4.88E-01	1.00E+00	3.98E-01	1.00E+00	6.61E-01	1.00E+00	1.12E-01	1.00E+00	5.56E-01	1.00E+00	5.74E-01	1.00E+00	3.76E-01	1.00E+00	9.98E-01	1.00E+00	neuromuscular synaptic transmission	P
GO:0007275	2890	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	development	P
GO:0007276	318	9.30E-01	1.00E+00	4.91E-01	1.00E+00	7.32E-01	1.00E+00	2.45E-01	1.00E+00	8.23E-01	1.00E+00	4.94E-01	1.00E+00	9.97E-01	1.00E+00	8.13E-01	1.00E+00	gametogenesis	P
GO:0007281	39	4.88E-01	1.00E+00	6.06E-01	1.00E+00	6.97E-01	1.00E+00	5.55E-01	1.00E+00	4.73E-01	1.00E+00	6.50E-01	1.00E+00	5.57E-01	1.00E+00	4.69E-01	1.00E+00	germ cell development	P
GO:0007283	251	8.11E-01	1.00E+00	3.30E-01	1.00E+00	7.72E-01	1.00E+00	1.75E-01	1.00E+00	6.30E-01	1.00E+00	3.35E-01	1.00E+00	9.73E-01	1.00E+00	8.13E-01	1.00E+00	spermatogenesis	P
GO:0007286	38	2.87E-01	1.00E+00	4.11E-01	1.00E+00	6.48E-01	1.00E+00	7.73E-01	1.00E+00	2.47E-01	1.00E+00	2.09E-01	1.00E+00	3.66E-01	1.00E+00	9.71E-01	1.00E+00	spermatid development	P
GO:0007292	47	3.99E-01	1.00E+00	5.63E-01	1.00E+00	3.78E-01	1.00E+00	9.49E-01	1.00E+00	2.94E-01	1.00E+00	3.69E-01	1.00E+00	9.98E-01	1.00E+00	7.79E-01	1.00E+00	female gamete generation	P
GO:0007338	64	6.04E-01	1.00E+00	6.91E-01	1.00E+00	4.66E-01	1.00E+00	6.67E-01	1.00E+00	7.31E-01	1.00E+00	5.91E-01	1.00E+00	2.94E-01	1.00E+00	9.18E-01	1.00E+00	fertilization (sensu Metazoa)	P
GO:0007339	15	1.77E-01	1.00E+00	4.71E-02	1.00E+00	2.57E-01	1.00E+00	4.22E-02	1.00E+00	2.74E-01	1.00E+00	4.90E-02	1.00E+00	1.66E-01	1.00E+00	8.57E-01	1.00E+00	binding of sperm to zona pellucida	P

GO:0007340	12	2.99E-01	1.00E+00	7.67E-01	1.00E+00	5.49E-01	1.00E+00	8.10E-01	1.00E+00	6.87E-01	1.00E+00	8.49E-01	1.00E+00	2.20E-02	2.56E-01	2.77E-01	1.00E+00	acrosome reaction	P
GO:0007342	10	5.82E-01	1.00E+00	9.92E-01	1.00E+00	3.61E-01	1.00E+00	1.00E+00	1.00E+00	4.97E-01	1.00E+00	8.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	fusion of sperm to egg plasma membrane	P
GO:0007346	39	2.11E-01	1.00E+00	2.30E-01	1.00E+00	1.44E-01	1.00E+00	1.01E-01	1.00E+00	2.80E-01	1.00E+00	4.06E-01	1.00E+00	3.14E-01	1.00E+00	3.13E-01	1.00E+00	regulation of progression through mitotic ce	P
GO:0007368	33	7.13E-01	1.00E+00	7.73E-01	1.00E+00	3.53E-01	1.00E+00	8.46E-01	1.00E+00	8.18E-01	1.00E+00	7.67E-01	1.00E+00	7.24E-01	1.00E+00	5.18E-01	1.00E+00	determination of left/right symmetry	P
GO:0007369	55	9.86E-01	1.00E+00	9.75E-01	1.00E+00	9.19E-01	1.00E+00	3.23E-01	1.00E+00	9.60E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gastrulation	P
GO:0007379	10	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	6.18E-01	1.00E+00	5.13E-01	1.00E+00	segment specification	P
GO:0007389	214	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	pattern specification	P
GO:0007398	183	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ectoderm development	P
GO:0007399	847	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	nervous system development	P
GO:0007405	21	2.97E-01	1.00E+00	7.87E-01	1.00E+00	3.26E-01	1.00E+00	7.76E-01	1.00E+00	2.87E-01	1.00E+00	7.08E-01	1.00E+00	4.26E-01	1.00E+00	9.51E-01	1.00E+00	neuroblast proliferation	P
GO:0007409	167	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	axonogenesis	P
GO:0007411	88	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	axon guidance	P
GO:0007416	24	9.93E-01	1.00E+00	1.00E+00	1.00E+00	8.36E-01	1.00E+00	9.74E-01	1.00E+00	9.58E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synaptogenesis	P
GO:0007417	336	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	central nervous system development	P
GO:0007420	220	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	brain development	P
GO:0007422	33	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	peripheral nervous system development	P
GO:0007423	129	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	sensory organ development	P
GO:0007431	11	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.92E-01	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	salivary gland development	P
GO:0007492	12	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endoderm development	P
GO:0007498	64	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	7.71E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mesoderm development	P
GO:0007507	135	9.70E-01	1.00E+00	9.98E-01	1.00E+00	4.76E-01	1.00E+00	9.55E-01	1.00E+00	9.89E-01	1.00E+00	9.98E-01	1.00E+00	9.80E-01	1.00E+00	9.70E-01	1.00E+00	heart development	P
GO:0007512	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	adult heart development	P
GO:0007517	231	9.96E-01	1.00E+00	1.00E+00	1.00E+00	5.81E-01	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	muscle development	P
GO:0007519	143	9.61E-01	1.00E+00	1.00E+00	1.00E+00	5.97E-01	1.00E+00	9.81E-01	1.00E+00	9.04E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	striated muscle development	P
GO:0007528	25	8.30E-01	1.00E+00	6.06E-01	1.00E+00	8.75E-01	1.00E+00	2.75E-01	1.00E+00	5.64E-01	1.00E+00	4.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuromuscular junction development	P
GO:0007530	23	9.16E-01	1.00E+00	9.99E-01	1.00E+00	3.49E-01	1.00E+00	9.80E-01	1.00E+00	9.29E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	sex determination	P
GO:0007548	101	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.68E-01	1.00E+00	9.81E-01	1.00E+00	sex differentiation	P
GO:0007565	71	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.93E-01	1.00E+00	1.00E+00	1.00E+00	pregnancy	P
GO:0007566	16	9.90E-01	1.00E+00	8.53E-01	1.00E+00	4.85E-01	1.00E+00	8.46E-01	1.00E+00	1.00E+00	1.00E+00	6.36E-01	1.00E+00	9.53E-01	1.00E+00	9.97E-01	1.00E+00	embryo implantation	P
GO:0007568	44	6.08E-01	1.00E+00	5.02E-01	1.00E+00	9.98E-01	1.00E+00	5.89E-01	1.00E+00	3.10E-01	1.00E+00	3.79E-01	1.00E+00	5.81E-01	1.00E+00	8.13E-01	1.00E+00	aging	P
GO:0007569	20	3.63E-01	1.00E+00	2.11E-01	1.00E+00	7.01E-01	1.00E+00	1.77E-01	1.00E+00	2.99E-01	1.00E+00	1.94E-01	1.00E+00	4.08E-01	1.00E+00	7.55E-01	1.00E+00	cell aging	P
GO:0007582	12494	9.94E-01	1.00E+00	5.82E-01	1.00E+00	9.76E-10	0.00E+00	1.62E-09	0.00E+00	9.99E-01	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	physiological process	P
GO:0007584	65	9.03E-01	1.00E+00	6.16E-01	1.00E+00	3.21E-01	1.00E+00	8.44E-01	1.00E+00	9.30E-01	1.00E+00	4.76E-01	1.00E+00	9.24E-01	1.00E+00	6.57E-01	1.00E+00	response to nutrient	P
GO:0007585	39	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	respiratory gaseous exchange	P
GO:0007586	86	9.92E-01	1.00E+00	9.96E-01	1.00E+00	7.43E-01	1.00E+00	9.59E-01	1.00E+00	9.95E-01	1.00E+00	9.73E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	digestion	P
GO:0007588	49	9.81E-01	1.00E+00	9.86E-01	1.00E+00	2.14E-01	1.00E+00	6.77E-01	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	9.59E-01	1.00E+00	9.98E-01	1.00E+00	excretion	P
GO:0007595	20	9.55E-01	1.00E+00	1.00E+00	1.00E+00	9.61E-01	1.00E+00	7.95E-01	1.00E+00	9.11E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	lactation	P
GO:0007596	144	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	blood coagulation	P
GO:0007599	150	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hemostasis	P
GO:0007600	458	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception	P
GO:0007601	214	9.79E-01	1.00E+00	9.98E-01	1.00E+00	4.70E-01	1.00E+00	8.93E-01	1.00E+00	9.57E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	visual perception	P
GO:0007602	30	9.92E-01	1.00E+00	9.29E-01	1.00E+00	7.36E-01	1.00E+00	9.89E-01	1.00E+00	9.55E-01	1.00E+00	7.83E-01	1.00E+00	9.98E-01	1.00E+00	8.36E-01	1.00E+00	phototransduction	P
GO:0007605	143	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of sound	P
GO:0007606	88	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of chemical stimulus	P
GO:0007608	69	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of smell	P
GO:0007610	433	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	behavior	P
GO:0007611	71	9.85E-01	1.00E+00	9.74E-01	1.00E+00	5.45E-01	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	7.90E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	learning and/or memory	P
GO:0007612	39	9.42E-01	1.00E+00	9.34E-01	1.00E+00	7.33E-01	1.00E+00	9.81E-01	1.00E+00	9.31E-01	1.00E+00	7.46E-01	1.00E+00	9.77E-01	1.00E+00	9.96E-01	1.00E+00	learning	P
GO:0007613	20	9.84E-01	1.00E+00	1.00E+00	1.00E+00	4.50E-01	1.00E+00	8.48E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	memory	P
GO:0007617	13	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.00E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.43E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mating behavior	P
GO:0007623	32	9.95E-01	1.00E+00	8.51E-01	1.00E+00	9.90E-01	1.00E+00	3.51E-01	1.00E+00	8.59E-01	1.00E+00	8.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	circadian rhythm	P
GO:0007626	277	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	7.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	locomotory behavior	P
GO:0007628	17	9.90E-01	1.00E+00	1.00E+00	1.00E+00	6.79E-01	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	adult walking behavior	P
GO:0007631	46	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	feeding behavior	P
GO:0007632	21	9.12E-01	1.00E+00	9.92E-01	1.00E+00	4.01E-01	1.00E+00	8.32E-01	1.00E+00	9.76E-01	1.00E+00	9.80E-01	1.00E+00	9.07E-01	1.00E+00	9.99E-01	1.00E+00	visual behavior	P
GO:0008009	55	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.81E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	chemokine activity	F
GO:0008013	14	4.73E-04	1.60E-02	2.73E-02	1.00E+00	8.34E-05	4.57E-03	5.07E-03	6.84E-02	1.09E-02	3.01E-01	6.58E-02	1.00E+00	5.32E-02	1.00E+00	8.77E-02	1.00E+00	beta-catenin binding	F
GO:0008015	178	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	circulation	P
GO:0008016	51	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	1.00E+00	1.00E+00	regulation of heart contraction	P
GO:0008017	56	2.73E-02	1.00E+00	8.85E-03	3.84E-01	3.42E-02	5.87E-01	1.44E-02	2.81E-01	4.49E-02	1.00E+00	1.47E-02	5.65E-01	2.03E-01	1.00E+00	1.24E-01	1.00E+00	microtubule binding	F
GO:0008021	76	9.75E-01	1.00E+00	9.77E-01	1.00E+00	5.16E-01	1.00E+00	4.32E-01	1.00E+00	9.91E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	synaptic vesicle	C
GO:0008022	101	1.81E-01	1.00E+00	1.24E-01	1.00E+00	6.86E-02	1.00E+00	4.68E-02	1.00E+00	1.44E-01	1.00E+00	2.37E-01	1.00E+00	9.93E-01	1.00E+00	3.24E-01	1.00E+00	protein C-terminus binding	F
GO:0008023	12	9.57E-01	1.00E+00	4.34E-01	1.00E+00	6.14E-01	1.00E+00	2.08E-01	1.00E+00	9.53E-01	1.00E+00	8.89E-01	1.00E+00	9.79E-01	1.00E+00	1.68E-01	1.00E+00	transcription elongation factor complex	C
GO:0008026	106	3.85E-01	1.00E+00	1.78E-02	9.24E-01	1.72E-01	1.00E+00	9.70E-04	1.11E-02	6.08E-01	1.00E+00	4.46E-02	1.00E+00	4.11E-01	1.00E+00	6.76E-01	1.00E+00	ATP-dependent helicase activity	F
GO:0008028	19	9.21E-01	1.00E+00	8.73E-01	1.00E+00	5.76E-01	1.00E+00	4.99E-01	1.00E+00	9.42E-01	1.00E+00	8.55E-01	1.00E+00	9.66E-01	1.00E+00	9.60E-01	1.00E+00	monocarboxylic acid transporter activity	F
GO:0008033	60	1.82E-01	1.00E+00	3.26E-02	1.00E+00	3.95E-01	1.00E+00	5.13E-02	1.00E+00	7.48E-02	1.00E+00	2.25E-01	1.00E+00	6.90E-01	1.00E+00	2.50E-01	1.00E+00	tRNA processing	P
GO:0008034	29	9.17E-01	1.00E+00	8.12E-01	1.00E+00	2.92E-01	1.00E+00	9.90E-01	1.00E+00	9.43E-01	1.00E+00	5.90E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	lipoprotein binding	F
GO:0008037	28	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	cell recognition	P
GO:0008038	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron recognition	P
GO:0008045	10	1.00E+00	1.00E+00	9.73E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.18E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	motor axon guidance	P
GO:0008047	356	9.01E-01	1.00E+00	9.71E-01	1.00E+00	1.34E-01	1.00E+00	6.94E-01	1.00E+00	9.65E-01	1.00E+00	9.72E-01	1.00E+00	9.57E-01	1.00E+00	9.56E-01	1.00E+00	enzyme activator activity	F
GO:0008060	31	2.07E-02	1.00E+00	6.04E-01	1.00E+00	3.44E-02	5.87E-01	1.45E-01	1.00E+00	1.51E-01	1.00E+00	8.05E-01	1.00E+00	1.57E-02	2.07E-01	4.58E-01	1.00E+00	ARF GTPase activator activity	F
GO:0008064	54	4.43E-02	1.00E+00	2.30E-01	1.00E+00	4.28E-02	7.24E-01	7.32E-02	1.00E+00	2.63E-02	6.55E-01	2.77E-01	1.00E+00	8.92E-01	1.00E+00	6.25E-01	1.00E+00	regulation of actin polymerization and/or de	P
GO:0008066	53	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	glutamate receptor activity	F
GO:0008067	35	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	metabotropic glutamate, GABA-B-like recep	F

GO:0008076	155	9.98E-01	1.00E+00	9.95E-01	1.00E+00	9.75E-01	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	voltage-gated potassium channel complex	C
GO:0008080	57	7.38E-01	1.00E+00	4.46E-01	1.00E+00	1.90E-01	1.00E+00	1.82E-01	1.00E+00	8.29E-01	1.00E+00	4.08E-01	1.00E+00	8.88E-01	1.00E+00	9.57E-01	1.00E+00	N-acetyltransferase activity	F
GO:0008081	89	4.84E-01	1.00E+00	9.66E-01	1.00E+00	1.68E-01	1.00E+00	7.64E-01	1.00E+00	7.56E-01	1.00E+00	9.68E-01	1.00E+00	3.23E-01	1.00E+00	9.59E-01	1.00E+00	phosphoric diester hydrolase activity	F
GO:0008083	193	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.13E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	growth factor activity	F
GO:0008088	13	3.53E-01	1.00E+00	2.39E-01	1.00E+00	1.53E-01	1.00E+00	6.89E-02	1.00E+00	4.25E-01	1.00E+00	3.70E-01	1.00E+00	5.42E-01	1.00E+00	3.26E-01	1.00E+00	axon cargo transport	P
GO:0008092	467	2.76E-01	1.00E+00	5.72E-01	1.00E+00	1.56E-04	4.57E-03	7.08E-02	1.00E+00	5.89E-01	1.00E+00	7.03E-01	1.00E+00	9.98E-01	1.00E+00	8.74E-01	1.00E+00	cytoskeletal protein binding	F
GO:0008094	46	1.00E-02	1.77E-01	2.33E-03	5.10E-02	1.60E-02	1.92E-01	9.09E-03	1.12E-01	2.50E-02	6.55E-01	5.06E-03	7.40E-02	4.61E-02	1.00E+00	5.10E-02	8.10E-01	DNA-dependent ATPase activity	F
GO:0008104	963	2.95E-03	4.90E-02	5.14E-06	1.41E-03	2.43E-06	8.48E-04	6.92E-06	8.32E-04	1.55E-02	3.01E-01	6.55E-04	1.02E-02	9.38E-01	1.00E+00	3.08E-01	1.00E+00	protein localization	P
GO:0008105	12	9.95E-01	1.00E+00	9.61E-01	1.00E+00	4.91E-01	1.00E+00	4.29E-01	1.00E+00	9.98E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	asymmetric protein localization	P
GO:0008121	12	1.33E-01	1.00E+00	2.25E-01	1.00E+00	2.98E-01	1.00E+00	1.71E-01	1.00E+00	2.15E-01	1.00E+00	3.46E-01	1.00E+00	8.38E-02	1.00E+00	3.44E-01	1.00E+00	ubiquinol-cytochrome-c reductase activity	F
GO:0008134	462	9.83E-01	1.00E+00	4.25E-02	1.00E+00	2.14E-01	1.00E+00	1.90E-03	2.70E-02	9.85E-01	1.00E+00	9.61E-02	1.00E+00	1.00E+00	1.00E+00	7.51E-01	1.00E+00	transcription factor binding	F
GO:0008135	101	1.21E-02	2.72E-01	1.42E-03	3.90E-02	8.56E-03	1.57E-01	3.53E-03	5.60E-02	5.10E-02	1.00E+00	5.62E-03	7.40E-02	4.43E-01	1.00E+00	3.93E-02	8.10E-01	translation factor activity, nucleic acid bindir	F
GO:0008137	44	2.98E-02	1.00E+00	1.03E-02	3.84E-01	3.70E-01	1.00E+00	4.42E-02	1.00E+00	5.60E-03	1.35E-01	1.91E-02	5.65E-01	8.71E-01	1.00E+00	1.62E-01	1.00E+00	NADH dehydrogenase (ubiquinone) activity	F
GO:0008138	48	8.96E-01	1.00E+00	5.07E-01	1.00E+00	1.55E-01	1.00E+00	3.76E-01	1.00E+00	9.82E-01	1.00E+00	6.71E-01	1.00E+00	9.99E-01	1.00E+00	2.48E-01	1.00E+00	protein tyrosine/serine/threonine phosphata	F
GO:0008144	23	5.53E-01	1.00E+00	5.21E-01	1.00E+00	7.32E-01	1.00E+00	2.91E-01	1.00E+00	4.69E-01	1.00E+00	8.90E-01	1.00E+00	5.78E-01	1.00E+00	1.82E-01	1.00E+00	drug binding	F
GO:0008146	46	4.03E-01	1.00E+00	5.02E-01	1.00E+00	1.46E-01	1.00E+00	5.10E-01	1.00E+00	3.41E-01	1.00E+00	3.39E-01	1.00E+00	9.37E-01	1.00E+00	9.64E-01	1.00E+00	sulfotransferase activity	F
GO:0008150	14254	1.00E+00	1.00E+00	9.97E-01	1.00E+00	6.43E-07	8.48E-04	5.09E-06	8.32E-04	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	biological_process	P
GO:0008152	8605	5.26E-02	1.00E+00	4.39E-08	1.00E-03	4.74E-16	0.00E+00	1.89E-20	0.00E+00	5.16E-01	1.00E+00	1.32E-03	1.70E-02	9.99E-01	1.00E+00	8.71E-01	1.00E+00	metabolism	P
GO:0008154	72	1.33E-01	1.00E+00	5.15E-01	1.00E+00	9.22E-02	1.00E+00	1.39E-01	1.00E+00	8.42E-02	1.00E+00	6.11E-01	1.00E+00	9.28E-01	1.00E+00	6.83E-01	1.00E+00	actin polymerization and/or depolymerizatio	P
GO:0008156	18	6.37E-02	1.00E+00	8.96E-02	1.00E+00	1.83E-02	2.36E-01	6.02E-02	1.00E+00	1.25E-01	1.00E+00	2.47E-01	1.00E+00	1.24E-01	1.00E+00	8.81E-02	1.00E+00	negative regulation of DNA replication	P
GO:0008168	178	5.02E-04	1.60E-02	2.64E-04	8.26E-03	3.50E-04	7.18E-03	1.41E-04	7.00E-03	1.12E-02	3.01E-01	4.52E-03	7.40E-02	2.91E-01	1.00E+00	9.39E-02	1.00E+00	methyltransferase activity	F
GO:0008170	49	1.08E-01	1.00E+00	5.63E-02	1.00E+00	1.87E-02	2.36E-01	1.12E-01	1.00E+00	1.57E-01	1.00E+00	1.94E-01	1.00E+00	6.16E-01	1.00E+00	5.71E-02	1.00E+00	N-methyltransferase activity	F
GO:0008172	10	5.59E-01	1.00E+00	8.30E-01	1.00E+00	4.54E-01	1.00E+00	6.22E-01	1.00E+00	4.84E-01	1.00E+00	7.50E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	S-methyltransferase activity	F
GO:0008173	24	6.95E-02	1.00E+00	2.57E-02	1.00E+00	7.38E-02	1.00E+00	5.01E-02	1.00E+00	7.91E-02	1.00E+00	3.83E-02	1.00E+00	3.93E-01	1.00E+00	3.98E-01	1.00E+00	RNA methyltransferase activity	F
GO:0008175	11	2.20E-01	1.00E+00	5.62E-01	1.00E+00	3.50E-01	1.00E+00	5.57E-01	1.00E+00	1.75E-01	1.00E+00	5.24E-01	1.00E+00	3.14E-01	1.00E+00	5.14E-01	1.00E+00	tRNA methyltransferase activity	F
GO:0008180	10	2.21E-01	1.00E+00	2.34E-01	1.00E+00	6.62E-01	1.00E+00	4.99E-02	1.00E+00	1.90E-01	1.00E+00	5.38E-01	1.00E+00	3.20E-01	1.00E+00	7.18E-02	1.00E+00	signalosome complex	C
GO:0008186	23	5.77E-01	1.00E+00	9.95E-02	1.00E+00	2.53E-01	1.00E+00	8.11E-02	1.00E+00	9.27E-01	1.00E+00	7.95E-02	1.00E+00	1.54E-01	1.00E+00	9.09E-01	1.00E+00	RNA-dependent ATPase activity	F
GO:0008188	126	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	7.00E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuropeptide receptor activity	F
GO:0008191	10	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.90E-01	1.00E+00	4.99E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	metalloendopeptidase inhibitor activity	F
GO:0008194	103	1.00E+00	1.00E+00	9.76E-01	1.00E+00	6.57E-01	1.00E+00	8.61E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	UDP-glycosyltransferase activity	F
GO:0008199	11	8.58E-01	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.07E-01	1.00E+00	8.76E-01	1.00E+00	5.08E-01	1.00E+00	5.97E-01	1.00E+00	ferric iron binding	F
GO:0008201	86	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.69E-01	1.00E+00	heparin binding	F
GO:0008202	209	9.67E-01	1.00E+00	9.57E-01	1.00E+00	5.33E-02	1.00E+00	2.41E-01	1.00E+00	9.92E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	steroid metabolism	P
GO:0008203	87	5.09E-01	1.00E+00	3.31E-01	1.00E+00	3.88E-02	5.87E-01	1.05E-01	1.00E+00	7.52E-01	1.00E+00	5.29E-01	1.00E+00	8.67E-01	1.00E+00	7.48E-01	1.00E+00	cholesterol metabolism	P
GO:0008206	18	2.38E-01	1.00E+00	6.82E-01	1.00E+00	2.25E-02	2.63E-01	5.28E-01	1.00E+00	5.52E-01	1.00E+00	5.94E-01	1.00E+00	8.04E-01	1.00E+00	9.92E-01	1.00E+00	bile acid metabolism	P
GO:0008207	19	9.79E-01	1.00E+00	9.99E-01	1.00E+00	6.70E-01	1.00E+00	6.42E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	C21-steroid hormone metabolism	P
GO:0008209	10	9.13E-01	1.00E+00	6.85E-01	1.00E+00	3.24E-01	1.00E+00	1.19E-01	1.00E+00	9.96E-01	1.00E+00	9.39E-01	1.00E+00	9.45E-01	1.00E+00	8.56E-01	1.00E+00	androgen metabolism	P
GO:0008210	12	9.04E-01	1.00E+00	1.00E+00	1.00E+00	6.80E-01	1.00E+00	9.61E-01	1.00E+00	9.43E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	9.48E-01	1.00E+00	estrogen metabolism	P
GO:0008213	28	7.83E-02	1.00E+00	2.62E-02	1.00E+00	5.68E-02	1.00E+00	8.81E-03	1.12E-01	1.67E-01	1.00E+00	1.37E-01	1.00E+00	2.45E-01	1.00E+00	1.55E-02	1.38E-01	protein amino acid alkylation	P
GO:0008217	68	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.88E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	blood pressure regulation	P
GO:0008219	916	9.76E-01	1.00E+00	8.77E-01	1.00E+00	1.04E-02	1.57E-01	2.83E-01	1.00E+00	1.00E+00	1.00E+00	9.35E-01	1.00E+00	9.99E-01	1.00E+00	9.57E-01	1.00E+00	cell death	P
GO:0008227	157	9.77E-01	1.00E+00	9.89E-01	1.00E+00	9.45E-01	1.00E+00	6.15E-01	1.00E+00	9.33E-01	1.00E+00	9.81E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	amine receptor activity	F
GO:0008233	691	8.95E-01	1.00E+00	9.88E-01	1.00E+00	1.20E-01	1.00E+00	8.90E-02	1.00E+00	9.47E-01	1.00E+00	9.97E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	peptidase activity	F
GO:0008234	162	1.87E-01	1.00E+00	3.93E-03	6.30E-02	3.31E-03	3.50E-02	8.44E-05	3.91E-03	4.82E-01	1.00E+00	2.77E-02	1.00E+00	6.28E-01	1.00E+00	5.33E-01	1.00E+00	cysteine-type peptidase activity	F
GO:0008235	57	4.36E-01	1.00E+00	8.41E-01	1.00E+00	1.47E-01	1.00E+00	3.85E-01	1.00E+00	6.16E-01	1.00E+00	8.52E-01	1.00E+00	6.38E-01	1.00E+00	9.80E-01	1.00E+00	metalloexopeptidase activity	F
GO:0008236	238	9.45E-01	1.00E+00	1.00E+00	1.00E+00	6.36E-01	1.00E+00	7.98E-01	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	9.82E-01	1.00E+00	serine-type peptidase activity	F
GO:0008237	203	9.57E-01	1.00E+00	9.95E-01	1.00E+00	2.20E-01	1.00E+00	6.96E-01	1.00E+00	9.86E-01	1.00E+00	9.93E-01	1.00E+00	9.74E-01	1.00E+00	9.99E-01	1.00E+00	metallopeptidase activity	F
GO:0008238	106	5.47E-01	1.00E+00	7.23E-01	1.00E+00	3.14E-01	1.00E+00	4.10E-02	1.00E+00	5.76E-01	1.00E+00	8.18E-01	1.00E+00	8.52E-01	1.00E+00	9.99E-01	1.00E+00	exopeptidase activity	F
GO:0008239	12	2.66E-01	1.00E+00	4.16E-01	1.00E+00	3.01E-01	1.00E+00	4.73E-01	1.00E+00	2.97E-01	1.00E+00	3.29E-01	1.00E+00	4.93E-01	1.00E+00	5.95E-01	1.00E+00	dipeptidyl-peptidase activity	F
GO:0008270	2350	5.99E-01	1.00E+00	4.47E-07	1.00E-03	2.02E-03	1.80E-02	6.53E-07	0.00E+00	8.13E-01	1.00E+00	8.06E-05	2.29E-03	9.91E-01	1.00E+00	7.50E-02	1.00E+00	zinc ion binding	F
GO:0008271	10	1.75E-01	1.00E+00	6.85E-01	1.00E+00	1.43E-03	1.60E-02	4.20E-01	1.00E+00	4.90E-01	1.00E+00	6.58E-01	1.00E+00	5.39E-01	1.00E+00	9.96E-01	1.00E+00	sulfate porter activity	F
GO:0008272	15	1.92E-01	1.00E+00	2.27E-01	1.00E+00	9.59E-03	1.57E-01	1.15E-01	1.00E+00	3.77E-01	1.00E+00	2.50E-01	1.00E+00	7.13E-01	1.00E+00	5.48E-01	1.00E+00	sulfate transport	P
GO:0008276	44	4.26E-03	1.37E-01	2.08E-03	5.10E-02	3.19E-04	7.18E-03	1.88E-03	2.70E-02	1.56E-02	3.01E-01	1.81E-02	5.65E-01	4.61E-01	1.00E+00	1.10E-02	1.38E-01	protein methyltransferase activity	F
GO:0008277	37	6.90E-01	1.00E+00	9.97E-01	1.00E+00	9.68E-01	1.00E+00	9.42E-01	1.00E+00	5.18E-01	1.00E+00	9.98E-01	1.00E+00	6.04E-01	1.00E+00	8.85E-01	1.00E+00	regulation of G-protein coupled receptor pro	P
GO:0008283	883	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	cell proliferation	P
GO:0008284	289	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	9.82E-01	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	positive regulation of cell proliferation	P
GO:0008285	283	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of cell proliferation	P
GO:0008286	37	7.55E-01	1.00E+00	5.50E-01	1.00E+00	3.70E-01	1.00E+00	7.19E-02	1.00E+00	7.74E-01	1.00E+00	7.22E-01	1.00E+00	9.82E-01	1.00E+00	9.11E-01	1.00E+00	insulin receptor signaling pathway	P
GO:0008287	39	2.83E-01	1.00E+00	2.22E-01	1.00E+00	1.32E-01	1.00E+00	9.44E-02	1.00E+00	5.30E-01	1.00E+00	4.83E-01	1.00E+00	2.57E-01	1.00E+00	3.94E-01	1.00E+00	protein serine/threonine phosphatase comp	C
GO:0008289	337	1.13E-01	1.00E+00	2.10E-01	1.00E+00	7.00E-04	1.25E-02	2.34E-02	4.10E-01	1.72E-01	1.00E+00	1.81E-01	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	lipid binding	F
GO:0008299	16	5.33E-02	1.00E+00	7.49E-01	1.00E+00	5.50E-02	1.00E+00	1.70E-01	1.00E+00	5.17E-02	1.00E+00	9.47E-01	1.00E+00	4.83E-01	1.00E+00	5.62E-01	1.00E+00	isoprenoid biosynthesis	P
GO:0008305	30	1.43E-01	1.00E+00	8.90E-01	1.00E+00	4.40E-02	7.24E-01	3.06E-01	1.00E+00	1.99E-01	1.00E+00	9.17E-01	1.00E+00	4.00E-01	1.00E+00	1.00E+00	1.00E+00	integrin complex	C
GO:0008306	10	9.15E-01	1.00E+00	7.73E-01	1.00E+00	8.24E-01	1.00E+00	8.71E-01	1.00E+00	9.06E-01	1.00E+00	5.60E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	associative learning	P
GO:0008307	39	5.33E-01	1.00E+00	1.00E+00	1.00E+00	3.89E-01	1.00E+00	1.00E+00	1.00E+00	5.30E-01	1.00E+00	1.00E+00	1.00E+00	6.62E-01	1.00E+00	1.00E+00	1.00E+00	structural constituent of muscle	F
GO:0008312	11	9.14E-01	1.00E+00	1.76E-01	1.00E+00	8.54E-01	1.00E+00	1.94E-01	1.00E+00	8.97E-01	1.00E+00	1.97E-01	1.00E+00	9.13E-01	1.00E+00	4.07E-01	1.00E+00	7S RNA binding	F
GO:0008324	749	9.99E-01	1.00E+00	9.94E-01	1.00E+00	5.65E-01	1.00E+00	8.18E-01	1.00E+00	9.98E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cation transporter activity	F
GO:0008329	10	6.51E-01	1.00E+00	6.19E-01	1.00E+00	9.06E-01	1.00E+00	5.62E-01	1.00E+00	4.51E-01	1.00E+00	6.78E-01	1.00E+00	7.37E-01	1.00E+00	4.27E-01	1.00E+00	pattern recognition receptor activity	F
GO:0008344	38	6.97E-01	1.00E+00	7.95E-01	1.00E+00	2.47E-01	1.00E+00	6.07E-01	1.00E+00	8.26E-01	1.00E+00	7.14E-01	1.00E+00	9.20E-01	1.00E+00	9.96E-01	1.00E+00	adult locomotory behavior	P
GO:0008360	48	3.06E-01	1.00E+00	4.86E-01	1.00E+00	8.15E-02	1.00E+00	3.74E-01	1.00E+00	4.35E-01	1.00E+00	4.81E-01	1.00E+00	9.18E-01	1.00E+00	7.47E-01	1.00E+00	regulation of cell shape	P
GO:0008361	215	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.83E-01	1.00E+00	4.77E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of cell size	P
GO:0008366	36	4.50E-01	1.00E+00	8.02E-01	1.00E+00	1.02E-01	1.00E+00	3.89E-01	1.00E+00	7.14E-01	1.00E+00	7.41E-01	1.00E+00	8.47E-01	1.00E+00	9.15E-01	1.00E+00	axon ensheathment	P
GO:0008373	20	9.67E-01	1.00E+00	7.52E-01	1.00E+00	8.97E-01	1.00E+00	9.84E-01	1.00E+00	9.53E-01	1.00E+00	4.48E-01	1.00E+00	9.70E-01	1.00E+00	9.12E-01	1.00E+00	sialyltransferase activity	F
GO:0008374	40	6.26E-01	1.00E+00	5.36E-01	1.00E+00	6.89E-01	1.00E+00	2.79E-01	1.00E+00	6.97E-01	1.00E+00	5.41E-01	1.00E+00	4.87E-01	1.00E+00	9.17E-01	1.00E+00	O-acyltransferase activity	F
GO:0008375	32	9.94E-01	1.00E+00	4.63E-01	1.00E+00	5.00E-01	1.00E+00	5.34E-01	1.00E+00	9.97E-01	1.00E+00	3.64E-01	1.00E+00	9.74E-01	1.00E+00	9.98E-01	1.00E+00	acetylglucosaminyltransferase activity	F
GO:0008376	29	9.97E-01	1.00E+00	1.00E+00	1.00E+00	8.51E-01	1.00E+00	7.23E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	acetylgalactosaminyltransferase activity	F

GO:0008378	30	9.97E-01	1.00E+00	8.29E-01	1.00E+00	6.35E-01	1.00E+00	2.07E-01	1.00E+00	9.90E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	galactosyltransferase activity	F
GO:0008380	275	7.24E-05	5.00E-03	2.45E-08	1.00E-03	1.06E-05	9.71E-04	9.65E-07	0.00E+00	1.67E-02	3.81E-01	2.98E-06	2.29E-03	9.86E-02	1.00E+00	1.27E-02	1.38E-01	RNA splicing	P
GO:0008395	13	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	8.99E-01	1.00E+00	steroid hydroxylase activity	F
GO:0008406	71	9.96E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.29E-01	1.00E+00	1.00E+00	1.00E+00	gonad development	P
GO:0008408	26	4.56E-01	1.00E+00	5.77E-02	1.00E+00	1.64E-01	1.00E+00	5.87E-02	1.00E+00	4.32E-01	1.00E+00	6.97E-02	1.00E+00	9.25E-01	1.00E+00	6.40E-01	1.00E+00	3'-5' exonuclease activity	F
GO:0008415	187	1.60E-01	1.00E+00	6.73E-02	1.00E+00	3.04E-03	3.50E-02	1.14E-02	1.27E-01	6.37E-01	1.00E+00	2.32E-01	1.00E+00	9.12E-01	1.00E+00	3.48E-01	1.00E+00	acyltransferase activity	F
GO:0008417	13	3.65E-01	1.00E+00	2.11E-02	9.24E-01	2.17E-01	1.00E+00	6.26E-02	1.00E+00	5.22E-01	1.00E+00	3.96E-02	1.00E+00	6.74E-01	1.00E+00	4.82E-02	8.10E-01	fucosyltransferase activity	F
GO:0008430	29	2.31E-01	1.00E+00	5.26E-01	1.00E+00	1.71E-01	1.00E+00	2.06E-01	1.00E+00	2.73E-01	1.00E+00	7.37E-01	1.00E+00	5.01E-01	1.00E+00	2.42E-01	1.00E+00	selenium binding	F
GO:0008443	12	8.91E-01	1.00E+00	4.53E-01	1.00E+00	4.87E-01	1.00E+00	1.96E-01	1.00E+00	9.48E-01	1.00E+00	6.32E-01	1.00E+00	9.88E-01	1.00E+00	4.96E-01	1.00E+00	phosphofructokinase activity	F
GO:0008483	23	3.48E-02	1.00E+00	1.66E-01	1.00E+00	5.63E-02	1.00E+00	2.62E-02	4.10E-01	1.40E-01	1.00E+00	2.88E-01	1.00E+00	2.38E-01	1.00E+00	7.12E-01	1.00E+00	transaminase activity	F
GO:0008484	20	8.37E-01	1.00E+00	8.88E-01	1.00E+00	2.17E-01	1.00E+00	1.29E-01	1.00E+00	9.61E-01	1.00E+00	9.89E-01	1.00E+00	9.49E-01	1.00E+00	9.93E-01	1.00E+00	sulfuric ester hydrolase activity	F
GO:0008493	27	9.52E-01	1.00E+00	9.51E-01	1.00E+00	9.24E-01	1.00E+00	9.04E-01	1.00E+00	8.77E-01	1.00E+00	8.79E-01	1.00E+00	8.86E-01	1.00E+00	9.99E-01	1.00E+00	tetracycline transporter activity	F
GO:0008509	187	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.60E-01	1.00E+00	8.29E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	anion transporter activity	F
GO:0008514	10	3.36E-01	1.00E+00	1.00E+00	1.00E+00	7.59E-01	1.00E+00	5.79E-01	1.00E+00	2.51E-01	1.00E+00	9.99E-01	1.00E+00	3.34E-01	1.00E+00	1.00E+00	1.00E+00	organic anion transporter activity	F
GO:0008528	261	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.70E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity, G-protein coupled	F
GO:0008533	14	9.73E-01	1.00E+00	9.97E-01	1.00E+00	9.43E-01	1.00E+00	3.78E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	5.05E-01	1.00E+00	9.98E-01	1.00E+00	astacin activity	F
GO:0008536	10	4.45E-01	1.00E+00	1.46E-02	3.84E-01	9.90E-01	1.00E+00	2.98E-02	5.42E-01	2.15E-01	1.00E+00	6.11E-02	1.00E+00	8.16E-01	1.00E+00	2.34E-02	2.52E-01	Ran GTPase binding	F
GO:0008542	18	8.99E-01	1.00E+00	9.86E-01	1.00E+00	5.29E-01	1.00E+00	8.68E-01	1.00E+00	9.58E-01	1.00E+00	9.40E-01	1.00E+00	8.47E-01	1.00E+00	1.00E+00	1.00E+00	visual learning	P
GO:0008543	31	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.42E-01	1.00E+00	9.98E-01	1.00E+00	fibroblast growth factor receptor signaling p	P
GO:0008544	169	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	epidermis development	P
GO:0008553	10	2.33E-01	1.00E+00	3.50E-02	1.00E+00	4.35E-01	1.00E+00	1.43E-01	1.00E+00	3.77E-01	1.00E+00	5.46E-02	1.00E+00	1.19E-01	1.00E+00	2.94E-01	1.00E+00	hydrogen-exporting ATPase activity, phosph	F
GO:0008565	93	2.14E-02	1.00E+00	4.78E-06	1.41E-03	1.67E-03	1.60E-02	6.63E-06	8.32E-04	5.25E-02	1.00E+00	5.67E-05	2.29E-03	5.45E-01	1.00E+00	1.05E-01	1.00E+00	protein transporter activity	F
GO:0008584	30	9.98E-01	1.00E+00	9.82E-01	1.00E+00	9.60E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.44E-01	1.00E+00	6.17E-01	1.00E+00	9.95E-01	1.00E+00	male gonad development	P
GO:0008585	41	7.31E-01	1.00E+00	9.77E-01	1.00E+00	4.88E-01	1.00E+00	9.48E-01	1.00E+00	9.37E-01	1.00E+00	9.60E-01	1.00E+00	2.50E-01	1.00E+00	9.41E-01	1.00E+00	female gonad development	P
GO:0008589	14	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.17E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	regulation of smoothened signaling pathwa	P
GO:0008601	23	3.18E-01	1.00E+00	5.45E-01	1.00E+00	3.76E-01	1.00E+00	3.03E-01	1.00E+00	2.40E-01	1.00E+00	5.49E-01	1.00E+00	5.96E-01	1.00E+00	7.99E-01	1.00E+00	protein phosphatase type 2A regulator activ	F
GO:0008603	28	9.01E-01	1.00E+00	9.59E-01	1.00E+00	9.81E-01	1.00E+00	9.88E-01	1.00E+00	9.01E-01	1.00E+00	9.58E-01	1.00E+00	6.62E-01	1.00E+00	7.19E-01	1.00E+00	cAMP-dependent protein kinase regulator a	F
GO:0008610	315	8.61E-01	1.00E+00	5.00E-01	1.00E+00	8.90E-02	1.00E+00	7.55E-03	8.10E-02	9.21E-01	1.00E+00	8.37E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	lipid biosynthesis	P
GO:0008624	48	8.29E-01	1.00E+00	4.59E-01	1.00E+00	7.96E-01	1.00E+00	1.98E-01	1.00E+00	8.54E-01	1.00E+00	6.35E-01	1.00E+00	7.07E-01	1.00E+00	4.20E-01	1.00E+00	induction of apoptosis by extracellular signa	P
GO:0008625	17	9.08E-01	1.00E+00	5.57E-01	1.00E+00	6.78E-01	1.00E+00	1.90E-01	1.00E+00	9.82E-01	1.00E+00	7.49E-01	1.00E+00	3.72E-01	1.00E+00	3.56E-01	1.00E+00	induction of apoptosis via death domain rec	P
GO:0008629	42	3.39E-01	1.00E+00	4.37E-02	1.00E+00	4.26E-01	1.00E+00	2.11E-03	2.70E-02	4.06E-01	1.00E+00	1.44E-01	1.00E+00	2.88E-01	1.00E+00	3.99E-01	1.00E+00	induction of apoptosis by intracellular signal	P
GO:0008630	23	2.74E-01	1.00E+00	3.96E-02	1.00E+00	7.60E-01	1.00E+00	7.81E-03	8.10E-02	1.57E-01	1.00E+00	7.63E-02	1.00E+00	6.46E-01	1.00E+00	3.38E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0008632	104	1.50E-01	1.00E+00	2.52E-02	1.00E+00	3.29E-01	1.00E+00	1.77E-02	4.10E-01	1.83E-01	1.00E+00	6.54E-02	1.00E+00	3.26E-01	1.00E+00	2.22E-01	1.00E+00	apoptotic program	P
GO:0008633	21	8.77E-01	1.00E+00	2.91E-01	1.00E+00	4.88E-01	1.00E+00	3.75E-01	1.00E+00	9.46E-01	1.00E+00	4.82E-01	1.00E+00	7.85E-01	1.00E+00	1.10E-01	1.00E+00	activation of pro-apoptotic gene products	P
GO:0008637	22	5.26E-01	1.00E+00	8.76E-02	1.00E+00	4.86E-01	1.00E+00	1.59E-01	1.00E+00	5.60E-01	1.00E+00	8.90E-02	1.00E+00	4.11E-01	1.00E+00	5.26E-01	1.00E+00	apoptotic mitochondrial changes	P
GO:0008643	75	8.24E-01	1.00E+00	4.31E-01	1.00E+00	5.12E-01	1.00E+00	1.75E-01	1.00E+00	7.62E-01	1.00E+00	4.17E-01	1.00E+00	9.99E-01	1.00E+00	9.31E-01	1.00E+00	carbohydrate transport	P
GO:0008645	45	9.48E-01	1.00E+00	5.75E-01	1.00E+00	8.23E-01	1.00E+00	5.58E-01	1.00E+00	8.95E-01	1.00E+00	4.59E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	hexose transport	P
GO:0008652	91	7.76E-01	1.00E+00	6.43E-01	1.00E+00	1.66E-01	1.00E+00	3.01E-01	1.00E+00	9.47E-01	1.00E+00	4.96E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	amino acid biosynthesis	P
GO:0008654	86	7.82E-01	1.00E+00	2.61E-01	1.00E+00	4.47E-01	1.00E+00	8.20E-02	1.00E+00	7.03E-01	1.00E+00	5.39E-01	1.00E+00	9.97E-01	1.00E+00	6.09E-01	1.00E+00	phospholipid biosynthesis	P
GO:0008656	15	1.19E-01	1.00E+00	1.78E-01	1.00E+00	2.58E-01	1.00E+00	1.18E-01	1.00E+00	1.48E-01	1.00E+00	2.60E-01	1.00E+00	6.14E-02	1.00E+00	1.87E-01	1.00E+00	caspase activator activity	F
GO:0008667	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	2,3-dihydro-2,3-dihydroxybenzoate dehydro	F
GO:0008757	78	1.69E-03	4.90E-02	5.84E-04	1.90E-02	1.94E-03	1.80E-02	9.59E-04	1.11E-02	2.07E-03	4.30E-02	1.35E-02	5.65E-01	4.28E-01	1.00E+00	1.46E-02	1.38E-01	S-adenosylmethionine-dependent methyltra	F
GO:0009055	350	4.13E-01	1.00E+00	6.43E-01	1.00E+00	2.77E-01	1.00E+00	8.43E-02	1.00E+00	6.45E-01	1.00E+00	7.81E-01	1.00E+00	4.30E-01	1.00E+00	9.39E-01	1.00E+00	electron carrier activity	F
GO:0009056	784	9.47E-04	1.60E-02	4.59E-05	4.00E-03	7.19E-05	4.57E-03	8.38E-07	0.00E+00	4.70E-02	1.00E+00	1.31E-03	1.70E-02	6.76E-01	1.00E+00	3.14E-01	1.00E+00	catabolism	P
GO:0009057	462	2.29E-04	1.10E-02	5.20E-07	1.00E-03	1.21E-03	1.25E-02	9.98E-09	0.00E+00	7.61E-03	2.02E-01	7.58E-05	2.29E-03	6.29E-01	1.00E+00	4.97E-02	8.10E-01	macromolecule catabolism	P
GO:0009058	1540	2.02E-02	1.00E+00	1.27E-02	3.84E-01	2.44E-04	6.00E-03	1.01E-04	7.00E-03	8.19E-02	1.00E+00	7.38E-02	1.00E+00	8.87E-01	1.00E+00	6.73E-01	1.00E+00	biosynthesis	P
GO:0009059	894	1.77E-02	5.62E-01	3.61E-03	6.30E-02	5.98E-02	1.00E+00	1.33E-03	1.80E-02	3.40E-02	6.55E-01	1.44E-02	5.65E-01	5.38E-01	1.00E+00	3.96E-01	1.00E+00	macromolecule biosynthesis	P
GO:0009060	37	2.28E-01	1.00E+00	1.57E-01	1.00E+00	9.99E-02	1.00E+00	4.79E-01	1.00E+00	4.81E-01	1.00E+00	5.87E-02	1.00E+00	3.44E-01	1.00E+00	8.92E-01	1.00E+00	aerobic respiration	P
GO:0009063	64	1.97E-01	1.00E+00	3.08E-01	1.00E+00	1.37E-01	1.00E+00	3.63E-01	1.00E+00	2.18E-01	1.00E+00	2.96E-01	1.00E+00	5.95E-01	1.00E+00	5.20E-01	1.00E+00	amino acid catabolism	P
GO:0009064	52	3.95E-01	1.00E+00	9.36E-01	1.00E+00	1.87E-01	1.00E+00	7.39E-01	1.00E+00	5.27E-01	1.00E+00	8.75E-01	1.00E+00	6.08E-01	1.00E+00	9.98E-01	1.00E+00	glutamine family amino acid metabolism	P
GO:0009065	18	5.46E-01	1.00E+00	9.04E-01	1.00E+00	2.81E-01	1.00E+00	8.55E-01	1.00E+00	5.47E-01	1.00E+00	8.81E-01	1.00E+00	9.98E-01	1.00E+00	7.13E-01	1.00E+00	glutamine family amino acid catabolism	P
GO:0009066	26	3.64E-01	1.00E+00	7.79E-01	1.00E+00	4.65E-02	8.68E-01	2.62E-01	1.00E+00	7.10E-01	1.00E+00	8.14E-01	1.00E+00	5.49E-01	1.00E+00	9.98E-01	1.00E+00	aspartate family amino acid metabolism	P
GO:0009067	14	8.06E-02	1.00E+00	5.99E-01	1.00E+00	1.12E-02	1.57E-01	4.04E-01	1.00E+00	3.41E-01	1.00E+00	6.01E-01	1.00E+00	5.24E-01	1.00E+00	9.27E-01	1.00E+00	aspartate family amino acid biosynthesis	P
GO:0009069	24	6.14E-02	1.00E+00	7.73E-02	1.00E+00	1.48E-01	1.00E+00	9.63E-02	1.00E+00	1.56E-01	1.00E+00	8.22E-02	1.00E+00	1.38E-01	1.00E+00	2.22E-01	1.00E+00	serine family amino acid metabolism	P
GO:0009072	73	6.33E-01	1.00E+00	4.30E-01	1.00E+00	2.21E-01	1.00E+00	6.87E-01	1.00E+00	6.76E-01	1.00E+00	2.49E-01	1.00E+00	9.57E-01	1.00E+00	9.02E-01	1.00E+00	aromatic amino acid family metabolism	P
GO:0009073	45	8.62E-01	1.00E+00	2.81E-01	1.00E+00	4.92E-01	1.00E+00	4.44E-01	1.00E+00	9.05E-01	1.00E+00	1.66E-01	1.00E+00	9.27E-01	1.00E+00	9.27E-01	1.00E+00	aromatic amino acid family biosynthesis	P
GO:0009074	15	1.73E-01	1.00E+00	4.59E-01	1.00E+00	1.58E-01	1.00E+00	9.41E-01	1.00E+00	1.80E-01	1.00E+00	3.81E-01	1.00E+00	6.03E-01	1.00E+00	2.72E-01	1.00E+00	aromatic amino acid family catabolism	P
GO:0009075	12	9.58E-01	1.00E+00	9.38E-01	1.00E+00	4.65E-01	1.00E+00	3.47E-01	1.00E+00	9.11E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	histidine family amino acid metabolism	P
GO:0009081	13	2.42E-01	1.00E+00	2.56E-02	1.00E+00	1.39E-01	1.00E+00	2.90E-02	5.42E-01	3.55E-01	1.00E+00	5.75E-02	1.00E+00	7.25E-01	1.00E+00	6.00E-01	1.00E+00	branched chain family amino acid metabolis	P
GO:0009084	20	4.95E-01	1.00E+00	8.89E-01	1.00E+00	2.55E-01	1.00E+00	6.47E-01	1.00E+00	6.43E-01	1.00E+00	7.82E-01	1.00E+00	5.25E-01	1.00E+00	9.98E-01	1.00E+00	glutamine family amino acid biosynthesis	P
GO:0009100	148	3.63E-01	1.00E+00	1.11E-01	1.00E+00	3.90E-02	5.87E-01	2.71E-02	4.10E-01	5.35E-01	1.00E+00	1.50E-01	1.00E+00	8.64E-01	1.00E+00	8.57E-01	1.00E+00	glycoprotein metabolism	P
GO:0009101	122	6.40E-01	1.00E+00	1.41E-01	1.00E+00	1.07E-01	1.00E+00	4.21E-02	1.00E+00	7.78E-01	1.00E+00	1.91E-01	1.00E+00	9.01E-01	1.00E+00	8.15E-01	1.00E+00	glycoprotein biosynthesis	P
GO:0009108	86	8.07E-03	1.56E-01	1.60E-02	3.84E-01	2.26E-03	1.80E-02	6.31E-02	1.00E+00	7.41E-02	1.00E+00	5.14E-02	1.00E+00	3.59E-01	1.00E+00	9.00E-02	1.00E+00	coenzyme biosynthesis	P
GO:0009109	27	3.60E-01	1.00E+00	1.60E-01	1.00E+00	9.29E-02	1.00E+00	6.06E-01	1.00E+00	4.63E-01	1.00E+00	5.60E-02	1.00E+00	9.72E-01	1.00E+00	8.78E-01	1.00E+00	coenzyme catabolism	P
GO:0009110	26	3.79E-01	1.00E+00	4.29E-01	1.00E+00	1.33E-01	1.00E+00	2.43E-01	1.00E+00	3.82E-01	1.00E+00	4.66E-01	1.00E+00	7.96E-01	1.00E+00	8.46E-01	1.00E+00	vitamin biosynthesis	P
GO:0009112	19	1.27E-02	2.72E-01	2.77E-02	1.00E+00	3.60E-02	5.87E-01	1.33E-02	2.81E-01	1.09E-01	1.00E+00	5.23E-02	1.00E+00	1.63E-01	1.00E+00	2.82E-01	1.00E+00	nucleobase metabolism	P
GO:0009116	33	4.02E-01	1.00E+00	5.30E-02	1.00E+00	7.09E-02	1.00E+00	6.37E-03	8.10E-02	9.06E-01	1.00E+00	1.18E-01	1.00E+00	5.18E-01	1.00E+00	4.89E-01	1.00E+00	nucleoside metabolism	P
GO:0009117	202	1.59E-01	1.00E+00	1.71E-01	1.00E+00	1.14E-02	1.57E-01	3.05E-02	5.42E-01	4.14E-01	1.00E+00	2.63E-01	1.00E+00	8.24E-01	1.00E+00	8.33E-01	1.00E+00	nucleotide metabolism	P
GO:0009119	13	3.99E-01	1.00E+00	6.75E-02	1.00E+00	6.48E-02	1.00E+00	7.61E-03	8.10E-02	9.78E-01	1.00E+00	9.86E-02	1.00E+00	4.14E-01	1.00E+00	6.17E-01	1.00E+00	ribonucleoside metabolism	P
GO:0009123	24	3.57E-01	1.00E+00	8.10E-02	1.00E+00	2.92E-01	1.00E+00	2.31E-02	4.10E-01	5.37E-01	1.00E+00	1.56E-01	1.00E+00	2.23E-01	1.00E+00	3.06E-01	1.00E+00	nucleoside monophosphate metabolism	P
GO:0009124	24	3.57E-01	1.00E+00	8.10E-02	1.00E+00	2.92E-01	1.00E+00	2.31E-02	4.10E-01	5.37E-01	1.00E+00	1.56E-01	1.00E+00	2.23E-01	1.00E+00	3.06E-01	1.00E+00	nucleoside monophosphate biosynthesis	P
GO:0009126	18	5.59E-01	1.00E+00	1.33E-01	1.00E+00	5.09E-01	1.00E+00	1.35E-01	1.00E+00	6.59E-01	1.00E+00	1.19E-01	1.00E+00	2.40E-01	1.00E+00	3.89E-01	1.00E+00	purine nucleoside monophosphate metabol	P
GO:0009127	18	5.59E-01	1.00E+00	1.33E-01	1.00E+00	5.09E-01	1.00E+00	1.35E-01	1.00E+00	6.59E-01	1.00E+00	1.19E-01	1.00E+00	2.40E-01	1.00E+00	3.89E-01	1.00E+00	purine nucleoside monophosphate biosynth	P
GO:0009132	13	6.62E-01	1.00E+00	3.21E-01	1.00E+00	7.73E-01	1.00E+00	2.00E-01	1.00E+00	8.05E-01	1.00E+00	4.13E-01	1.00E+00	2.53E-01	1.00E+00	5.96E-01	1.00E+00	nucleoside diphosphate metabolism	P
GO:0009141	62	2.38E-02	1.00E+00	2.50E-01	1.00E+00	1.63E-02	1.92E-01	9.86E-02	1.00E+00	6.17E-02	1.00E+00	3.27E-01	1.00E+00	7.29E-01	1.00E+00	8.65E-01	1.00E+00	nucleoside triphosphate metabolism	P

GO:0009142	42	5.92E-02	1.00E+00	2.93E-01	1.00E+00	5.42E-02	1.00E+00	2.00E-01	1.00E+00	1.34E-01	1.00E+00	3.10E-01	1.00E+00	4.16E-01	1.00E+00	7.44E-01	1.00E+00	nucleoside triphosphate biosynthesis	P
GO:0009143	10	5.97E-02	1.00E+00	5.39E-01	1.00E+00	7.15E-02	1.00E+00	2.68E-01	1.00E+00	5.10E-02	1.00E+00	5.92E-01	1.00E+00	3.92E-01	1.00E+00	9.97E-01	1.00E+00	nucleoside triphosphate catabolism	P
GO:0009144	51	5.88E-03	1.37E-01	1.80E-01	1.00E+00	1.35E-02	1.92E-01	1.49E-01	1.00E+00	1.76E-02	3.81E-01	2.13E-01	1.00E+00	6.00E-01	1.00E+00	7.49E-01	1.00E+00	purine nucleoside triphosphate metabolism	P
GO:0009145	37	2.24E-02	1.00E+00	3.53E-01	1.00E+00	3.54E-02	5.87E-01	3.70E-01	1.00E+00	6.57E-02	1.00E+00	3.04E-01	1.00E+00	3.72E-01	1.00E+00	7.43E-01	1.00E+00	purine nucleoside triphosphate biosynthesis	P
GO:0009147	17	7.07E-01	1.00E+00	7.02E-01	1.00E+00	4.95E-01	1.00E+00	2.73E-01	1.00E+00	7.25E-01	1.00E+00	9.17E-01	1.00E+00	8.21E-01	1.00E+00	9.57E-01	1.00E+00	pyrimidine nucleoside triphosphate metabol	P
GO:0009150	70	1.46E-02	2.72E-01	1.01E-01	1.00E+00	1.71E-02	2.36E-01	9.46E-02	1.00E+00	3.70E-02	1.00E+00	1.21E-01	1.00E+00	4.98E-01	1.00E+00	7.09E-01	1.00E+00	purine ribonucleotide metabolism	P
GO:0009152	57	4.90E-02	1.00E+00	2.37E-01	1.00E+00	4.60E-02	8.68E-01	2.59E-01	1.00E+00	1.16E-01	1.00E+00	2.05E-01	1.00E+00	2.89E-01	1.00E+00	6.97E-01	1.00E+00	purine ribonucleotide biosynthesis	P
GO:0009156	23	3.36E-01	1.00E+00	6.79E-02	1.00E+00	2.34E-01	1.00E+00	1.18E-02	1.27E-01	5.25E-01	1.00E+00	1.60E-01	1.00E+00	1.77E-01	1.00E+00	2.44E-01	1.00E+00	ribonucleoside monophosphate biosynthesi	P
GO:0009161	23	3.36E-01	1.00E+00	6.79E-02	1.00E+00	2.34E-01	1.00E+00	1.18E-02	1.27E-01	5.25E-01	1.00E+00	1.60E-01	1.00E+00	1.77E-01	1.00E+00	2.44E-01	1.00E+00	ribonucleoside monophosphate metabolism	P
GO:0009165	130	3.05E-01	1.00E+00	2.71E-01	1.00E+00	8.00E-02	1.00E+00	1.34E-01	1.00E+00	5.60E-01	1.00E+00	3.02E-01	1.00E+00	5.19E-01	1.00E+00	9.25E-01	1.00E+00	nucleotide biosynthesis	P
GO:0009166	24	4.27E-01	1.00E+00	6.27E-01	1.00E+00	2.42E-01	1.00E+00	4.76E-01	1.00E+00	5.54E-01	1.00E+00	5.64E-01	1.00E+00	7.77E-01	1.00E+00	8.11E-01	1.00E+00	nucleotide catabolism	P
GO:0009167	18	5.59E-01	1.00E+00	1.33E-01	1.00E+00	5.09E-01	1.00E+00	1.35E-01	1.00E+00	6.59E-01	1.00E+00	1.19E-01	1.00E+00	2.40E-01	1.00E+00	3.89E-01	1.00E+00	purine ribonucleoside monophosphate meta	P
GO:0009168	18	5.59E-01	1.00E+00	1.33E-01	1.00E+00	5.09E-01	1.00E+00	1.35E-01	1.00E+00	6.59E-01	1.00E+00	1.19E-01	1.00E+00	2.40E-01	1.00E+00	3.89E-01	1.00E+00	purine ribonucleoside monophosphate biosy	P
GO:0009187	44	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.42E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cyclic nucleotide metabolism	P
GO:0009190	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.47E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cyclic nucleotide biosynthesis	P
GO:0009199	50	6.38E-03	1.37E-01	1.90E-01	1.00E+00	1.41E-02	1.92E-01	1.28E-01	1.00E+00	2.05E-02	3.81E-01	2.40E-01	1.00E+00	5.98E-01	1.00E+00	7.71E-01	1.00E+00	ribonucleoside triphosphate metabolism	P
GO:0009201	38	2.38E-02	1.00E+00	3.43E-01	1.00E+00	3.51E-02	5.87E-01	3.07E-01	1.00E+00	7.38E-02	1.00E+00	3.06E-01	1.00E+00	3.73E-01	1.00E+00	7.77E-01	1.00E+00	ribonucleoside triphosphate biosynthesis	P
GO:0009205	49	5.96E-03	1.37E-01	1.96E-01	1.00E+00	1.43E-02	1.92E-01	1.54E-01	1.00E+00	1.77E-02	3.81E-01	2.38E-01	1.00E+00	5.98E-01	1.00E+00	7.39E-01	1.00E+00	purine ribonucleoside triphosphate metabol	P
GO:0009206	37	2.24E-02	1.00E+00	3.53E-01	1.00E+00	3.54E-02	5.87E-01	3.70E-01	1.00E+00	6.57E-02	1.00E+00	3.04E-01	1.00E+00	3.72E-01	1.00E+00	7.43E-01	1.00E+00	purine ribonucleoside triphosphate biosynth	P
GO:0009208	11	3.10E-01	1.00E+00	7.53E-01	1.00E+00	3.54E-01	1.00E+00	3.31E-01	1.00E+00	2.73E-01	1.00E+00	9.12E-01	1.00E+00	6.29E-01	1.00E+00	9.66E-01	1.00E+00	pyrimidine ribonucleoside triphosphate meta	P
GO:0009209	11	3.10E-01	1.00E+00	7.53E-01	1.00E+00	3.54E-01	1.00E+00	3.31E-01	1.00E+00	2.73E-01	1.00E+00	9.12E-01	1.00E+00	6.29E-01	1.00E+00	9.66E-01	1.00E+00	pyrimidine ribonucleoside triphosphate bios	P
GO:0009218	16	1.53E-01	1.00E+00	4.51E-01	1.00E+00	1.29E-01	1.00E+00	1.04E-01	1.00E+00	2.06E-01	1.00E+00	6.81E-01	1.00E+00	3.69E-01	1.00E+00	7.08E-01	1.00E+00	pyrimidine ribonucleotide metabolism	P
GO:0009220	15	1.32E-01	1.00E+00	4.31E-01	1.00E+00	9.92E-02	1.00E+00	9.96E-02	1.00E+00	1.85E-01	1.00E+00	6.43E-01	1.00E+00	3.83E-01	1.00E+00	7.78E-01	1.00E+00	pyrimidine ribonucleotide biosynthesis	P
GO:0009225	15	1.72E-01	1.00E+00	1.05E-01	1.00E+00	1.75E-01	1.00E+00	4.90E-02	1.00E+00	1.72E-01	1.00E+00	2.39E-01	1.00E+00	2.96E-01	1.00E+00	3.78E-01	1.00E+00	nucleotide-sugar metabolism	P
GO:0009237	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	siderophore metabolism	P
GO:0009238	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	enterobactin metabolism	P
GO:0009239	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	enterobactin biosynthesis	P
GO:0009247	14	8.79E-01	1.00E+00	2.24E-01	1.00E+00	3.52E-01	1.00E+00	1.54E-01	1.00E+00	8.77E-01	1.00E+00	1.38E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	glycolipid biosynthesis	P
GO:0009250	30	6.64E-01	1.00E+00	1.00E+00	1.00E+00	1.89E-01	1.00E+00	9.64E-01	1.00E+00	8.40E-01	1.00E+00	9.98E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	glucan biosynthesis	P
GO:0009259	79	6.71E-03	1.37E-01	3.47E-02	1.00E+00	1.17E-02	1.57E-01	1.86E-02	4.10E-01	2.30E-02	4.78E-01	8.36E-02	1.00E+00	4.11E-01	1.00E+00	5.02E-01	1.00E+00	ribonucleotide metabolism	P
GO:0009260	64	2.82E-02	1.00E+00	1.03E-01	1.00E+00	2.62E-02	4.97E-01	5.16E-02	1.00E+00	9.74E-02	1.00E+00	1.48E-01	1.00E+00	2.24E-01	1.00E+00	5.42E-01	1.00E+00	ribonucleotide biosynthesis	P
GO:0009261	10	6.85E-02	1.00E+00	1.95E-01	1.00E+00	7.98E-02	1.00E+00	1.10E-01	1.00E+00	5.72E-02	1.00E+00	3.10E-01	1.00E+00	4.49E-01	1.00E+00	7.77E-01	1.00E+00	ribonucleotide catabolism	P
GO:0009262	16	9.21E-01	1.00E+00	5.03E-01	1.00E+00	5.47E-01	1.00E+00	4.16E-01	1.00E+00	9.96E-01	1.00E+00	5.39E-01	1.00E+00	3.81E-01	1.00E+00	5.71E-01	1.00E+00	deoxyribonucleotide metabolism	P
GO:0009266	229	9.97E-01	1.00E+00	9.95E-01	1.00E+00	2.70E-01	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.82E-01	1.00E+00	9.99E-01	1.00E+00	response to temperature stimulus	P
GO:0009267	10	2.19E-01	1.00E+00	9.72E-01	1.00E+00	4.11E-01	1.00E+00	9.26E-01	1.00E+00	2.41E-01	1.00E+00	9.83E-01	1.00E+00	2.83E-01	1.00E+00	2.63E-01	1.00E+00	cellular response to starvation	P
GO:0009288	39	8.84E-01	1.00E+00	9.87E-01	1.00E+00	7.12E-01	1.00E+00	9.11E-01	1.00E+00	7.24E-01	1.00E+00	9.72E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	flagellum (sensu Bacteria)	C
GO:0009296	14	4.77E-01	1.00E+00	2.93E-01	1.00E+00	3.84E-01	1.00E+00	3.31E-01	1.00E+00	5.41E-01	1.00E+00	1.95E-01	1.00E+00	4.50E-01	1.00E+00	7.44E-01	1.00E+00	flagellum biogenesis	P
GO:0009303	14	1.28E-01	1.00E+00	1.86E-01	1.00E+00	1.98E-01	1.00E+00	4.96E-01	1.00E+00	1.50E-01	1.00E+00	1.49E-01	1.00E+00	8.24E-01	1.00E+00	9.11E-01	1.00E+00	rRNA transcription	P
GO:0009306	70	8.09E-01	1.00E+00	9.48E-01	1.00E+00	9.40E-01	1.00E+00	9.05E-01	1.00E+00	5.01E-01	1.00E+00	9.51E-01	1.00E+00	9.96E-01	1.00E+00	9.10E-01	1.00E+00	protein secretion	P
GO:0009308	558	3.75E-01	1.00E+00	6.32E-01	1.00E+00	5.78E-03	9.30E-02	4.43E-01	1.00E+00	5.73E-01	1.00E+00	4.74E-01	1.00E+00	9.78E-01	1.00E+00	9.80E-01	1.00E+00	amine metabolism	P
GO:0009309	123	8.43E-01	1.00E+00	7.34E-01	1.00E+00	2.19E-01	1.00E+00	5.70E-01	1.00E+00	9.70E-01	1.00E+00	4.68E-01	1.00E+00	8.52E-01	1.00E+00	1.00E+00	1.00E+00	amine biosynthesis	P
GO:0009310	72	1.58E-01	1.00E+00	3.92E-01	1.00E+00	6.93E-02	1.00E+00	3.27E-01	1.00E+00	1.93E-01	1.00E+00	3.95E-01	1.00E+00	6.93E-01	1.00E+00	6.10E-01	1.00E+00	amine catabolism	P
GO:0009311	19	3.63E-01	1.00E+00	9.50E-01	1.00E+00	9.81E-01	1.00E+00	7.30E-01	1.00E+00	3.23E-01	1.00E+00	9.75E-01	1.00E+00	2.50E-01	1.00E+00	8.06E-01	1.00E+00	oligosaccharide metabolism	P
GO:0009314	135	9.48E-01	1.00E+00	6.61E-01	1.00E+00	6.41E-01	1.00E+00	1.86E-01	1.00E+00	8.73E-01	1.00E+00	8.04E-01	1.00E+00	1.00E+00	1.00E+00	7.32E-01	1.00E+00	response to radiation	P
GO:0009331	13	7.91E-01	1.00E+00	5.71E-01	1.00E+00	4.04E-01	1.00E+00	2.55E-01	1.00E+00	8.93E-01	1.00E+00	7.97E-01	1.00E+00	7.86E-01	1.00E+00	7.70E-01	1.00E+00	glycerol-3-phosphate dehydrogenase comp	C
GO:0009395	15	8.92E-01	1.00E+00	6.99E-01	1.00E+00	2.75E-01	1.00E+00	5.01E-01	1.00E+00	9.69E-01	1.00E+00	6.80E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	phospholipid catabolism	P
GO:0009396	12	9.35E-01	1.00E+00	1.92E-01	1.00E+00	8.41E-01	1.00E+00	5.46E-01	1.00E+00	9.92E-01	1.00E+00	1.00E-01	1.00E+00	9.48E-01	1.00E+00	4.61E-01	1.00E+00	folic acid and derivative biosynthesis	P
GO:0009405	35	3.82E-01	1.00E+00	9.20E-01	1.00E+00	2.77E-01	1.00E+00	8.33E-01	1.00E+00	4.05E-01	1.00E+00	9.83E-01	1.00E+00	4.18E-01	1.00E+00	1.54E-01	1.00E+00	pathogenesis	P
GO:0009408	17	4.13E-01	1.00E+00	7.46E-01	1.00E+00	1.48E-01	1.00E+00	7.00E-01	1.00E+00	7.23E-01	1.00E+00	8.57E-01	1.00E+00	6.33E-01	1.00E+00	2.66E-01	1.00E+00	response to heat	P
GO:0009409	204	9.98E-01	1.00E+00	9.98E-01	1.00E+00	4.19E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	response to cold	P
GO:0009410	34	9.52E-01	1.00E+00	9.41E-01	1.00E+00	5.66E-01	1.00E+00	8.59E-01	1.00E+00	9.96E-01	1.00E+00	8.36E-01	1.00E+00	5.18E-01	1.00E+00	1.00E+00	1.00E+00	response to xenobiotic stimulus	P
GO:0009411	48	4.10E-01	1.00E+00	1.01E-01	1.00E+00	7.11E-01	1.00E+00	2.47E-02	4.10E-01	2.52E-01	1.00E+00	3.36E-01	1.00E+00	7.08E-01	1.00E+00	1.86E-01	1.00E+00	response to UV	P
GO:0009416	106	8.60E-01	1.00E+00	5.13E-01	1.00E+00	6.41E-01	1.00E+00	2.18E-01	1.00E+00	6.84E-01	1.00E+00	6.66E-01	1.00E+00	9.93E-01	1.00E+00	5.39E-01	1.00E+00	response to light stimulus	P
GO:0009434	15	9.96E-01	1.00E+00	6.48E-01	1.00E+00	1.00E+00	1.00E+00	4.82E-01	1.00E+00	9.61E-01	1.00E+00	6.37E-01	1.00E+00	1.00E+00	1.00E+00	9.11E-01	1.00E+00	flagellum (sensu Eukaryota)	C
GO:0009451	36	1.18E-02	2.72E-01	1.19E-02	3.84E-01	3.69E-02	5.87E-01	4.68E-02	1.00E+00	2.29E-02	4.78E-01	9.38E-02	1.00E+00	4.55E-01	1.00E+00	1.02E-01	1.00E+00	RNA modification	P
GO:0009566	74	5.44E-01	1.00E+00	4.86E-01	1.00E+00	4.14E-01	1.00E+00	6.45E-01	1.00E+00	6.87E-01	1.00E+00	3.51E-01	1.00E+00	2.40E-01	1.00E+00	9.24E-01	1.00E+00	fertilization	P
GO:0009581	60	1.00E+00	1.00E+00	9.45E-01	1.00E+00	9.56E-01	1.00E+00	7.75E-01	1.00E+00	9.93E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	detection of external stimulus	P
GO:0009582	53	1.00E+00	1.00E+00	9.50E-01	1.00E+00	8.89E-01	1.00E+00	6.81E-01	1.00E+00	9.95E-01	1.00E+00	9.18E-01	1.00E+00	1.00E+00	1.00E+00	8.89E-01	1.00E+00	detection of abiotic stimulus	P
GO:0009583	33	9.81E-01	1.00E+00	9.20E-01	1.00E+00	6.16E-01	1.00E+00	9.74E-01	1.00E+00	9.33E-01	1.00E+00	8.07E-01	1.00E+00	9.98E-01	1.00E+00	7.47E-01	1.00E+00	detection of light stimulus	P
GO:0009593	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	detection of chemical stimulus	P
GO:0009595	15	8.04E-01	1.00E+00	5.51E-01	1.00E+00	8.55E-01	1.00E+00	3.05E-01	1.00E+00	5.88E-01	1.00E+00	6.49E-01	1.00E+00	8.63E-01	1.00E+00	5.00E-01	1.00E+00	detection of biotic stimulus	P
GO:0009605	851	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to external stimulus	P
GO:0009607	323	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.89E-01	1.00E+00	9.54E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to biotic stimulus	P
GO:0009611	566	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to wounding	P
GO:0009612	32	9.99E-01	1.00E+00	8.80E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.04E-01	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	response to mechanical stimulus	P
GO:0009615	106	7.39E-01	1.00E+00	9.53E-01	1.00E+00	9.30E-01	1.00E+00	4.76E-01	1.00E+00	4.80E-01	1.00E+00	9.51E-01	1.00E+00	9.72E-01	1.00E+00	9.91E-01	1.00E+00	response to virus	P
GO:0009617	122	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	response to bacterium	P
GO:0009620	23	7.49E-01	1.00E+00	9.61E-01	1.00E+00	2.80E-01	1.00E+00	9.96E-01	1.00E+00	9.09E-01	1.00E+00	8.91E-01	1.00E+00	4.95E-01	1.00E+00	8.14E-01	1.00E+00	response to fungus	P
GO:0009628	422	1.00E+00	1.00E+00	9.96E-01	1.00E+00	4.08E-01	1.00E+00	8.66E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	response to abiotic stimulus	P
GO:0009636	27	7.82E-01	1.00E+00	4.21E-01	1.00E+00	8.63E-01	1.00E+00	2.77E-01	1.00E+00	5.39E-01	1.00E+00	4.36E-01	1.00E+00	7.92E-01	1.00E+00	8.30E-01	1.00E+00	response to toxin	P
GO:0009650	10	4.38E-01	1.00E+00	2.29E-01	1.00E+00	6.49E-01	1.00E+00	8.44E-01	1.00E+00	4.69E-01	1.00E+00	1.43E-01	1.00E+00	3.07E-01	1.00E+00	7.86E-01	1.00E+00	UV protection	P
GO:0009653	1354	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	morphogenesis	P
GO:0009698	45	8.62E-01	1.00E+00	2.81E-01	1.00E+00	4.92E-01	1.00E+00	4.44E-01	1.00E+00	9.05E-01	1.00E+00	1.66E-01	1.00E+00	9.27E-01	1.00E+00	9.27E-01	1.00E+00	phenylpropanoid metabolism	P
GO:0009712	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	catechol metabolism	P
GO:0009719	502	1.28E-01	1.00E+00	1.70E-03	3.90E-02	5.91E-04	1.25E-02	1.50E-04	7.00E-03	2.60E-01	1.00E+00	1.87E-02	5.65E-01	9.99E-01	1.00E+00	2.95E-01	1.00E+00	response to endogenous stimulus	P

GO:0009725	124	9.66E-01	1.00E+00	9.81E-01	1.00E+00	3.48E-01	1.00E+00	2.85E-01	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	9.51E-01	1.00E+00	9.93E-01	1.00E+00	response to hormone stimulus	P
GO:0009743	26	6.41E-01	1.00E+00	9.41E-01	1.00E+00	1.29E-01	1.00E+00	6.22E-01	1.00E+00	8.37E-01	1.00E+00	9.85E-01	1.00E+00	9.19E-01	1.00E+00	7.75E-01	1.00E+00	response to carbohydrate stimulus	P
GO:0009746	19	5.04E-01	1.00E+00	8.26E-01	1.00E+00	1.21E-01	1.00E+00	5.30E-01	1.00E+00	7.66E-01	1.00E+00	9.02E-01	1.00E+00	8.02E-01	1.00E+00	7.83E-01	1.00E+00	response to hexose stimulus	P
GO:0009749	19	5.04E-01	1.00E+00	8.26E-01	1.00E+00	1.21E-01	1.00E+00	5.30E-01	1.00E+00	7.66E-01	1.00E+00	9.02E-01	1.00E+00	8.02E-01	1.00E+00	7.83E-01	1.00E+00	response to glucose stimulus	P
GO:0009755	37	5.91E-01	1.00E+00	7.95E-01	1.00E+00	2.92E-01	1.00E+00	3.25E-01	1.00E+00	7.64E-01	1.00E+00	8.45E-01	1.00E+00	6.31E-01	1.00E+00	9.73E-01	1.00E+00	hormone-mediated signaling	P
GO:0009790	438	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	embryonic development	P
GO:0009791	69	8.61E-01	1.00E+00	8.56E-01	1.00E+00	5.16E-01	1.00E+00	7.09E-01	1.00E+00	9.75E-01	1.00E+00	8.99E-01	1.00E+00	5.16E-01	1.00E+00	7.23E-01	1.00E+00	post-embryonic development	P
GO:0009792	242	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.09E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.54E-01	1.00E+00	embryonic development (sensu Metazoa)	P
GO:0009798	20	9.26E-01	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	9.84E-01	1.00E+00	7.93E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.81E-01	1.00E+00	axis specification	P
GO:0009799	34	7.60E-01	1.00E+00	8.09E-01	1.00E+00	3.95E-01	1.00E+00	8.81E-01	1.00E+00	8.51E-01	1.00E+00	8.00E-01	1.00E+00	7.57E-01	1.00E+00	5.34E-01	1.00E+00	determination of symmetry	P
GO:0009855	34	7.60E-01	1.00E+00	8.09E-01	1.00E+00	3.95E-01	1.00E+00	8.81E-01	1.00E+00	8.51E-01	1.00E+00	8.00E-01	1.00E+00	7.57E-01	1.00E+00	5.34E-01	1.00E+00	determination of bilateral symmetry	P
GO:0009880	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.86E-01	1.00E+00	embryonic pattern specification	P
GO:0009881	15	7.32E-01	1.00E+00	1.00E+00	1.00E+00	2.95E-01	1.00E+00	6.99E-01	1.00E+00	6.12E-01	1.00E+00	1.00E+00	1.00E+00	9.12E-01	1.00E+00	1.00E+00	1.00E+00	photoreceptor activity	F
GO:0009887	700	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organ morphogenesis	P
GO:0009888	430	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tissue development	P
GO:0009889	236	4.32E-01	1.00E+00	2.69E-01	1.00E+00	6.09E-02	1.00E+00	7.90E-02	1.00E+00	5.08E-01	1.00E+00	2.60E-01	1.00E+00	9.94E-01	1.00E+00	9.40E-01	1.00E+00	regulation of biosynthesis	P
GO:0009890	55	3.98E-01	1.00E+00	3.76E-01	1.00E+00	4.01E-01	1.00E+00	1.35E-01	1.00E+00	4.13E-01	1.00E+00	6.27E-01	1.00E+00	5.00E-01	1.00E+00	2.90E-01	1.00E+00	negative regulation of biosynthesis	P
GO:0009891	96	7.83E-01	1.00E+00	8.81E-01	1.00E+00	2.09E-01	1.00E+00	5.69E-01	1.00E+00	6.86E-01	1.00E+00	7.75E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	positive regulation of biosynthesis	P
GO:0009892	510	7.41E-01	1.00E+00	4.47E-01	1.00E+00	1.25E-01	1.00E+00	1.70E-02	4.10E-01	6.26E-01	1.00E+00	7.06E-01	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	negative regulation of metabolism	P
GO:0009893	551	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	9.62E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of metabolism	P
GO:0009894	39	7.38E-01	1.00E+00	8.20E-01	1.00E+00	4.75E-01	1.00E+00	4.55E-01	1.00E+00	5.44E-01	1.00E+00	8.81E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	regulation of catabolism	P
GO:0009895	12	9.61E-01	1.00E+00	9.26E-01	1.00E+00	2.70E-01	1.00E+00	7.18E-01	1.00E+00	9.91E-01	1.00E+00	9.32E-01	1.00E+00	9.77E-01	1.00E+00	9.97E-01	1.00E+00	negative regulation of catabolism	P
GO:0009897	97	9.80E-01	1.00E+00	1.00E+00	1.00E+00	5.69E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.34E-01	1.00E+00	external side of plasma membrane	C
GO:0009898	11	5.54E-01	1.00E+00	5.57E-01	1.00E+00	5.40E-01	1.00E+00	4.53E-01	1.00E+00	6.15E-01	1.00E+00	5.23E-01	1.00E+00	5.22E-01	1.00E+00	8.38E-01	1.00E+00	internal side of plasma membrane	C
GO:0009913	67	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.96E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	epidermal cell differentiation	P
GO:0009925	25	7.88E-01	1.00E+00	9.56E-01	1.00E+00	7.19E-01	1.00E+00	1.00E+00	1.00E+00	7.57E-01	1.00E+00	8.74E-01	1.00E+00	6.72E-01	1.00E+00	7.44E-01	1.00E+00	basal plasma membrane	C
GO:0009948	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.96E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	anterior/posterior axis specification	P
GO:0009952	117	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	anterior/posterior pattern formation	P
GO:0009953	45	8.83E-01	1.00E+00	1.00E+00	1.00E+00	5.91E-01	1.00E+00	9.50E-01	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	7.98E-01	1.00E+00	9.78E-01	1.00E+00	dorsal/ventral pattern formation	P
GO:0009954	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	proximal/distal pattern formation	P
GO:0009966	540	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	8.05E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of signal transduction	P
GO:0009967	189	9.94E-01	1.00E+00	9.43E-01	1.00E+00	3.81E-01	1.00E+00	5.33E-01	1.00E+00	9.98E-01	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	positive regulation of signal transduction	P
GO:0009968	128	9.91E-01	1.00E+00	9.83E-01	1.00E+00	9.94E-01	1.00E+00	9.43E-01	1.00E+00	9.40E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	negative regulation of signal transduction	P
GO:0009975	23	9.73E-01	1.00E+00	9.22E-01	1.00E+00	6.51E-01	1.00E+00	3.93E-01	1.00E+00	9.75E-01	1.00E+00	9.92E-01	1.00E+00	9.59E-01	1.00E+00	9.38E-01	1.00E+00	cyclase activity	F
GO:0009982	39	8.22E-01	1.00E+00	8.45E-01	1.00E+00	3.55E-01	1.00E+00	7.92E-01	1.00E+00	8.95E-01	1.00E+00	9.15E-01	1.00E+00	8.56E-01	1.00E+00	3.31E-01	1.00E+00	pseudouridine synthase activity	F
GO:0009986	232	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.32E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cell surface	C
GO:0009987	12845	9.99E-01	1.00E+00	7.61E-01	1.00E+00	3.53E-09	0.00E+00	1.68E-08	0.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cellular process	P
GO:0009991	97	8.57E-01	1.00E+00	8.33E-01	1.00E+00	2.12E-01	1.00E+00	8.58E-01	1.00E+00	9.15E-01	1.00E+00	7.74E-01	1.00E+00	9.24E-01	1.00E+00	6.64E-01	1.00E+00	response to extracellular stimulus	P
GO:0009994	14	2.62E-01	1.00E+00	9.31E-01	1.00E+00	7.00E-01	1.00E+00	7.10E-01	1.00E+00	2.26E-01	1.00E+00	9.77E-01	1.00E+00	7.11E-01	1.00E+00	6.20E-01	1.00E+00	oocyte differentiation	P
GO:0010001	38	9.92E-01	1.00E+00	1.00E+00	1.00E+00	7.92E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.84E-01	1.00E+00	9.93E-01	1.00E+00	glial cell differentiation	P
GO:0010008	114	2.53E-02	1.00E+00	8.01E-03	3.40E-01	2.58E-02	4.97E-01	1.41E-04	7.00E-03	2.90E-02	6.55E-01	3.24E-02	1.00E+00	7.73E-01	1.00E+00	3.54E-01	1.00E+00	endosome membrane	C
GO:0010033	80	9.24E-01	1.00E+00	9.57E-01	1.00E+00	8.66E-02	1.00E+00	9.75E-01	1.00E+00	9.73E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	response to organic substance	P
GO:0010035	58	8.84E-01	1.00E+00	8.02E-01	1.00E+00	2.36E-01	1.00E+00	4.28E-01	1.00E+00	9.98E-01	1.00E+00	8.28E-01	1.00E+00	4.33E-01	1.00E+00	9.76E-01	1.00E+00	response to inorganic substance	P
GO:0010038	51	9.67E-01	1.00E+00	9.42E-01	1.00E+00	2.44E-01	1.00E+00	4.23E-01	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	6.93E-01	1.00E+00	9.99E-01	1.00E+00	response to metal ion	P
GO:0010092	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	specification of organ identity	P
GO:0010165	11	2.15E-01	1.00E+00	2.49E-01	1.00E+00	5.22E-01	1.00E+00	2.18E-01	1.00E+00	1.97E-01	1.00E+00	2.17E-01	1.00E+00	1.70E-01	1.00E+00	7.69E-01	1.00E+00	response to X-ray	P
GO:0010181	13	4.52E-01	1.00E+00	8.25E-01	1.00E+00	9.19E-02	1.00E+00	3.33E-01	1.00E+00	5.81E-01	1.00E+00	8.83E-01	1.00E+00	8.33E-01	1.00E+00	8.91E-01	1.00E+00	FMN binding	F
GO:0010212	12	5.83E-01	1.00E+00	3.45E-01	1.00E+00	2.98E-01	1.00E+00	7.77E-02	1.00E+00	6.37E-01	1.00E+00	6.39E-01	1.00E+00	8.19E-01	1.00E+00	6.12E-01	1.00E+00	response to ionizing radiation	P
GO:0012501	867	9.69E-01	1.00E+00	8.72E-01	1.00E+00	1.22E-02	1.92E-01	2.63E-01	1.00E+00	9.99E-01	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	programmed cell death	P
GO:0012502	244	6.02E-01	1.00E+00	8.64E-02	1.00E+00	2.67E-02	4.97E-01	1.47E-02	2.81E-01	9.30E-01	1.00E+00	2.33E-01	1.00E+00	7.21E-01	1.00E+00	8.18E-01	1.00E+00	induction of programmed cell death	P
GO:0012505	1119	2.74E-01	1.00E+00	8.92E-03	3.84E-01	3.23E-07	0.00E+00	8.90E-06	9.66E-04	5.20E-01	1.00E+00	8.81E-02	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	endomembrane system	C
GO:0012506	126	2.32E-01	1.00E+00	2.29E-01	1.00E+00	1.33E-02	1.92E-01	7.95E-02	1.00E+00	1.86E-01	1.00E+00	3.00E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	vesicle membrane	C
GO:0012510	13	7.45E-02	1.00E+00	4.37E-01	1.00E+00	2.74E-03	1.80E-02	2.29E-01	1.00E+00	1.09E-01	1.00E+00	6.12E-01	1.00E+00	9.45E-01	1.00E+00	7.34E-01	1.00E+00	trans-Golgi network transport vesicle membr	C
GO:0014003	10	5.74E-01	1.00E+00	7.52E-01	1.00E+00	1.59E-01	1.00E+00	3.70E-01	1.00E+00	9.26E-01	1.00E+00	8.90E-01	1.00E+00	6.04E-01	1.00E+00	5.93E-01	1.00E+00	oligodendrocyte development	P
GO:0014013	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	regulation of gliogenesis	P
GO:0014020	29	8.69E-01	1.00E+00	6.95E-01	1.00E+00	6.43E-01	1.00E+00	4.78E-01	1.00E+00	8.10E-01	1.00E+00	7.75E-01	1.00E+00	9.50E-01	1.00E+00	6.63E-01	1.00E+00	primary neural tube formation	P
GO:0014031	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	1.00E+00	1.00E+00	mesenchymal cell development	P
GO:0014032	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	1.00E+00	1.00E+00	neural crest cell development	P
GO:0014033	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	1.00E+00	1.00E+00	neural crest cell differentiation	P
GO:0014065	10	6.37E-01	1.00E+00	7.94E-01	1.00E+00	6.20E-01	1.00E+00	8.99E-01	1.00E+00	6.40E-01	1.00E+00	6.04E-01	1.00E+00	5.57E-01	1.00E+00	9.84E-01	1.00E+00	phosphoinositide 3-kinase cascade	P
GO:0014069	22	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	postsynaptic density	C
GO:0015002	28	2.35E-01	1.00E+00	1.49E-01	1.00E+00	9.00E-01	1.00E+00	4.42E-01	1.00E+00	1.43E-01	1.00E+00	1.48E-01	1.00E+00	9.27E-01	1.00E+00	3.06E-01	1.00E+00	heme-copper terminal oxidase activity	F
GO:0015012	10	1.00E+00	1.00E+00	7.95E-01	1.00E+00	6.67E-01	1.00E+00	9.17E-01	1.00E+00	9.92E-01	1.00E+00	3.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	heparan sulfate proteoglycan biosynthesis	P
GO:0015020	22	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	7.55E-01	1.00E+00	glucuronosyltransferase activity	F
GO:0015026	16	6.21E-01	1.00E+00	5.31E-01	1.00E+00	2.68E-01	1.00E+00	7.85E-01	1.00E+00	8.69E-01	1.00E+00	4.18E-01	1.00E+00	8.69E-01	1.00E+00	6.31E-01	1.00E+00	coreceptor activity	F
GO:0015031	827	1.01E-04	5.00E-03	1.14E-07	1.00E-03	3.81E-08	0.00E+00	2.50E-06	0.00E+00	1.61E-03	4.30E-02	5.66E-05	2.29E-03	8.29E-01	1.00E+00	1.17E-01	1.00E+00	protein transport	P
GO:0015035	14	9.85E-01	1.00E+00	4.88E-01	1.00E+00	9.94E-01	1.00E+00	1.64E-01	1.00E+00	8.66E-01	1.00E+00	6.05E-01	1.00E+00	9.73E-01	1.00E+00	9.39E-01	1.00E+00	protein disulfide oxidoreductase activity	F
GO:0015036	18	8.35E-01	1.00E+00	1.40E-01	1.00E+00	6.26E-01	1.00E+00	5.52E-02	1.00E+00	7.58E-01	1.00E+00	3.60E-01	1.00E+00	9.25E-01	1.00E+00	4.18E-01	1.00E+00	disulfide oxidoreductase activity	F
GO:0015057	38	9.44E-01	1.00E+00	9.93E-01	1.00E+00	8.90E-01	1.00E+00	8.38E-01	1.00E+00	8.92E-01	1.00E+00	9.87E-01	1.00E+00	8.82E-01	1.00E+00	1.00E+00	1.00E+00	thrombin receptor activity	F
GO:0015074	15	8.56E-01	1.00E+00	3.05E-01	1.00E+00	6.95E-01	1.00E+00	6.30E-01	1.00E+00	9.17E-01	1.00E+00	4.65E-01	1.00E+00	6.29E-01	1.00E+00	9.02E-02	1.00E+00	DNA integration	F
GO:0015075	913	1.00E+00	1.00E+00	9.98E-01	1.00E+00	6.18E-01	1.00E+00	9.49E-01	1.00E+00	9.99E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ion transporter activity	F
GO:0015077	132	1.11E-01	1.00E+00	1.20E-01	1.00E+00	1.56E-01	1.00E+00	9.40E-02	1.00E+00	1.31E-01	1.00E+00	1.46E-01	1.00E+00	6.14E-01	1.00E+00	5.76E-01	1.00E+00	monovalent inorganic cation transporter act	F
GO:0015078	121	8.86E-02	1.00E+00	6.05E-02	1.00E+00	2.19E-01	1.00E+00	5.57E-02	1.00E+00	1.02E-01	1.00E+00	9.00E-02	1.00E+00	5.28E-01	1.00E+00	4.93E-01	1.00E+00	hydrogen ion transporter activity	F
GO:0015082	48	5.02E-01	1.00E+00	2.13E-01	1.00E+00	4.27E-01	1.00E+00	1.35E-01	1.00E+00	3.98E-01	1.00E+00	1.55E-01	1.00E+00	8.41E-01	1.00E+00	9.53E-01	1.00E+00	di-, tri-valent inorganic cation transporter ac	F
GO:0015085	13	4.27E-01	1.00E+00	7.42E-01	1.00E+00	2.97E-01	1.00E+00	5.71E-01	1.00E+00	3.48E-01	1.00E+00	6.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	calcium ion transporter activity	F

GO:0015103	46	4.75E-01	1.00E+00	8.18E-01	1.00E+00	2.36E-01	1.00E+00	8.44E-01	1.00E+00	6.99E-01	1.00E+00	6.51E-01	1.00E+00	2.96E-01	1.00E+00	9.77E-01	1.00E+00	inorganic anion transporter activity	F
GO:0015106	22	6.85E-01	1.00E+00	9.85E-01	1.00E+00	2.87E-01	1.00E+00	9.62E-01	1.00E+00	8.96E-01	1.00E+00	9.21E-01	1.00E+00	3.14E-01	1.00E+00	9.94E-01	1.00E+00	bicarbonate transporter activity	F
GO:0015108	23	7.01E-01	1.00E+00	9.77E-01	1.00E+00	1.72E-01	1.00E+00	8.89E-01	1.00E+00	9.44E-01	1.00E+00	9.07E-01	1.00E+00	2.59E-01	1.00E+00	9.96E-01	1.00E+00	chloride transporter activity	F
GO:0015114	13	9.68E-01	1.00E+00	6.62E-01	1.00E+00	9.76E-01	1.00E+00	9.03E-01	1.00E+00	8.79E-01	1.00E+00	5.04E-01	1.00E+00	9.43E-01	1.00E+00	7.95E-01	1.00E+00	phosphate transporter activity	F
GO:0015116	12	2.10E-01	1.00E+00	6.36E-01	1.00E+00	8.12E-03	1.57E-01	3.97E-01	1.00E+00	4.39E-01	1.00E+00	5.94E-01	1.00E+00	4.55E-01	1.00E+00	9.90E-01	1.00E+00	sulfate transporter activity	F
GO:0015125	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.95E-01	1.00E+00	bile acid transporter activity	F
GO:0015144	46	3.81E-01	1.00E+00	5.50E-01	1.00E+00	3.91E-01	1.00E+00	1.21E-01	1.00E+00	3.38E-01	1.00E+00	7.06E-01	1.00E+00	8.85E-01	1.00E+00	8.52E-01	1.00E+00	carbohydrate transporter activity	F
GO:0015145	17	3.69E-01	1.00E+00	7.19E-01	1.00E+00	7.10E-01	1.00E+00	7.60E-01	1.00E+00	2.95E-01	1.00E+00	6.58E-01	1.00E+00	8.68E-01	1.00E+00	8.91E-01	1.00E+00	monosaccharide transporter activity	F
GO:0015149	16	2.77E-01	1.00E+00	6.18E-01	1.00E+00	6.34E-01	1.00E+00	6.88E-01	1.00E+00	2.20E-01	1.00E+00	5.68E-01	1.00E+00	8.17E-01	1.00E+00	8.36E-01	1.00E+00	hexose transporter activity	F
GO:0015171	54	7.98E-01	1.00E+00	9.17E-01	1.00E+00	7.35E-01	1.00E+00	6.72E-01	1.00E+00	6.78E-01	1.00E+00	8.93E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	amino acid transporter activity	F
GO:0015172	11	9.86E-01	1.00E+00	9.48E-01	1.00E+00	5.34E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	9.12E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	acidic amino acid transporter activity	F
GO:0015175	18	9.71E-01	1.00E+00	5.03E-01	1.00E+00	7.06E-01	1.00E+00	1.82E-01	1.00E+00	9.98E-01	1.00E+00	5.93E-01	1.00E+00	5.14E-01	1.00E+00	9.78E-01	1.00E+00	neutral amino acid transporter activity	F
GO:0015179	35	9.68E-01	1.00E+00	8.69E-01	1.00E+00	6.20E-01	1.00E+00	7.15E-01	1.00E+00	9.68E-01	1.00E+00	8.38E-01	1.00E+00	9.90E-01	1.00E+00	9.95E-01	1.00E+00	L-amino acid transporter activity	F
GO:0015197	24	9.81E-01	1.00E+00	4.71E-01	1.00E+00	5.91E-01	1.00E+00	3.71E-01	1.00E+00	9.83E-01	1.00E+00	4.73E-01	1.00E+00	1.00E+00	1.00E+00	7.39E-01	1.00E+00	peptide transporter activity	F
GO:0015198	13	9.73E-01	1.00E+00	9.92E-01	1.00E+00	7.17E-01	1.00E+00	8.85E-01	1.00E+00	9.64E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	7.28E-01	1.00E+00	oligopeptide transporter activity	F
GO:0015203	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	polyamine transporter activity	F
GO:0015232	11	5.99E-01	1.00E+00	4.81E-01	1.00E+00	9.29E-02	1.00E+00	4.86E-02	1.00E+00	9.57E-01	1.00E+00	7.76E-01	1.00E+00	4.58E-01	1.00E+00	6.96E-01	1.00E+00	heme transporter activity	F
GO:0015238	35	9.52E-01	1.00E+00	7.30E-01	1.00E+00	9.70E-01	1.00E+00	2.17E-01	1.00E+00	8.70E-01	1.00E+00	8.83E-01	1.00E+00	7.99E-01	1.00E+00	9.99E-01	1.00E+00	drug transporter activity	F
GO:0015247	15	7.94E-01	1.00E+00	6.54E-01	1.00E+00	2.33E-01	1.00E+00	8.73E-01	1.00E+00	9.17E-01	1.00E+00	4.85E-01	1.00E+00	9.99E-01	1.00E+00	9.25E-01	1.00E+00	aminophospholipid transporter activity	F
GO:0015248	14	9.91E-01	1.00E+00	5.89E-01	1.00E+00	1.33E-01	1.00E+00	7.57E-01	1.00E+00	1.00E+00	1.00E+00	3.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sterol transporter activity	F
GO:0015267	505	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.83E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	channel or pore class transporter activity	F
GO:0015268	502	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	alpha-type channel activity	F
GO:0015269	14	8.98E-01	1.00E+00	8.71E-01	1.00E+00	5.79E-01	1.00E+00	9.84E-01	1.00E+00	9.70E-01	1.00E+00	6.29E-01	1.00E+00	8.32E-01	1.00E+00	9.77E-01	1.00E+00	calcium-activated potassium channel activit	F
GO:0015276	105	9.55E-01	1.00E+00	1.00E+00	1.00E+00	4.58E-01	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.58E-01	1.00E+00	ligand-gated ion channel activity	F
GO:0015290	288	9.98E-01	1.00E+00	9.98E-01	1.00E+00	8.43E-01	1.00E+00	7.85E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.34E-01	1.00E+00	1.00E+00	1.00E+00	electrochemical potential-driven transporter	F
GO:0015291	288	9.98E-01	1.00E+00	9.98E-01	1.00E+00	8.43E-01	1.00E+00	7.85E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.34E-01	1.00E+00	1.00E+00	1.00E+00	porter activity	F
GO:0015293	166	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.45E-01	1.00E+00	8.34E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	symporter activity	F
GO:0015294	103	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.70E-01	1.00E+00	6.39E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	solute:cation symporter activity	F
GO:0015296	71	9.94E-01	1.00E+00	8.04E-01	1.00E+00	8.54E-01	1.00E+00	2.76E-01	1.00E+00	9.95E-01	1.00E+00	7.50E-01	1.00E+00	9.42E-01	1.00E+00	9.99E-01	1.00E+00	anion:cation symporter activity	F
GO:0015297	88	8.98E-01	1.00E+00	9.09E-01	1.00E+00	4.05E-01	1.00E+00	8.88E-01	1.00E+00	9.54E-01	1.00E+00	8.05E-01	1.00E+00	8.32E-01	1.00E+00	9.91E-01	1.00E+00	antiporter activity	F
GO:0015298	42	9.84E-01	1.00E+00	9.85E-01	1.00E+00	9.52E-01	1.00E+00	9.10E-01	1.00E+00	9.01E-01	1.00E+00	9.45E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	solute:cation antiporter activity	F
GO:0015299	42	9.84E-01	1.00E+00	9.85E-01	1.00E+00	9.52E-01	1.00E+00	9.10E-01	1.00E+00	9.01E-01	1.00E+00	9.45E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	solute:hydrogen antiporter activity	F
GO:0015300	47	9.20E-01	1.00E+00	9.38E-01	1.00E+00	5.16E-01	1.00E+00	9.50E-01	1.00E+00	9.19E-01	1.00E+00	8.46E-01	1.00E+00	9.54E-01	1.00E+00	9.89E-01	1.00E+00	solute:solute antiporter activity	F
GO:0015301	23	7.68E-01	1.00E+00	9.93E-01	1.00E+00	3.75E-01	1.00E+00	9.77E-01	1.00E+00	9.32E-01	1.00E+00	9.51E-01	1.00E+00	3.67E-01	1.00E+00	9.97E-01	1.00E+00	anion:anion antiporter activity	F
GO:0015307	26	9.21E-01	1.00E+00	9.21E-01	1.00E+00	8.93E-01	1.00E+00	8.62E-01	1.00E+00	8.27E-01	1.00E+00	8.28E-01	1.00E+00	8.47E-01	1.00E+00	9.98E-01	1.00E+00	drug:hydrogen antiporter activity	F
GO:0015370	99	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.84E-01	1.00E+00	5.90E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	solute:sodium symporter activity	F
GO:0015380	21	6.80E-01	1.00E+00	9.73E-01	1.00E+00	2.65E-01	1.00E+00	9.38E-01	1.00E+00	9.12E-01	1.00E+00	8.95E-01	1.00E+00	2.63E-01	1.00E+00	9.89E-01	1.00E+00	anion exchanger activity	F
GO:0015385	14	9.02E-01	1.00E+00	3.31E-01	1.00E+00	9.87E-01	1.00E+00	4.69E-01	1.00E+00	7.08E-01	1.00E+00	2.54E-01	1.00E+00	8.07E-01	1.00E+00	4.95E-01	1.00E+00	sodium:hydrogen antiporter activity	F
GO:0015399	111	2.48E-01	1.00E+00	1.30E-01	1.00E+00	2.53E-02	4.97E-01	5.77E-02	1.00E+00	4.45E-01	1.00E+00	1.32E-01	1.00E+00	7.66E-01	1.00E+00	9.63E-01	1.00E+00	primary active transporter activity	F
GO:0015405	111	2.48E-01	1.00E+00	1.30E-01	1.00E+00	2.53E-02	4.97E-01	5.77E-02	1.00E+00	4.45E-01	1.00E+00	1.32E-01	1.00E+00	7.66E-01	1.00E+00	9.63E-01	1.00E+00	P-P-bond-hydrolysis-driven transporter acti	F
GO:0015450	21	7.61E-01	1.00E+00	6.52E-02	1.00E+00	4.62E-01	1.00E+00	6.98E-02	1.00E+00	7.38E-01	1.00E+00	8.33E-02	1.00E+00	9.27E-01	1.00E+00	4.81E-01	1.00E+00	protein translocase activity	F
GO:0015457	43	9.37E-01	1.00E+00	1.00E+00	1.00E+00	5.34E-01	1.00E+00	9.79E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	5.86E-01	1.00E+00	9.94E-01	1.00E+00	auxiliary transport protein activity	F
GO:0015459	18	6.79E-01	1.00E+00	9.76E-01	1.00E+00	7.66E-01	1.00E+00	6.02E-01	1.00E+00	8.29E-01	1.00E+00	9.75E-01	1.00E+00	2.86E-01	1.00E+00	9.92E-01	1.00E+00	potassium channel regulator activity	F
GO:0015464	29	7.39E-01	1.00E+00	7.93E-01	1.00E+00	4.55E-01	1.00E+00	5.14E-01	1.00E+00	7.14E-01	1.00E+00	6.95E-01	1.00E+00	8.67E-01	1.00E+00	9.76E-01	1.00E+00	acetylcholine receptor activity	F
GO:0015485	19	9.65E-01	1.00E+00	7.15E-01	1.00E+00	3.05E-01	1.00E+00	8.95E-01	1.00E+00	9.66E-01	1.00E+00	5.04E-01	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	cholesterol binding	F
GO:0015491	21	8.11E-01	1.00E+00	3.28E-01	1.00E+00	8.82E-01	1.00E+00	3.89E-01	1.00E+00	6.38E-01	1.00E+00	2.51E-01	1.00E+00	8.52E-01	1.00E+00	6.29E-01	1.00E+00	cation:cation antiporter activity	F
GO:0015520	26	9.21E-01	1.00E+00	9.21E-01	1.00E+00	8.93E-01	1.00E+00	8.62E-01	1.00E+00	8.27E-01	1.00E+00	8.28E-01	1.00E+00	8.47E-01	1.00E+00	9.98E-01	1.00E+00	tetracycline:hydrogen antiporter activity	F
GO:0015629	313	2.65E-01	1.00E+00	8.35E-01	1.00E+00	4.99E-03	9.30E-02	5.08E-01	1.00E+00	3.92E-01	1.00E+00	8.40E-01	1.00E+00	9.71E-01	1.00E+00	8.91E-01	1.00E+00	actin cytoskeleton	C
GO:0015630	430	1.07E-01	1.00E+00	1.02E-03	2.00E-02	1.01E-04	4.57E-03	1.13E-04	7.00E-03	5.15E-01	1.00E+00	3.32E-03	6.40E-02	8.65E-01	1.00E+00	4.23E-01	1.00E+00	microtubule cytoskeleton	C
GO:0015631	73	2.38E-02	1.00E+00	2.25E-03	5.10E-02	6.06E-02	1.00E+00	8.98E-03	1.12E-01	2.71E-02	6.55E-01	3.22E-03	6.40E-02	2.10E-01	1.00E+00	1.37E-01	1.00E+00	tubulin binding	F
GO:0015645	11	1.78E-01	1.00E+00	3.31E-01	1.00E+00	9.46E-03	1.57E-01	5.77E-01	1.00E+00	5.32E-01	1.00E+00	3.33E-01	1.00E+00	7.02E-02	1.00E+00	2.78E-01	1.00E+00	fatty-acid ligase activity	F
GO:0015662	60	5.88E-01	1.00E+00	4.83E-01	1.00E+00	1.32E-01	1.00E+00	8.31E-01	1.00E+00	7.56E-01	1.00E+00	2.97E-01	1.00E+00	9.54E-01	1.00E+00	9.43E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0015669	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.24E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	gas transport	P
GO:0015671	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.01E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen transport	P
GO:0015672	450	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.09E-01	1.00E+00	8.55E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	monovalent inorganic cation transport	P
GO:0015674	238	9.87E-01	1.00E+00	9.63E-01	1.00E+00	5.81E-01	1.00E+00	7.30E-01	1.00E+00	9.68E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	di-, tri-valent inorganic cation transport	P
GO:0015695	10	9.82E-01	1.00E+00	9.60E-01	1.00E+00	8.62E-01	1.00E+00	9.99E-01	1.00E+00	9.12E-01	1.00E+00	8.05E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organic cation transport	P
GO:0015698	194	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inorganic anion transport	P
GO:0015711	14	8.33E-01	1.00E+00	9.45E-01	1.00E+00	7.65E-01	1.00E+00	6.01E-01	1.00E+00	9.47E-01	1.00E+00	9.60E-01	1.00E+00	3.48E-01	1.00E+00	9.22E-01	1.00E+00	organic anion transport	P
GO:0015718	16	2.90E-01	1.00E+00	6.34E-01	1.00E+00	1.01E-01	1.00E+00	3.35E-01	1.00E+00	4.82E-01	1.00E+00	6.43E-01	1.00E+00	7.78E-01	1.00E+00	7.17E-01	1.00E+00	monocarboxylic acid transport	P
GO:0015749	45	9.48E-01	1.00E+00	5.75E-01	1.00E+00	8.23E-01	1.00E+00	5.58E-01	1.00E+00	8.95E-01	1.00E+00	4.59E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	monosaccharide transport	P
GO:0015758	44	9.40E-01	1.00E+00	5.48E-01	1.00E+00	7.89E-01	1.00E+00	5.14E-01	1.00E+00	8.93E-01	1.00E+00	4.50E-01	1.00E+00	1.00E+00	1.00E+00	9.11E-01	1.00E+00	glucose transport	P
GO:0015800	20	9.99E-01	1.00E+00	5.32E-01	1.00E+00	8.36E-01	1.00E+00	9.80E-01	1.00E+00	9.99E-01	1.00E+00	3.15E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	acidic amino acid transport	P
GO:0015804	16	9.41E-01	1.00E+00	4.57E-01	1.00E+00	6.63E-01	1.00E+00	1.35E-01	1.00E+00	9.93E-01	1.00E+00	6.09E-01	1.00E+00	4.62E-01	1.00E+00	9.36E-01	1.00E+00	neutral amino acid transport	P
GO:0015807	14	5.80E-01	1.00E+00	1.81E-01	1.00E+00	3.80E-01	1.00E+00	3.04E-01	1.00E+00	5.37E-01	1.00E+00	1.52E-01	1.00E+00	9.75E-01	1.00E+00	5.05E-01	1.00E+00	L-amino acid transport	P
GO:0015813	20	9.99E-01	1.00E+00	5.32E-01	1.00E+00	8.36E-01	1.00E+00	9.80E-01	1.00E+00	9.99E-01	1.00E+00	3.15E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	glutamate transport	P
GO:0015833	61	1.00E+00	1.00E+00	9.25E-01	1.00E+00	9.47E-01	1.00E+00	3.57E-01	1.00E+00	9.99E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	peptide transport	P
GO:0015837	91	7.02E-01	1.00E+00	7.29E-01	1.00E+00	3.16E-01	1.00E+00	6.05E-01	1.00E+00	6.11E-01	1.00E+00	4.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	amine transport	P
GO:0015849	144	9.28E-01	1.00E+00	8.72E-01	1.00E+00	4.50E-01	1.00E+00	4.86E-01	1.00E+00	9.23E-01	1.00E+00	7.05E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	organic acid transport	P
GO:0015886	10	4.52E-01	1.00E+00	3.87E-01	1.00E+00	5.23E-02	1.00E+00	2.83E-02	5.42E-01	9.21E-01	1.00E+00	7.10E-01	1.00E+00	3.87E-01	1.00E+00	5.97E-01	1.00E+00	heme transport	P
GO:0015893	30	9.29E-01	1.00E+00	7.83E-01	1.00E+00	8.85E-01	1.00E+00	6.20E-01	1.00E+00	8.72E-01	1.00E+00	6.90E-01	1.00E+00	7.85E-01	1.00E+00	9.94E-01	1.00E+00	drug transport	P
GO:0015904	26	9.21E-01	1.00E+00	9.21E-01	1.00E+00	8.93E-01	1.00E+00	8.62E-01	1.00E+00	8.27E-01	1.00E+00	8.28E-01	1.00E+00	8.47E-01	1.00E+00	9.98E-01	1.00E+00	tetracycline transport	P
GO:0015908	12	7.07E-03	1.37E-01	7.55E-02	1.00E+00	4.24E-03	3.50E-02	2.91E-02	5.42E-01	3.11E-02	6.55E-01	8.62E-02	1.00E+00	1.14E-01	1.00E+00	7.43E-01	1.00E+00	fatty acid transport	P
GO:0015914	18	7.75E-01	1.00E+00	6.07E-01	1.00E+00	1.31E-01	1.00E+00	9.35E-01	1.00E+00	8.88E-01	1.00E+00	2.93E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	phospholipid transport	P
GO:0015918	17	8.22E-01	1.00E+00	4.04E-01	1.00E+00	2.21E-01	1.00E+00	4.67E-01	1.00E+00	8.93E-01	1.00E+00	3.48E-01	1.00E+00	9.96E-01	1.00E+00	6.87E-01	1.00E+00	sterol transport	P

GO:0015923	16	3.99E-01	1.00E+00	1.94E-01	1.00E+00	1.60E-01	1.00E+00	4.38E-01	1.00E+00	7.22E-01	1.00E+00	1.39E-01	1.00E+00	2.82E-01	1.00E+00	5.17E-01	1.00E+00	mannosidase activity	F
GO:0015924	10	6.07E-01	1.00E+00	2.12E-01	1.00E+00	2.26E-01	1.00E+00	2.91E-01	1.00E+00	8.69E-01	1.00E+00	1.81E-01	1.00E+00	9.57E-01	1.00E+00	5.02E-01	1.00E+00	mannosyl-oligosaccharide mannosidase ac	F
GO:0015926	11	2.38E-01	1.00E+00	7.26E-01	1.00E+00	3.93E-01	1.00E+00	8.97E-01	1.00E+00	3.96E-01	1.00E+00	6.82E-01	1.00E+00	1.63E-01	1.00E+00	7.54E-01	1.00E+00	glucosidase activity	F
GO:0015929	12	1.79E-01	1.00E+00	7.56E-02	1.00E+00	1.16E-01	1.00E+00	4.54E-01	1.00E+00	4.46E-01	1.00E+00	6.18E-02	1.00E+00	1.69E-01	1.00E+00	5.01E-01	1.00E+00	hexosaminidase activity	F
GO:0015931	105	3.29E-02	1.00E+00	4.39E-05	4.00E-03	2.23E-03	1.80E-02	2.87E-06	0.00E+00	9.53E-02	1.00E+00	5.17E-04	1.02E-02	6.24E-01	1.00E+00	7.05E-02	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	P
GO:0015932	23	7.19E-02	1.00E+00	3.84E-01	1.00E+00	1.07E-02	1.57E-01	4.93E-02	1.00E+00	4.99E-01	1.00E+00	5.39E-01	1.00E+00	1.00E+00	1.00E+00	7.52E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	F
GO:0015934	29	2.64E-01	1.00E+00	4.40E-01	1.00E+00	9.62E-01	1.00E+00	3.16E-01	1.00E+00	1.17E-01	1.00E+00	3.60E-01	1.00E+00	9.54E-01	1.00E+00	9.75E-01	1.00E+00	large ribosomal subunit	C
GO:0015935	39	1.50E-01	1.00E+00	4.36E-01	1.00E+00	9.88E-01	1.00E+00	2.15E-01	1.00E+00	5.46E-02	1.00E+00	6.52E-01	1.00E+00	4.74E-01	1.00E+00	5.53E-01	1.00E+00	small ribosomal subunit	C
GO:0015936	13	8.01E-01	1.00E+00	7.52E-01	1.00E+00	3.46E-01	1.00E+00	6.69E-01	1.00E+00	9.73E-01	1.00E+00	7.22E-01	1.00E+00	2.80E-01	1.00E+00	8.86E-01	1.00E+00	coenzyme A metabolism	P
GO:0015980	204	4.54E-02	1.00E+00	2.21E-01	1.00E+00	1.77E-03	1.60E-02	1.27E-01	1.00E+00	1.07E-01	1.00E+00	3.04E-01	1.00E+00	9.47E-01	1.00E+00	7.56E-01	1.00E+00	energy derivation by oxidation of organic cc	P
GO:0015985	19	7.20E-03	1.37E-01	3.49E-01	1.00E+00	3.84E-02	5.87E-01	4.42E-01	1.00E+00	7.08E-02	1.00E+00	2.81E-01	1.00E+00	1.28E-01	1.00E+00	7.69E-01	1.00E+00	energy coupled proton transport, down elec	P
GO:0015986	19	7.20E-03	1.37E-01	3.49E-01	1.00E+00	3.84E-02	5.87E-01	4.42E-01	1.00E+00	7.08E-02	1.00E+00	2.81E-01	1.00E+00	1.28E-01	1.00E+00	7.69E-01	1.00E+00	ATP synthesis coupled proton transport	P
GO:0015992	73	2.87E-02	1.00E+00	1.87E-01	1.00E+00	9.34E-03	1.57E-01	6.41E-02	1.00E+00	1.15E-01	1.00E+00	2.32E-01	1.00E+00	6.52E-01	1.00E+00	8.51E-01	1.00E+00	proton transport	P
GO:0016010	17	9.92E-01	1.00E+00	8.02E-01	1.00E+00	7.22E-01	1.00E+00	8.49E-01	1.00E+00	9.99E-01	1.00E+00	8.92E-01	1.00E+00	9.74E-01	1.00E+00	3.27E-01	1.00E+00	dystrophin-associated glycoprotein complex	C
GO:0016020	6912	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.22E-01	1.00E+00	7.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	membrane	C
GO:0016021	5021	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.25E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	integral to membrane	C
GO:0016023	415	6.64E-01	1.00E+00	5.12E-01	1.00E+00	1.63E-01	1.00E+00	1.51E-01	1.00E+00	5.36E-01	1.00E+00	5.51E-01	1.00E+00	1.00E+00	1.00E+00	9.27E-01	1.00E+00	cytoplasmic membrane-bound vesicle	C
GO:0016032	72	9.36E-01	1.00E+00	9.81E-01	1.00E+00	7.86E-01	1.00E+00	7.06E-01	1.00E+00	7.93E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.22E-01	1.00E+00	viral life cycle	P
GO:0016042	145	5.60E-01	1.00E+00	3.89E-01	1.00E+00	8.06E-02	1.00E+00	4.51E-01	1.00E+00	7.68E-01	1.00E+00	3.80E-01	1.00E+00	6.31E-01	1.00E+00	7.99E-01	1.00E+00	lipid catabolism	P
GO:0016043	2253	1.88E-01	1.00E+00	2.43E-02	1.00E+00	2.10E-10	0.00E+00	4.99E-06	8.32E-04	6.64E-01	1.00E+00	2.06E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	cell organization and biogenesis	P
GO:0016044	123	2.82E-01	1.00E+00	2.33E-01	1.00E+00	2.33E-01	1.00E+00	1.69E-01	1.00E+00	3.19E-01	1.00E+00	1.96E-01	1.00E+00	7.22E-01	1.00E+00	8.26E-01	1.00E+00	membrane organization and biogenesis	P
GO:0016049	204	9.98E-01	1.00E+00	1.00E+00	1.00E+00	6.74E-01	1.00E+00	5.70E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cell growth	P
GO:0016051	136	5.50E-01	1.00E+00	7.40E-01	1.00E+00	1.18E-01	1.00E+00	2.79E-01	1.00E+00	5.28E-01	1.00E+00	6.45E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	carbohydrate biosynthesis	P
GO:0016052	113	2.12E-02	1.00E+00	2.67E-02	1.00E+00	7.23E-03	1.57E-01	7.73E-02	1.00E+00	6.48E-02	1.00E+00	5.20E-02	1.00E+00	4.74E-01	1.00E+00	1.12E-01	1.00E+00	carbohydrate catabolism	P
GO:0016053	93	7.18E-01	1.00E+00	7.40E-01	1.00E+00	3.44E-01	1.00E+00	2.65E-01	1.00E+00	7.29E-01	1.00E+00	8.34E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	organic acid biosynthesis	P
GO:0016054	10	6.67E-03	1.37E-01	1.32E-02	3.84E-01	1.42E-05	9.71E-04	3.31E-01	1.00E+00	3.21E-02	6.55E-01	1.39E-02	5.65E-01	3.15E-01	1.00E+00	1.13E-01	1.00E+00	organic acid catabolism	P
GO:0016055	122	9.88E-01	1.00E+00	9.97E-01	1.00E+00	8.22E-01	1.00E+00	9.24E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	8.71E-01	1.00E+00	Wnt receptor signaling pathway	P
GO:0016064	114	9.97E-01	1.00E+00	9.99E-01	1.00E+00	8.96E-01	1.00E+00	9.57E-01	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	immunoglobulin mediated immune respons	P
GO:0016068	46	9.91E-01	1.00E+00	9.99E-01	1.00E+00	8.45E-01	1.00E+00	9.12E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.60E-01	1.00E+00	9.92E-01	1.00E+00	type I hypersensitivity	P
GO:0016070	637	6.27E-07	1.25E-04	2.12E-14	0.00E+00	3.33E-09	0.00E+00	1.86E-08	0.00E+00	5.93E-04	4.90E-03	1.03E-10	1.05E-04	1.28E-01	1.00E+00	1.81E-02	1.77E-01	RNA metabolism	P
GO:0016071	342	7.88E-05	5.00E-03	2.88E-09	1.00E-03	3.07E-05	4.57E-03	2.45E-08	0.00E+00	7.60E-03	2.02E-01	5.96E-07	2.22E-04	9.95E-02	1.00E+00	1.57E-02	1.38E-01	mRNA metabolism	P
GO:0016072	74	8.11E-02	1.00E+00	3.44E-02	1.00E+00	2.08E-02	2.36E-01	2.37E-02	4.10E-01	1.63E-01	1.00E+00	1.11E-01	1.00E+00	5.56E-01	1.00E+00	8.91E-01	1.00E+00	rRNA metabolism	P
GO:0016073	12	1.26E-01	1.00E+00	5.61E-02	1.00E+00	2.63E-02	4.97E-01	2.42E-02	4.10E-01	4.29E-01	1.00E+00	6.98E-02	1.00E+00	1.64E-01	1.00E+00	7.30E-01	1.00E+00	snRNA metabolism	P
GO:0016079	13	9.25E-01	1.00E+00	7.66E-01	1.00E+00	7.50E-01	1.00E+00	2.44E-01	1.00E+00	8.99E-01	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synaptic vesicle exocytosis	P
GO:0016089	45	8.62E-01	1.00E+00	2.81E-01	1.00E+00	4.92E-01	1.00E+00	4.44E-01	1.00E+00	9.05E-01	1.00E+00	1.66E-01	1.00E+00	9.27E-01	1.00E+00	9.27E-01	1.00E+00	aromatic amino acid family biosynthesis, sh	P
GO:0016125	95	6.37E-01	1.00E+00	4.04E-01	1.00E+00	3.73E-02	5.87E-01	1.54E-01	1.00E+00	8.32E-01	1.00E+00	6.88E-01	1.00E+00	9.50E-01	1.00E+00	4.21E-01	1.00E+00	sterol metabolism	P
GO:0016126	34	5.63E-01	1.00E+00	2.17E-01	1.00E+00	2.12E-01	1.00E+00	1.23E-01	1.00E+00	6.35E-01	1.00E+00	5.25E-01	1.00E+00	7.84E-01	1.00E+00	3.27E-01	1.00E+00	sterol biosynthesis	P
GO:0016127	10	1.74E-01	1.00E+00	2.91E-01	1.00E+00	7.52E-02	1.00E+00	8.19E-01	1.00E+00	4.79E-01	1.00E+00	2.76E-01	1.00E+00	9.09E-01	1.00E+00	3.81E-01	1.00E+00	sterol catabolism	P
GO:0016180	12	1.26E-01	1.00E+00	5.61E-02	1.00E+00	2.63E-02	4.97E-01	2.42E-02	4.10E-01	4.29E-01	1.00E+00	6.98E-02	1.00E+00	1.64E-01	1.00E+00	7.30E-01	1.00E+00	snRNA processing	P
GO:0016192	546	2.51E-04	1.10E-02	3.09E-04	8.26E-03	6.23E-07	8.48E-04	4.03E-06	8.32E-04	2.15E-03	4.30E-02	9.29E-03	1.43E-01	8.57E-01	1.00E+00	1.53E-01	1.00E+00	vesicle-mediated transport	P
GO:0016197	45	4.42E-01	1.00E+00	1.69E-01	1.00E+00	4.02E-02	5.87E-01	8.78E-02	1.00E+00	6.70E-01	1.00E+00	1.49E-01	1.00E+00	9.88E-01	1.00E+00	6.61E-01	1.00E+00	endosome transport	P
GO:0016202	15	4.06E-01	1.00E+00	7.94E-01	1.00E+00	1.89E-01	1.00E+00	1.00E+00	1.00E+00	4.78E-01	1.00E+00	7.08E-01	1.00E+00	9.98E-01	1.00E+00	5.01E-01	1.00E+00	regulation of striated muscle development	P
GO:0016208	25	9.37E-01	1.00E+00	7.92E-01	1.00E+00	7.16E-01	1.00E+00	7.35E-01	1.00E+00	9.61E-01	1.00E+00	7.17E-01	1.00E+00	9.34E-01	1.00E+00	8.58E-01	1.00E+00	AMP binding	F
GO:0016209	61	6.12E-01	1.00E+00	9.85E-01	1.00E+00	1.50E-01	1.00E+00	6.88E-01	1.00E+00	8.21E-01	1.00E+00	9.87E-01	1.00E+00	5.71E-01	1.00E+00	9.92E-01	1.00E+00	antioxidant activity	F
GO:0016229	38	9.63E-01	1.00E+00	9.57E-01	1.00E+00	5.40E-01	1.00E+00	3.96E-01	1.00E+00	9.94E-01	1.00E+00	9.41E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	steroid dehydrogenase activity	F
GO:0016236	14	8.71E-02	1.00E+00	4.85E-02	1.00E+00	1.13E-01	1.00E+00	3.66E-01	1.00E+00	1.30E-01	1.00E+00	2.22E-02	7.69E-01	3.28E-01	1.00E+00	3.39E-01	1.00E+00	macroautophagy	P
GO:0016247	40	8.76E-01	1.00E+00	1.00E+00	1.00E+00	4.08E-01	1.00E+00	9.66E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	5.27E-01	1.00E+00	9.86E-01	1.00E+00	channel regulator activity	F
GO:0016251	36	3.83E-02	1.00E+00	5.03E-05	4.00E-03	2.59E-02	4.97E-01	1.25E-03	1.30E-02	5.00E-02	1.00E+00	1.12E-04	2.29E-03	5.14E-01	1.00E+00	3.75E-03	6.60E-02	general RNA polymerase II transcription fac	F
GO:0016254	16	7.58E-01	1.00E+00	2.97E-01	1.00E+00	9.61E-01	1.00E+00	2.62E-01	1.00E+00	4.97E-01	1.00E+00	3.92E-01	1.00E+00	9.63E-01	1.00E+00	3.95E-01	1.00E+00	preassembly of GPI anchor in ER membran	P
GO:0016265	919	9.77E-01	1.00E+00	8.75E-01	1.00E+00	1.12E-02	1.57E-01	2.98E-01	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	9.59E-01	1.00E+00	death	P
GO:0016272	12	8.24E-01	1.00E+00	6.36E-01	1.00E+00	5.44E-01	1.00E+00	9.98E-01	1.00E+00	7.25E-01	1.00E+00	2.71E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	prefoldin complex	C
GO:0016278	29	3.50E-02	1.00E+00	3.91E-02	1.00E+00	7.11E-03	1.57E-01	7.69E-02	1.00E+00	5.65E-02	1.00E+00	1.21E-01	1.00E+00	5.74E-01	1.00E+00	2.40E-02	2.52E-01	lysine N-methyltransferase activity	F
GO:0016279	29	3.50E-02	1.00E+00	3.91E-02	1.00E+00	7.11E-03	1.57E-01	7.69E-02	1.00E+00	5.65E-02	1.00E+00	1.21E-01	1.00E+00	5.74E-01	1.00E+00	2.40E-02	2.52E-01	protein-lysine N-methyltransferase activity	F
GO:0016282	16	6.10E-03	1.37E-01	1.34E-03	3.90E-02	1.11E-02	1.57E-01	1.88E-02	4.10E-01	8.00E-02	1.00E+00	5.48E-03	7.40E-02	9.52E-02	1.00E+00	5.63E-03	6.60E-02	eukaryotic 43S preinitiation complex	C
GO:0016284	12	9.49E-01	1.00E+00	7.39E-01	1.00E+00	9.62E-01	1.00E+00	5.11E-01	1.00E+00	9.33E-01	1.00E+00	7.26E-01	1.00E+00	8.86E-01	1.00E+00	9.19E-01	1.00E+00	alanine aminopeptidase activity	F
GO:0016289	15	2.20E-02	1.00E+00	1.03E-03	2.00E-02	3.67E-01	1.00E+00	1.04E-01	1.00E+00	2.51E-02	6.55E-01	2.25E-04	7.00E-03	1.67E-01	1.00E+00	1.00E+00	1.00E+00	CoA hydrolase activity	F
GO:0016298	107	7.26E-01	1.00E+00	9.80E-01	1.00E+00	1.87E-01	1.00E+00	6.80E-01	1.00E+00	9.08E-01	1.00E+00	9.96E-01	1.00E+00	5.64E-01	1.00E+00	7.78E-01	1.00E+00	lipase activity	F
GO:0016301	902	6.83E-01	1.00E+00	3.13E-01	1.00E+00	2.32E-04	6.00E-03	2.41E-04	7.00E-03	8.14E-01	1.00E+00	5.71E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	kinase activity	F
GO:0016303	11	1.40E-01	1.00E+00	1.58E-01	1.00E+00	1.83E-02	2.36E-01	1.48E-01	1.00E+00	2.62E-01	1.00E+00	1.74E-01	1.00E+00	8.72E-01	1.00E+00	7.19E-01	1.00E+00	phosphatidylinositol 3-kinase activity	F
GO:0016307	11	2.02E-01	1.00E+00	4.32E-01	1.00E+00	3.75E-02	5.87E-01	7.42E-01	1.00E+00	2.99E-01	1.00E+00	3.32E-01	1.00E+00	4.45E-01	1.00E+00	8.25E-01	1.00E+00	phosphatidylinositol phosphate kinase activ	F
GO:0016310	851	1.31E-01	1.00E+00	3.58E-01	1.00E+00	5.31E-05	4.57E-03	2.13E-02	4.10E-01	3.11E-01	1.00E+00	3.83E-01	1.00E+00	9.97E-01	1.00E+00	9.88E-01	1.00E+00	phosphorylation	P
GO:0016311	161	7.46E-01	1.00E+00	2.14E-01	1.00E+00	2.71E-02	4.97E-01	2.40E-02	4.10E-01	9.51E-01	1.00E+00	5.80E-01	1.00E+00	9.78E-01	1.00E+00	3.21E-01	1.00E+00	dephosphorylation	P
GO:0016323	133	7.92E-01	1.00E+00	9.89E-01	1.00E+00	2.45E-01	1.00E+00	8.22E-01	1.00E+00	6.14E-01	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	basolateral plasma membrane	C
GO:0016324	96	9.45E-01	1.00E+00	9.86E-01	1.00E+00	4.62E-01	1.00E+00	6.29E-01	1.00E+00	9.64E-01	1.00E+00	9.84E-01	1.00E+00	9.53E-01	1.00E+00	1.00E+00	1.00E+00	apical plasma membrane	C
GO:0016327	100	3.25E-01	1.00E+00	8.10E-01	1.00E+00	2.82E-01	1.00E+00	4.39E-01	1.00E+00	2.53E-01	1.00E+00	6.54E-01	1.00E+00	7.96E-01	1.00E+00	1.00E+00	1.00E+00	apicolateral plasma membrane	C
GO:0016328	12	5.18E-01	1.00E+00	4.97E-01	1.00E+00	4.30E-01	1.00E+00	2.07E-01	1.00E+00	5.81E-01	1.00E+00	6.06E-01	1.00E+00	6.27E-01	1.00E+00	5.05E-01	1.00E+00	lateral plasma membrane	C
GO:0016331	54	9.93E-01	1.00E+00	9.59E-01	1.00E+00	9.50E-01	1.00E+00	8.38E-01	1.00E+00	9.80E-01	1.00E+00	9.64E-01	1.00E+00	9.96E-01	1.00E+00	9.15E-01	1.00E+00	morphogenesis of embryonic epithelium	P
GO:0016337	230	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell-cell adhesion	P
GO:0016338	16	2.35E-01	1.00E+00	1.00E+00	1.00E+00	2.78E-01	1.00E+00	9.97E-01	1.00E+00	2.51E-01	1.00E+00	1.00E+00	1.00E+00	3.60E-01	1.00E+00	1.00E+00	1.00E+00	calcium-independent cell-cell adhesion	P
GO:0016339	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	calcium-dependent cell-cell adhesion	P
GO:0016358	40	9.99E-01	1.00E+00	9.15E-01	1.00E+00	5.96E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	7.76E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	dendrite development	P
GO:0016363	46	1.44E-01	1.00E+00	6.54E-03	1.50E-01	8.00E-02	1.00E+00	9.95E-04	1.11E-02	2.86E-01	1.00E+00	6.20E-02	1.00E+00	1.21E-01	1.00E+00	1.25E-01	1.00E+00	nuclear matrix	C
GO:0016407	69	5.44E-01	1.00E+00	3.07E-01	1.00E+00	1.04E-01	1.00E+00	1.67E-01	1.00E+00	7.61E-01	1.00E+00	2.92E-01	1.00E+00	7.38E-01	1.00E+00	8.11E-01	1.00E+00	acetyltransferase activity	F
GO:0016408	12	2.00E-01	1.00E+00	1.90E-01	1.00E+00	7.79E-02	1.00E+00	1.13E-01	1.00E+00	4.55E-01	1.00E+00	3.19E-01	1.00E+00	2.35E-01	1.00E+00	2.01E-01	1.00E+00	C-acyltransferase activity	F
GO:0016409	14	3.88E-01	1.00E+00	2.97E-01	1.00E+00	3.28E-01	1.00E+00	1.72E-01	1.00E+00	5.38E-01	1.00E+00	2.35E-01	1.00E+00	1.99E-01	1.00E+00	8.69E-01	1.00E+00	palmitoyltransferase activity	F

GO:0016410	70	6.22E-01	1.00E+00	3.41E-01	1.00E+00	4.66E-02	8.68E-01	7.51E-02	1.00E+00	7.87E-01	1.00E+00	3.93E-01	1.00E+00	9.34E-01	1.00E+00	8.01E-01	1.00E+00	N-acyltransferase activity	F
GO:0016411	18	8.88E-01	1.00E+00	8.76E-01	1.00E+00	8.71E-01	1.00E+00	9.94E-01	1.00E+00	7.51E-01	1.00E+00	6.14E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	acylglycerol O-acyltransferase activity	F
GO:0016439	33	9.96E-01	1.00E+00	8.46E-01	1.00E+00	9.65E-01	1.00E+00	6.04E-01	1.00E+00	9.92E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	3.58E-01	1.00E+00	tRNA-pseudouridine synthase activity	F
GO:0016444	26	3.16E-01	1.00E+00	2.08E-01	1.00E+00	5.29E-01	1.00E+00	4.98E-01	1.00E+00	1.67E-01	1.00E+00	1.51E-01	1.00E+00	9.03E-01	1.00E+00	4.96E-01	1.00E+00	somatic cell DNA recombination	P
GO:0016445	29	3.20E-01	1.00E+00	3.48E-01	1.00E+00	4.81E-01	1.00E+00	4.81E-01	1.00E+00	1.80E-01	1.00E+00	2.82E-01	1.00E+00	8.54E-01	1.00E+00	6.74E-01	1.00E+00	somatic diversification of immunoglobulins	P
GO:0016447	26	3.16E-01	1.00E+00	2.08E-01	1.00E+00	5.29E-01	1.00E+00	4.98E-01	1.00E+00	1.67E-01	1.00E+00	1.51E-01	1.00E+00	9.03E-01	1.00E+00	4.96E-01	1.00E+00	somatic recombination of immunoglobulin g	P
GO:0016455	16	3.64E-01	1.00E+00	6.64E-02	1.00E+00	4.82E-01	1.00E+00	1.65E-01	1.00E+00	3.48E-01	1.00E+00	5.86E-02	1.00E+00	4.11E-01	1.00E+00	7.45E-02	1.00E+00	RNA polymerase II transcription mediator a	F
GO:0016458	32	8.17E-02	1.00E+00	1.99E-02	9.24E-01	1.84E-01	1.00E+00	3.36E-02	5.42E-01	7.91E-02	1.00E+00	1.54E-02	5.65E-01	3.35E-01	1.00E+00	2.75E-01	1.00E+00	gene silencing	P
GO:0016459	59	2.30E-01	1.00E+00	1.00E+00	1.00E+00	8.15E-02	1.00E+00	9.63E-01	1.00E+00	3.02E-01	1.00E+00	9.99E-01	1.00E+00	7.41E-01	1.00E+00	1.00E+00	1.00E+00	myosin complex	C
GO:0016462	779	7.11E-02	1.00E+00	2.60E-03	5.10E-02	4.94E-06	9.71E-04	3.99E-04	7.17E-03	6.40E-01	1.00E+00	5.54E-02	1.00E+00	8.87E-01	1.00E+00	5.55E-01	1.00E+00	pyrophosphatase activity	F
GO:0016469	50	4.38E-02	1.00E+00	1.06E-01	1.00E+00	2.21E-02	2.63E-01	4.65E-02	1.00E+00	1.63E-01	1.00E+00	1.79E-01	1.00E+00	4.28E-01	1.00E+00	5.47E-01	1.00E+00	proton-transporting two-sector ATPase com	C
GO:0016477	347	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell migration	P
GO:0016478	12	1.87E-01	1.00E+00	3.20E-02	1.00E+00	2.88E-01	1.00E+00	7.34E-03	8.10E-02	1.73E-01	1.00E+00	6.50E-02	1.00E+00	6.69E-01	1.00E+00	1.66E-01	1.00E+00	negative regulation of translation	P
GO:0016481	349	8.43E-01	1.00E+00	5.11E-01	1.00E+00	3.74E-01	1.00E+00	4.79E-02	1.00E+00	7.24E-01	1.00E+00	6.95E-01	1.00E+00	1.00E+00	1.00E+00	8.77E-01	1.00E+00	negative regulation of transcription	P
GO:0016485	106	4.13E-01	1.00E+00	2.84E-01	1.00E+00	2.99E-01	1.00E+00	1.35E-01	1.00E+00	2.25E-01	1.00E+00	2.90E-01	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	protein processing	P
GO:0016491	874	2.57E-01	1.00E+00	6.68E-01	1.00E+00	8.32E-02	1.00E+00	2.25E-02	4.10E-01	4.47E-01	1.00E+00	6.74E-01	1.00E+00	6.09E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity	F
GO:0016493	40	9.81E-01	1.00E+00	9.82E-01	1.00E+00	9.35E-01	1.00E+00	5.23E-01	1.00E+00	8.82E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	C-C chemokine receptor activity	F
GO:0016494	35	9.98E-01	1.00E+00	9.84E-01	1.00E+00	9.82E-01	1.00E+00	5.26E-01	1.00E+00	9.81E-01	1.00E+00	9.74E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	C-X-C chemokine receptor activity	F
GO:0016500	27	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.55E-01	1.00E+00	9.44E-01	1.00E+00	protein-hormone receptor activity	F
GO:0016502	107	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.69E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	nucleotide receptor activity	F
GO:0016504	21	1.91E-01	1.00E+00	4.06E-01	1.00E+00	3.53E-01	1.00E+00	4.07E-01	1.00E+00	1.99E-01	1.00E+00	5.59E-01	1.00E+00	1.46E-01	1.00E+00	8.93E-02	1.00E+00	protease activator activity	F
GO:0016505	17	1.60E-01	1.00E+00	2.77E-01	1.00E+00	2.46E-01	1.00E+00	1.82E-01	1.00E+00	1.91E-01	1.00E+00	4.03E-01	1.00E+00	1.22E-01	1.00E+00	1.69E-01	1.00E+00	apoptotic protease activator activity	F
GO:0016525	20	9.98E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.55E-01	1.00E+00	8.70E-01	1.00E+00	9.81E-01	1.00E+00	9.95E-01	1.00E+00	negative regulation of angiogenesis	P
GO:0016527	10	8.02E-01	1.00E+00	9.49E-01	1.00E+00	5.40E-01	1.00E+00	9.97E-01	1.00E+00	8.33E-01	1.00E+00	8.51E-01	1.00E+00	9.96E-01	1.00E+00	9.98E-01	1.00E+00	brain-specific angiogenesis inhibitor activity	F
GO:0016528	17	6.76E-01	1.00E+00	7.34E-01	1.00E+00	1.61E-01	1.00E+00	2.88E-01	1.00E+00	9.03E-01	1.00E+00	8.87E-01	1.00E+00	9.87E-01	1.00E+00	7.53E-01	1.00E+00	sarcoplasm	C
GO:0016529	14	4.86E-01	1.00E+00	4.35E-01	1.00E+00	9.83E-02	1.00E+00	1.89E-01	1.00E+00	7.62E-01	1.00E+00	6.90E-01	1.00E+00	9.65E-01	1.00E+00	5.75E-01	1.00E+00	sarcoplasmic reticulum	C
GO:0016540	62	2.74E-01	1.00E+00	2.87E-01	1.00E+00	2.88E-01	1.00E+00	2.32E-01	1.00E+00	1.74E-01	1.00E+00	2.39E-01	1.00E+00	9.94E-01	1.00E+00	8.45E-01	1.00E+00	protein autoprocessing	P
GO:0016558	10	3.34E-01	1.00E+00	6.62E-01	1.00E+00	2.73E-01	1.00E+00	4.16E-01	1.00E+00	4.20E-01	1.00E+00	8.93E-01	1.00E+00	6.45E-01	1.00E+00	2.62E-01	1.00E+00	protein import into peroxisome matrix	P
GO:0016563	327	9.30E-01	1.00E+00	3.72E-01	1.00E+00	8.40E-02	1.00E+00	2.53E-02	4.10E-01	9.92E-01	1.00E+00	6.55E-01	1.00E+00	9.99E-01	1.00E+00	6.51E-01	1.00E+00	transcriptional activator activity	F
GO:0016564	239	9.98E-01	1.00E+00	8.31E-01	1.00E+00	9.64E-01	1.00E+00	2.67E-01	1.00E+00	9.83E-01	1.00E+00	8.53E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	transcriptional repressor activity	F
GO:0016566	18	9.48E-01	1.00E+00	8.55E-01	1.00E+00	8.52E-01	1.00E+00	9.77E-01	1.00E+00	6.47E-01	1.00E+00	6.18E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	specific transcriptional repressor activity	F
GO:0016567	103	2.11E-01	1.00E+00	3.27E-02	1.00E+00	3.20E-02	5.87E-01	2.28E-03	2.70E-02	4.20E-01	1.00E+00	8.01E-02	1.00E+00	4.82E-01	1.00E+00	2.75E-01	1.00E+00	protein ubiquitination	P
GO:0016568	214	2.02E-03	4.90E-02	2.20E-06	1.41E-03	5.00E-06	9.71E-04	2.70E-05	3.91E-03	2.21E-02	4.78E-01	3.22E-05	2.29E-03	9.17E-01	1.00E+00	2.30E-02	2.52E-01	chromatin modification	P
GO:0016569	58	1.66E-01	1.00E+00	2.55E-02	1.00E+00	1.92E-02	2.36E-01	5.50E-03	8.10E-02	3.96E-01	1.00E+00	1.08E-01	1.00E+00	8.89E-01	1.00E+00	9.56E-02	1.00E+00	covalent chromatin modification	P
GO:0016570	55	2.04E-01	1.00E+00	7.90E-02	1.00E+00	2.57E-02	4.97E-01	2.08E-02	4.10E-01	4.79E-01	1.00E+00	2.31E-01	1.00E+00	8.52E-01	1.00E+00	1.61E-01	1.00E+00	histone modification	P
GO:0016571	15	5.32E-01	1.00E+00	3.70E-02	1.00E+00	7.30E-01	1.00E+00	1.46E-02	2.81E-01	4.79E-01	1.00E+00	1.75E-01	1.00E+00	5.32E-01	1.00E+00	1.24E-02	1.38E-01	histone methylation	P
GO:0016573	14	8.42E-02	1.00E+00	2.64E-01	1.00E+00	2.58E-01	1.00E+00	2.97E-01	1.00E+00	6.95E-02	1.00E+00	3.07E-01	1.00E+00	4.30E-01	1.00E+00	4.95E-01	1.00E+00	histone acetylation	P
GO:0016575	14	5.89E-02	1.00E+00	3.30E-01	1.00E+00	8.48E-03	1.57E-01	4.42E-01	1.00E+00	1.90E-01	1.00E+00	2.50E-01	1.00E+00	8.80E-01	1.00E+00	9.21E-01	1.00E+00	histone deacetylation	P
GO:0016585	30	1.56E-02	3.10E-01	7.41E-03	3.40E-01	8.11E-02	1.00E+00	1.63E-01	1.00E+00	1.33E-02	3.01E-01	5.26E-03	7.40E-02	3.79E-01	1.00E+00	2.50E-01	1.00E+00	chromatin remodeling complex	C
GO:0016591	96	1.01E-02	1.77E-01	1.23E-04	4.00E-03	2.27E-03	1.80E-02	2.19E-02	4.10E-01	7.24E-02	1.00E+00	3.23E-05	2.29E-03	4.19E-01	1.00E+00	2.82E-01	1.00E+00	DNA-directed RNA polymerase II, holoenzy	C
GO:0016597	19	9.45E-01	1.00E+00	8.29E-01	1.00E+00	5.77E-01	1.00E+00	8.25E-01	1.00E+00	9.60E-01	1.00E+00	9.20E-01	1.00E+00	9.11E-01	1.00E+00	4.19E-01	1.00E+00	amino acid binding	F
GO:0016599	19	1.25E-01	1.00E+00	8.41E-01	1.00E+00	2.04E-01	1.00E+00	7.12E-01	1.00E+00	1.55E-01	1.00E+00	9.23E-01	1.00E+00	5.05E-01	1.00E+00	4.65E-01	1.00E+00	caveolar membrane	C
GO:0016600	12	5.55E-02	1.00E+00	9.12E-01	1.00E+00	1.64E-01	1.00E+00	7.45E-01	1.00E+00	6.92E-02	1.00E+00	9.74E-01	1.00E+00	4.71E-01	1.00E+00	5.26E-01	1.00E+00	flotillin complex	C
GO:0016601	14	2.97E-01	1.00E+00	6.86E-01	1.00E+00	2.86E-01	1.00E+00	6.34E-01	1.00E+00	2.62E-01	1.00E+00	6.39E-01	1.00E+00	5.56E-01	1.00E+00	7.41E-01	1.00E+00	Rac protein signal transduction	P
GO:0016604	124	8.37E-03	1.56E-01	4.95E-05	4.00E-03	3.74E-03	3.50E-02	5.94E-04	7.17E-03	7.79E-02	1.00E+00	3.28E-04	1.02E-02	1.05E-01	1.00E+00	2.00E-02	1.77E-01	nuclear body	C
GO:0016605	23	5.99E-02	1.00E+00	4.36E-02	1.00E+00	1.02E-02	1.57E-01	1.14E-01	1.00E+00	9.09E-02	1.00E+00	3.78E-02	1.00E+00	5.79E-01	1.00E+00	2.92E-01	1.00E+00	PML body	C
GO:0016607	85	1.18E-01	1.00E+00	9.73E-03	3.84E-01	2.87E-02	5.65E-01	9.35E-03	1.12E-01	4.43E-01	1.00E+00	2.32E-02	7.69E-01	1.26E-01	1.00E+00	1.25E-01	1.00E+00	nuclear speck	C
GO:0016614	151	8.98E-01	1.00E+00	8.70E-01	1.00E+00	2.72E-01	1.00E+00	2.98E-01	1.00E+00	9.83E-01	1.00E+00	7.70E-01	1.00E+00	9.19E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on CH-OH g	F
GO:0016616	134	8.33E-01	1.00E+00	9.44E-01	1.00E+00	2.68E-01	1.00E+00	5.22E-01	1.00E+00	9.60E-01	1.00E+00	8.46E-01	1.00E+00	8.31E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on the CH-O	F
GO:0016620	23	1.12E-01	1.00E+00	2.63E-01	1.00E+00	2.04E-01	1.00E+00	7.65E-02	1.00E+00	7.99E-02	1.00E+00	2.39E-01	1.00E+00	3.60E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016627	93	1.96E-01	1.00E+00	7.12E-02	1.00E+00	1.66E-01	1.00E+00	3.41E-01	1.00E+00	2.17E-01	1.00E+00	3.95E-02	1.00E+00	8.75E-01	1.00E+00	6.62E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016628	59	6.88E-01	1.00E+00	3.02E-01	1.00E+00	3.74E-01	1.00E+00	3.15E-01	1.00E+00	7.69E-01	1.00E+00	2.28E-01	1.00E+00	7.92E-01	1.00E+00	8.96E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016634	10	6.19E-01	1.00E+00	4.56E-01	1.00E+00	5.12E-01	1.00E+00	9.89E-01	1.00E+00	6.76E-01	1.00E+00	3.63E-01	1.00E+00	5.11E-01	1.00E+00	3.31E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016638	16	8.60E-01	1.00E+00	6.91E-01	1.00E+00	4.58E-01	1.00E+00	2.95E-01	1.00E+00	9.10E-01	1.00E+00	8.04E-01	1.00E+00	8.13E-01	1.00E+00	9.65E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016641	14	9.00E-01	1.00E+00	8.67E-01	1.00E+00	6.20E-01	1.00E+00	3.44E-01	1.00E+00	9.11E-01	1.00E+00	9.62E-01	1.00E+00	8.49E-01	1.00E+00	9.94E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016645	29	2.86E-01	1.00E+00	3.71E-01	1.00E+00	1.75E-01	1.00E+00	6.98E-02	1.00E+00	5.16E-01	1.00E+00	4.20E-01	1.00E+00	6.72E-01	1.00E+00	9.86E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016646	19	6.29E-01	1.00E+00	4.38E-01	1.00E+00	5.57E-01	1.00E+00	1.95E-01	1.00E+00	9.01E-01	1.00E+00	4.78E-01	1.00E+00	4.60E-01	1.00E+00	9.46E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016651	74	4.68E-02	1.00E+00	4.49E-02	1.00E+00	3.71E-01	1.00E+00	2.66E-02	4.10E-01	1.85E-02	3.81E-01	9.30E-02	1.00E+00	4.96E-01	1.00E+00	3.44E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016652	10	3.18E-01	1.00E+00	2.91E-01	1.00E+00	5.63E-01	1.00E+00	2.75E-02	4.10E-01	3.46E-01	1.00E+00	3.71E-01	1.00E+00	1.90E-01	1.00E+00	9.95E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016655	49	1.79E-02	5.62E-01	8.78E-03	3.84E-01	2.83E-01	1.00E+00	2.02E-02	4.10E-01	3.44E-03	6.24E-02	1.94E-02	5.65E-01	7.30E-01	1.00E+00	1.94E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016667	20	8.84E-01	1.00E+00	1.02E-01	1.00E+00	3.65E-01	1.00E+00	7.30E-02	1.00E+00	8.98E-01	1.00E+00	1.41E-01	1.00E+00	9.92E-01	1.00E+00	3.57E-01	1.00E+00	oxidoreductase activity, acting on sulfur gro	F
GO:0016675	28	2.35E-01	1.00E+00	1.49E-01	1.00E+00	9.00E-01	1.00E+00	4.42E-01	1.00E+00	1.43E-01	1.00E+00	1.48E-01	1.00E+00	9.27E-01	1.00E+00	3.06E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016676	28	2.35E-01	1.00E+00	1.49E-01	1.00E+00	9.00E-01	1.00E+00	4.42E-01	1.00E+00	1.43E-01	1.00E+00	1.48E-01	1.00E+00	9.27E-01	1.00E+00	3.06E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016679	12	1.33E-01	1.00E+00	2.25E-01	1.00E+00	2.98E-01	1.00E+00	1.71E-01	1.00E+00	2.15E-01	1.00E+00	3.46E-01	1.00E+00	8.38E-02	1.00E+00	3.44E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F
GO:0016681	12	1.33E-01	1.00E+00	2.25E-01	1.00E+00	2.98E-01	1.00E+00	1.71E-01	1.00E+00	2.15E-01	1.00E+00	3.46E-01	1.00E+00	8.38E-02	1.00E+00	3.44E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F
GO:0016684	47	4.34E-01	1.00E+00	1.00E+00	1.00E+00	1.98E-01	1.00E+00	9.08E-01	1.00E+00	6.10E-01	1.00E+00	9.99E-01	1.00E+00	5.13E-01	1.00E+00	9.99E-01	1.00E+00	oxidoreductase activity, acting on peroxide a	F
GO:0016701	61	1.75E-01	1.00E+00	4.88E-01	1.00E+00	1.03E-01	1.00E+00	5.20E-01	1.00E+00	1.70E-01	1.00E+00	4.77E-01	1.00E+00	9.98E-01	1.00E+00	6.24E-01	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016702	60	1.45E-01	1.00E+00	4.22E-01	1.00E+00	8.97E-02	1.00E+00	4.74E-01	1.00E+00	1.44E-01	1.00E+00	4.16E-01	1.00E+00	9.96E-01	1.00E+00	5.87E-01	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016705	135	9.36E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	9.26E-01	1.00E+00	8.61E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016706	26	5.53E-02	1.00E+00	3.45E-01	1.00E+00	1.24E-01	1.00E+00	1.40E-01	1.00E+00	4.09E-02	1.00E+00	4.85E-01	1.00E+00	8.76E-01	1.00E+00	4.47E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016709	34	6.83E-01	1.00E+00	6.91E-01	1.00E+00	7.30E-01	1.00E+00	4.54E-01	1.00E+00	7.32E-01	1.00E+00	6.59E-01	1.00E+00	3.14E-01	1.00E+00	8.90E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016712	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016740	1836	4.92E-02	1.00E+00	9.05E-04	2.00E-02	5.66E-12	0.00E+00	8.82E-10	0.00E+00	4.65E-01	1.00E+00	4.85E-02	1.00E+00	1.00E+00	1.00E+00	8.34E-01	1.00E+00	transferase activity	F
GO:0016741	185	3.67E-04	1.60E-02	9.55E-05	4.00E-03	3.72E-04	7.18E-03	8.73E-05	3.91E-03	7.60E-03	2.02E-01	2.32E-03	5.10E-02	2.54E-01	1.00E+00	4.69E-02	8.10E-01	transferase activity, transferring one-carbon	F
GO:0016746	203	1.70E-01	1.00E+00	1.27E-01	1.00E+00	2.94E-03	3.50E-02	2.59E-02	4.10E-01	5.86E-01	1.00E+00	3.82E-01	1.00E+00	9.61E-01	1.00E+00	2.74E-01	1.00E+00	transferase activity, transferring acyl groups	F

GO:0016747	189	1.73E-01	1.00E+00	6.61E-02	1.00E+00	3.16E-03	3.50E-02	1.19E-02	1.27E-01	6.53E-01	1.00E+00	2.26E-01	1.00E+00	9.22E-01	1.00E+00	3.51E-01	1.00E+00	transferase activity, transferring groups othe	F
GO:0016755	24	3.78E-01	1.00E+00	9.55E-01	1.00E+00	4.17E-02	5.87E-01	9.69E-01	1.00E+00	5.22E-01	1.00E+00	9.93E-01	1.00E+00	9.98E-01	1.00E+00	2.24E-01	1.00E+00	transferase activity, transferring amino-acyl	F
GO:0016757	250	9.50E-01	1.00E+00	3.64E-01	1.00E+00	7.27E-02	1.00E+00	5.94E-02	1.00E+00	9.83E-01	1.00E+00	4.29E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	transferase activity, transferring glycosyl gro	F
GO:0016758	167	9.81E-01	1.00E+00	4.45E-01	1.00E+00	1.44E-01	1.00E+00	8.18E-02	1.00E+00	9.94E-01	1.00E+00	5.37E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	transferase activity, transferring hexosyl gro	F
GO:0016763	49	1.34E-01	1.00E+00	2.26E-01	1.00E+00	5.76E-02	1.00E+00	4.37E-02	1.00E+00	3.38E-01	1.00E+00	3.09E-01	1.00E+00	8.22E-01	1.00E+00	5.13E-01	1.00E+00	transferase activity, transferring pentosyl gr	F
GO:0016765	48	3.78E-01	1.00E+00	9.66E-01	1.00E+00	3.69E-01	1.00E+00	1.00E-01	1.00E+00	5.53E-01	1.00E+00	9.92E-01	1.00E+00	2.86E-01	1.00E+00	1.00E+00	1.00E+00	transferase activity, transferring alkyl or aryl	F
GO:0016769	31	3.34E-02	1.00E+00	9.23E-02	1.00E+00	1.53E-02	1.92E-01	3.96E-02	1.00E+00	1.42E-01	1.00E+00	1.87E-01	1.00E+00	4.69E-01	1.00E+00	2.44E-01	1.00E+00	transferase activity, transferring nitrogenous	F
GO:0016772	1053	3.05E-01	1.00E+00	2.86E-02	1.00E+00	3.91E-06	9.71E-04	1.79E-05	2.00E-03	5.15E-01	1.00E+00	1.83E-01	1.00E+00	1.00E+00	1.00E+00	8.64E-01	1.00E+00	transferase activity, transferring phosphorus	F
GO:0016773	808	5.99E-01	1.00E+00	4.99E-01	1.00E+00	2.59E-04	6.00E-03	1.99E-03	2.70E-02	7.52E-01	1.00E+00	6.51E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	phosphotransferase activity, alcohol group a	F
GO:0016775	18	5.14E-01	1.00E+00	9.98E-01	1.00E+00	1.49E-01	1.00E+00	9.95E-01	1.00E+00	7.62E-01	1.00E+00	9.88E-01	1.00E+00	4.25E-01	1.00E+00	9.95E-01	1.00E+00	phosphotransferase activity, nitrogenous gr	F
GO:0016776	38	1.99E-01	1.00E+00	9.25E-02	1.00E+00	3.46E-02	5.87E-01	2.63E-03	5.60E-02	3.19E-01	1.00E+00	3.46E-01	1.00E+00	7.55E-01	1.00E+00	5.66E-01	1.00E+00	phosphotransferase activity, phosphate gro	F
GO:0016779	128	3.02E-02	1.00E+00	7.19E-04	1.90E-02	4.90E-03	9.30E-02	2.26E-02	4.10E-01	1.11E-01	1.00E+00	1.39E-02	5.65E-01	7.42E-01	1.00E+00	2.98E-02	2.52E-01	nucleotidyltransferase activity	F
GO:0016780	17	8.19E-01	1.00E+00	2.45E-01	1.00E+00	2.74E-01	1.00E+00	4.65E-02	1.00E+00	8.59E-01	1.00E+00	6.30E-01	1.00E+00	9.95E-01	1.00E+00	4.82E-01	1.00E+00	phosphotransferase activity, for other substi	F
GO:0016782	52	5.48E-01	1.00E+00	3.88E-01	1.00E+00	2.38E-01	1.00E+00	3.57E-01	1.00E+00	4.41E-01	1.00E+00	2.92E-01	1.00E+00	9.71E-01	1.00E+00	8.39E-01	1.00E+00	transferase activity, transferring sulfur-conta	F
GO:0016787	2476	6.42E-02	1.00E+00	6.26E-02	1.00E+00	2.35E-10	0.00E+00	1.58E-07	0.00E+00	7.07E-01	1.00E+00	5.27E-01	1.00E+00	9.64E-01	1.00E+00	9.90E-01	1.00E+00	hydrolase activity	F
GO:0016788	703	5.86E-02	1.00E+00	3.76E-02	1.00E+00	2.49E-05	1.00E-03	2.50E-05	3.91E-03	3.66E-01	1.00E+00	2.98E-01	1.00E+00	7.53E-01	1.00E+00	9.41E-01	1.00E+00	hydrolase activity, acting on ester bonds	F
GO:0016789	147	1.36E-01	1.00E+00	9.02E-01	1.00E+00	4.97E-02	8.68E-01	2.58E-01	1.00E+00	4.10E-01	1.00E+00	9.56E-01	1.00E+00	1.28E-01	1.00E+00	9.62E-01	1.00E+00	carboxylic ester hydrolase activity	F
GO:0016790	89	7.11E-02	1.00E+00	7.51E-05	4.00E-03	5.49E-02	1.00E+00	1.14E-04	7.00E-03	8.86E-02	1.00E+00	6.05E-04	1.02E-02	7.02E-01	1.00E+00	2.02E-01	1.00E+00	thiolester hydrolase activity	F
GO:0016791	266	3.09E-01	1.00E+00	8.99E-02	1.00E+00	4.12E-03	3.50E-02	1.11E-03	1.30E-02	7.03E-01	1.00E+00	3.76E-01	1.00E+00	9.03E-01	1.00E+00	4.95E-01	1.00E+00	phosphoric monoester hydrolase activity	F
GO:0016796	21	5.98E-01	1.00E+00	1.74E-01	1.00E+00	1.59E-01	1.00E+00	2.75E-01	1.00E+00	6.64E-01	1.00E+00	1.08E-01	1.00E+00	9.06E-01	1.00E+00	9.97E-01	1.00E+00	exonuclease activity, active with either ribo-	F
GO:0016798	157	2.14E-01	1.00E+00	7.57E-02	1.00E+00	1.21E-01	1.00E+00	5.47E-02	1.00E+00	4.62E-01	1.00E+00	1.12E-01	1.00E+00	3.04E-01	1.00E+00	7.79E-01	1.00E+00	hydrolase activity, acting on glycosyl bonds	F
GO:0016799	20	3.94E-01	1.00E+00	1.91E-01	1.00E+00	2.78E-01	1.00E+00	4.56E-01	1.00E+00	2.79E-01	1.00E+00	8.77E-02	1.00E+00	9.78E-01	1.00E+00	9.88E-01	1.00E+00	hydrolase activity, hydrolyzing N-glycosyl co	F
GO:0016805	13	4.49E-01	1.00E+00	6.67E-01	1.00E+00	2.12E-01	1.00E+00	8.16E-01	1.00E+00	5.12E-01	1.00E+00	5.12E-01	1.00E+00	8.95E-01	1.00E+00	7.07E-01	1.00E+00	dipeptidase activity	F
GO:0016806	12	2.66E-01	1.00E+00	4.16E-01	1.00E+00	3.01E-01	1.00E+00	4.73E-01	1.00E+00	2.97E-01	1.00E+00	3.29E-01	1.00E+00	4.93E-01	1.00E+00	5.95E-01	1.00E+00	dipeptidyl-peptidase and tripeptidyl-peptidas	F
GO:0016810	123	2.85E-02	1.00E+00	3.38E-01	1.00E+00	3.66E-03	3.50E-02	7.61E-01	1.00E+00	7.58E-02	1.00E+00	1.57E-01	1.00E+00	5.20E-01	1.00E+00	7.06E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016811	58	1.52E-02	3.10E-01	1.79E-01	1.00E+00	1.39E-02	1.92E-01	8.55E-01	1.00E+00	3.84E-02	1.00E+00	7.06E-02	1.00E+00	1.70E-01	1.00E+00	4.26E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016812	11	3.77E-01	1.00E+00	9.94E-01	1.00E+00	7.48E-02	1.00E+00	5.51E-01	1.00E+00	4.68E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016813	15	4.71E-01	1.00E+00	8.40E-01	1.00E+00	5.25E-01	1.00E+00	3.88E-01	1.00E+00	3.27E-01	1.00E+00	8.78E-01	1.00E+00	9.46E-01	1.00E+00	9.49E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016814	32	1.84E-01	1.00E+00	1.32E-01	1.00E+00	2.07E-01	1.00E+00	4.47E-01	1.00E+00	2.51E-01	1.00E+00	7.31E-02	1.00E+00	3.46E-01	1.00E+00	4.04E-01	1.00E+00	hydrolase activity, acting on carbon-nitrogen	F
GO:0016817	785	5.99E-02	1.00E+00	1.62E-03	3.90E-02	4.25E-06	9.71E-04	3.53E-04	7.00E-03	6.03E-01	1.00E+00	3.68E-02	1.00E+00	8.79E-01	1.00E+00	5.40E-01	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016818	783	7.06E-02	1.00E+00	1.90E-03	3.90E-02	5.50E-06	9.71E-04	3.87E-04	7.17E-03	6.34E-01	1.00E+00	4.20E-02	1.00E+00	8.82E-01	1.00E+00	5.39E-01	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016820	140	3.10E-01	1.00E+00	7.88E-01	1.00E+00	1.56E-02	1.92E-01	2.43E-01	1.00E+00	5.15E-01	1.00E+00	7.40E-01	1.00E+00	8.94E-01	1.00E+00	1.00E+00	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016829	167	2.11E-01	1.00E+00	8.03E-01	1.00E+00	1.22E-03	1.25E-02	4.90E-01	1.00E+00	3.31E-01	1.00E+00	8.14E-01	1.00E+00	9.95E-01	1.00E+00	9.76E-01	1.00E+00	lyase activity	F
GO:0016830	45	4.31E-01	1.00E+00	5.29E-01	1.00E+00	2.80E-02	4.97E-01	3.16E-01	1.00E+00	5.19E-01	1.00E+00	5.39E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	carbon-carbon lyase activity	F
GO:0016831	33	6.15E-01	1.00E+00	4.51E-01	1.00E+00	5.94E-02	1.00E+00	3.06E-01	1.00E+00	6.68E-01	1.00E+00	4.77E-01	1.00E+00	1.00E+00	1.00E+00	8.24E-01	1.00E+00	carboxy-lyase activity	F
GO:0016835	59	1.29E-01	1.00E+00	7.24E-01	1.00E+00	1.27E-01	1.00E+00	8.16E-01	1.00E+00	1.48E-01	1.00E+00	5.51E-01	1.00E+00	4.28E-01	1.00E+00	9.60E-01	1.00E+00	carbon-oxygen lyase activity	F
GO:0016836	50	1.03E-01	1.00E+00	5.55E-01	1.00E+00	7.38E-02	1.00E+00	7.92E-01	1.00E+00	1.26E-01	1.00E+00	4.08E-01	1.00E+00	3.68E-01	1.00E+00	8.20E-01	1.00E+00	hydro-lyase activity	F
GO:0016846	16	2.83E-01	1.00E+00	7.46E-01	1.00E+00	9.93E-03	1.57E-01	4.69E-01	1.00E+00	5.04E-01	1.00E+00	7.56E-01	1.00E+00	8.09E-01	1.00E+00	7.60E-01	1.00E+00	carbon-sulfur lyase activity	F
GO:0016849	21	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.50E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	phosphorus-oxygen lyase activity	F
GO:0016853	186	1.92E-01	1.00E+00	1.23E-01	1.00E+00	1.58E-01	1.00E+00	3.73E-02	1.00E+00	4.01E-01	1.00E+00	2.49E-01	1.00E+00	2.21E-01	1.00E+00	4.13E-01	1.00E+00	isomerase activity	F
GO:0016854	17	3.04E-01	1.00E+00	2.58E-01	1.00E+00	3.13E-01	1.00E+00	4.64E-02	1.00E+00	2.48E-01	1.00E+00	6.47E-01	1.00E+00	6.87E-01	1.00E+00	2.73E-01	1.00E+00	racemase and epimerase activity	F
GO:0016857	10	2.46E-01	1.00E+00	1.41E-01	1.00E+00	1.69E-01	1.00E+00	6.62E-02	1.00E+00	2.50E-01	1.00E+00	3.27E-01	1.00E+00	8.49E-01	1.00E+00	2.92E-01	1.00E+00	racemase and epimerase activity, acting on	F
GO:0016859	39	9.45E-02	1.00E+00	7.05E-02	1.00E+00	1.04E-01	1.00E+00	1.13E-01	1.00E+00	3.42E-01	1.00E+00	1.07E-01	1.00E+00	1.61E-01	1.00E+00	5.00E-01	1.00E+00	cis-trans isomerase activity	F
GO:0016860	40	2.65E-01	1.00E+00	1.63E-01	1.00E+00	5.85E-01	1.00E+00	1.07E-01	1.00E+00	1.17E-01	1.00E+00	3.96E-01	1.00E+00	6.02E-01	1.00E+00	2.84E-01	1.00E+00	intramolecular oxidoreductase activity	F
GO:0016861	11	7.38E-01	1.00E+00	8.14E-01	1.00E+00	1.90E-01	1.00E+00	8.03E-01	1.00E+00	7.34E-01	1.00E+00	6.16E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	intramolecular oxidoreductase activity, inter	F
GO:0016862	10	2.99E-01	1.00E+00	3.62E-01	1.00E+00	4.53E-01	1.00E+00	3.96E-01	1.00E+00	2.80E-01	1.00E+00	2.55E-01	1.00E+00	1.68E-01	1.00E+00	8.78E-01	1.00E+00	intramolecular oxidoreductase activity, inter	F
GO:0016863	12	2.09E-01	1.00E+00	1.39E-01	1.00E+00	8.15E-01	1.00E+00	1.61E-01	1.00E+00	8.42E-02	1.00E+00	9.38E-01	1.00E+00	3.55E-01	1.00E+00	9.61E-02	1.00E+00	intramolecular oxidoreductase activity, trans	F
GO:0016866	55	9.02E-01	1.00E+00	9.15E-01	1.00E+00	5.62E-01	1.00E+00	7.68E-01	1.00E+00	9.05E-01	1.00E+00	9.61E-01	1.00E+00	9.37E-01	1.00E+00	4.41E-01	1.00E+00	intramolecular transferase activity	F
GO:0016868	14	7.95E-01	1.00E+00	8.00E-01	1.00E+00	8.57E-01	1.00E+00	5.07E-01	1.00E+00	5.58E-01	1.00E+00	8.14E-01	1.00E+00	9.99E-01	1.00E+00	6.97E-01	1.00E+00	intramolecular transferase activity, phospho	F
GO:0016874	424	2.19E-03	4.90E-02	2.89E-06	1.41E-03	7.47E-07	8.48E-04	3.57E-07	0.00E+00	5.53E-02	1.00E+00	4.72E-04	1.02E-02	3.67E-01	1.00E+00	2.13E-02	1.77E-01	ligase activity	F
GO:0016875	76	2.06E-03	4.90E-02	3.76E-03	6.30E-02	1.16E-02	1.57E-01	1.98E-01	1.00E+00	3.82E-03	6.24E-02	6.59E-03	1.05E-01	1.26E-01	1.00E+00	2.50E-02	2.52E-01	ligase activity, forming carbon-oxygen bond	F
GO:0016876	76	2.06E-03	4.90E-02	3.76E-03	6.30E-02	1.16E-02	1.57E-01	1.98E-01	1.00E+00	3.82E-03	6.24E-02	6.59E-03	1.05E-01	1.26E-01	1.00E+00	2.50E-02	2.52E-01	ligase activity, forming aminoacyl-tRNA and	F
GO:0016877	27	6.51E-01	1.00E+00	6.80E-01	1.00E+00	1.95E-01	1.00E+00	7.15E-01	1.00E+00	7.27E-01	1.00E+00	6.26E-01	1.00E+00	7.55E-01	1.00E+00	6.52E-01	1.00E+00	ligase activity, forming carbon-sulfur bonds	F
GO:0016878	18	8.18E-01	1.00E+00	5.79E-01	1.00E+00	4.88E-01	1.00E+00	8.57E-01	1.00E+00	6.06E-01	1.00E+00	4.62E-01	1.00E+00	1.00E+00	1.00E+00	5.82E-01	1.00E+00	acid-thiol ligase activity	F
GO:0016879	234	3.93E-02	1.00E+00	3.65E-04	1.10E-02	3.48E-04	7.18E-03	2.35E-06	0.00E+00	2.57E-01	1.00E+00	4.76E-03	7.40E-02	3.45E-01	1.00E+00	3.39E-01	1.00E+00	ligase activity, forming carbon-nitrogen bond	F
GO:0016881	195	1.14E-02	2.72E-01	2.90E-04	8.26E-03	3.34E-04	7.18E-03	1.68E-06	0.00E+00	7.18E-02	1.00E+00	5.29E-03	7.40E-02	2.68E-01	1.00E+00	2.09E-01	1.00E+00	acid-amino acid ligase activity	F
GO:0016884	10	4.44E-01	1.00E+00	4.97E-01	1.00E+00	3.52E-01	1.00E+00	7.26E-01	1.00E+00	6.98E-01	1.00E+00	3.53E-01	1.00E+00	1.59E-01	1.00E+00	8.54E-01	1.00E+00	carbon-nitrogen ligase activity, with glutamir	F
GO:0016887	372	2.20E-01	1.00E+00	4.29E-02	1.00E+00	9.00E-03	1.57E-01	6.39E-04	8.43E-03	4.65E-01	1.00E+00	1.03E-01	1.00E+00	7.92E-01	1.00E+00	9.12E-01	1.00E+00	ATPase activity	F
GO:0016891	23	5.21E-01	1.00E+00	1.31E-01	1.00E+00	2.52E-01	1.00E+00	8.76E-02	1.00E+00	5.31E-01	1.00E+00	5.41E-01	1.00E+00	9.80E-01	1.00E+00	9.97E-01	1.00E+00	endoribonuclease activity, producing 5'-pho	F
GO:0016892	15	8.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.13E-01	1.00E+00	9.96E-01	1.00E+00	5.69E-01	1.00E+00	9.95E-01	1.00E+00	endoribonuclease activity, producing 3'-pho	F
GO:0016893	29	3.89E-01	1.00E+00	1.01E-01	1.00E+00	1.66E-01	1.00E+00	7.37E-02	1.00E+00	5.38E-01	1.00E+00	4.68E-01	1.00E+00	8.08E-01	1.00E+00	9.78E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016894	17	5.60E-01	1.00E+00	9.32E-01	1.00E+00	8.03E-01	1.00E+00	9.51E-01	1.00E+00	4.57E-01	1.00E+00	8.41E-01	1.00E+00	3.46E-01	1.00E+00	9.99E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016895	10	8.19E-01	1.00E+00	5.21E-01	1.00E+00	2.91E-01	1.00E+00	9.87E-01	1.00E+00	9.37E-01	1.00E+00	2.80E-01	1.00E+00	9.92E-01	1.00E+00	9.96E-01	1.00E+00	exodeoxyribonuclease activity, producing 5'	F
GO:0016896	12	3.34E-01	1.00E+00	9.55E-02	1.00E+00	7.33E-02	1.00E+00	1.21E-01	1.00E+00	3.88E-01	1.00E+00	7.72E-02	1.00E+00	6.90E-01	1.00E+00	9.62E-01	1.00E+00	exoribonuclease activity, producing 5'-phos	F
GO:0016903	31	1.79E-01	1.00E+00	1.17E-01	1.00E+00	2.37E-01	1.00E+00	5.20E-02	1.00E+00	1.22E-01	1.00E+00	8.95E-02	1.00E+00	4.68E-01	1.00E+00	9.93E-01	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016917	60	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	GABA receptor activity	F
GO:0016918	12	3.82E-01	1.00E+00	6.80E-01	1.00E+00	7.37E-01	1.00E+00	9.54E-01	1.00E+00	1.46E-01	1.00E+00	4.58E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinal binding	F
GO:0016986	19	1.91E-01	1.00E+00	3.24E-03	6.30E-02	9.08E-02	1.00E+00	1.56E-02	2.81E-01	2.88E-01	1.00E+00	9.10E-03	1.43E-01	2.71E-01	1.00E+00	3.01E-01	1.00E+00	transcription initiation factor activity	F
GO:0016998	17	8.76E-01	1.00E+00	8.73E-01	1.00E+00	7.29E-01	1.00E+00	3.28E-01	1.00E+00	8.65E-01	1.00E+00	9.76E-01	1.00E+00	5.34E-01	1.00E+00	4.15E-01	1.00E+00	cell wall catabolism	P
GO:0017015	26	6.75E-01	1.00E+00	2.91E-01	1.00E+00	5.45E-01	1.00E+00	3.60E-01	1.00E+00	5.60E-01	1.00E+00	2.99E-01	1.00E+00	9.95E-01	1.00E+00	3.34E-01	1.00E+00	regulation of transforming growth factor beta	P
GO:0017016	66	6.62E-01	1.00E+00	3.65E-01	1.00E+00	5.95E-01	1.00E+00	1.55E-01	1.00E+00	6.28E-01	1.00E+00	5.84E-01	1.00E+00	6.13E-01	1.00E+00	2.56E-01	1.00E+00	Ras GTPase binding	F
GO:0017017	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.68E-01	1.00E+00	7.03E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	MAP kinase phosphatase activity	F
GO:0017022	19	5.41E-01	1.00E+00	6.17E-01	1.00E+00	1.85E-01	1.00E+00	8.72E-01	1.00E+00	6.01E-01	1.00E+00	4.03E-01	1.00E+00	9.41E-01	1.00E+00	9.51E-01	1.00E+00	myosin binding	F
GO:0017038	128	1.02E-01	1.00E+00	3.77E-02	1.00E+00	5.40E-02	1.00E+00	9.90E-03	1.23E-01	1.42E-01	1.00E+00	6.55E-02	1.00E+00	5.18E-01	1.00E+00	4.78E-01	1.00E+00	protein import	P
GO:0017040	10	7.31E-02	1.00E+00	1.74E-01	1.00E+00	8.65E-02	1.00E+00	4.59E-01	1.00E+00	9.34E-02	1.00E+00	1.59E-01	1.00E+00	1.34E-01	1.00E+00	2.57E-01	1.00E+00	ceramidase activity	F

GO:0017046	12	9.77E-01	1.00E+00	9.57E-01	1.00E+00	7.51E-01	1.00E+00	9.40E-01	1.00E+00	9.87E-01	1.00E+00	9.00E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	peptide hormone binding	F
GO:0017048	28	7.90E-01	1.00E+00	5.64E-01	1.00E+00	5.50E-01	1.00E+00	5.12E-01	1.00E+00	7.92E-01	1.00E+00	5.55E-01	1.00E+00	7.18E-01	1.00E+00	6.60E-01	1.00E+00	Rho GTPase binding	F
GO:0017053	12	4.70E-01	1.00E+00	9.79E-01	1.00E+00	5.70E-01	1.00E+00	8.64E-01	1.00E+00	4.00E-01	1.00E+00	9.63E-01	1.00E+00	5.22E-01	1.00E+00	9.82E-01	1.00E+00	transcriptional repressor complex	C
GO:0017076	2027	8.17E-04	1.60E-02	2.05E-05	2.21E-03	5.63E-11	0.00E+00	5.74E-07	0.00E+00	9.68E-02	1.00E+00	1.56E-03	3.00E-02	8.86E-01	1.00E+00	7.64E-01	1.00E+00	purine nucleotide binding	F
GO:0017111	751	7.85E-02	1.00E+00	3.35E-03	6.30E-02	9.33E-06	9.71E-04	6.80E-04	8.43E-03	6.50E-01	1.00E+00	5.78E-02	1.00E+00	8.59E-01	1.00E+00	5.79E-01	1.00E+00	nucleoside-triphosphatase activity	F
GO:0017124	29	5.07E-01	1.00E+00	7.05E-01	1.00E+00	7.72E-02	1.00E+00	3.12E-01	1.00E+00	8.28E-01	1.00E+00	7.84E-01	1.00E+00	8.51E-01	1.00E+00	7.28E-01	1.00E+00	SH3 domain binding	F
GO:0017127	12	9.91E-01	1.00E+00	5.75E-01	1.00E+00	1.88E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	3.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cholesterol transporter activity	F
GO:0017137	21	5.74E-01	1.00E+00	6.77E-01	1.00E+00	2.44E-01	1.00E+00	3.15E-01	1.00E+00	6.78E-01	1.00E+00	8.22E-01	1.00E+00	7.59E-01	1.00E+00	6.02E-01	1.00E+00	Rab GTPase binding	F
GO:0017148	41	4.20E-01	1.00E+00	4.31E-01	1.00E+00	4.24E-01	1.00E+00	1.30E-01	1.00E+00	4.61E-01	1.00E+00	6.48E-01	1.00E+00	4.51E-01	1.00E+00	3.66E-01	1.00E+00	negative regulation of protein biosynthesis	P
GO:0017153	55	9.96E-01	1.00E+00	8.49E-01	1.00E+00	8.17E-01	1.00E+00	3.06E-01	1.00E+00	9.99E-01	1.00E+00	8.12E-01	1.00E+00	7.98E-01	1.00E+00	9.99E-01	1.00E+00	sodium:dicarboxylate symporter activity	F
GO:0017156	21	5.94E-01	1.00E+00	9.86E-01	1.00E+00	4.63E-01	1.00E+00	9.75E-01	1.00E+00	9.46E-01	1.00E+00	9.92E-01	1.00E+00	6.93E-02	1.00E+00	7.06E-01	1.00E+00	calcium ion-dependent exocytosis	P
GO:0017157	18	3.66E-01	1.00E+00	4.96E-01	1.00E+00	3.63E-01	1.00E+00	2.79E-01	1.00E+00	3.52E-01	1.00E+00	6.76E-01	1.00E+00	9.88E-01	1.00E+00	8.20E-01	1.00E+00	regulation of exocytosis	P
GO:0018024	29	3.50E-02	1.00E+00	3.91E-02	1.00E+00	7.11E-03	1.57E-01	7.69E-02	1.00E+00	5.65E-02	1.00E+00	1.21E-01	1.00E+00	5.74E-01	1.00E+00	2.40E-02	2.52E-01	histone-lysine N-methyltransferase activity	F
GO:0018105	16	3.97E-01	1.00E+00	1.04E-01	1.00E+00	4.83E-01	1.00E+00	7.80E-02	1.00E+00	2.44E-01	1.00E+00	1.20E-01	1.00E+00	9.03E-01	1.00E+00	3.00E-01	1.00E+00	peptidyl-serine phosphorylation	P
GO:0018108	68	9.82E-01	1.00E+00	9.71E-01	1.00E+00	5.19E-01	1.00E+00	9.30E-01	1.00E+00	9.71E-01	1.00E+00	8.23E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptidyl-tyrosine phosphorylation	P
GO:0018149	18	9.90E-01	1.00E+00	1.00E+00	1.00E+00	4.76E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	peptide cross-linking	P
GO:0018193	144	6.56E-01	1.00E+00	3.16E-01	1.00E+00	3.13E-02	5.65E-01	2.06E-02	4.10E-01	6.83E-01	1.00E+00	4.05E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	peptidyl-amino acid modification	P
GO:0018205	10	2.29E-01	1.00E+00	1.95E-01	1.00E+00	6.86E-02	1.00E+00	2.05E-01	1.00E+00	3.40E-01	1.00E+00	2.88E-01	1.00E+00	9.99E-01	1.00E+00	2.88E-01	1.00E+00	peptidyl-lysine modification	P
GO:0018209	19	6.34E-01	1.00E+00	1.90E-01	1.00E+00	6.50E-01	1.00E+00	8.47E-02	1.00E+00	4.39E-01	1.00E+00	2.39E-01	1.00E+00	9.57E-01	1.00E+00	4.34E-01	1.00E+00	peptidyl-serine modification	P
GO:0018212	70	9.77E-01	1.00E+00	9.52E-01	1.00E+00	4.74E-01	1.00E+00	8.89E-01	1.00E+00	9.70E-01	1.00E+00	7.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptidyl-tyrosine modification	P
GO:0018298	16	9.12E-01	1.00E+00	1.00E+00	1.00E+00	2.59E-01	1.00E+00	9.95E-01	1.00E+00	8.07E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	protein-chromophore linkage	P
GO:0018958	77	9.86E-01	1.00E+00	6.00E-01	1.00E+00	5.51E-01	1.00E+00	2.99E-01	1.00E+00	9.92E-01	1.00E+00	4.48E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	phenol metabolism	P
GO:0019001	407	1.31E-01	1.00E+00	1.76E-01	1.00E+00	8.34E-04	1.25E-02	3.96E-02	1.00E+00	6.11E-01	1.00E+00	5.09E-01	1.00E+00	8.27E-01	1.00E+00	7.77E-01	1.00E+00	guanyl nucleotide binding	F
GO:0019012	15	1.00E+00	1.00E+00	9.63E-01	1.00E+00	5.58E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	2.44E-01	1.00E+00	virion	C
GO:0019028	15	1.00E+00	1.00E+00	9.63E-01	1.00E+00	5.58E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	2.44E-01	1.00E+00	viral capsid	C
GO:0019048	14	5.93E-01	1.00E+00	7.51E-01	1.00E+00	5.49E-01	1.00E+00	8.93E-01	1.00E+00	4.02E-01	1.00E+00	6.35E-01	1.00E+00	1.00E+00	1.00E+00	7.10E-01	1.00E+00	virus-host interaction	P
GO:0019058	55	9.31E-01	1.00E+00	9.94E-01	1.00E+00	8.60E-01	1.00E+00	9.79E-01	1.00E+00	7.59E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	8.26E-01	1.00E+00	viral infectious cycle	P
GO:0019059	21	8.31E-01	1.00E+00	6.42E-01	1.00E+00	4.58E-01	1.00E+00	6.59E-01	1.00E+00	8.27E-01	1.00E+00	7.24E-01	1.00E+00	9.77E-01	1.00E+00	3.82E-01	1.00E+00	initiation of viral infection	P
GO:0019079	30	9.84E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.31E-01	1.00E+00	9.96E-01	1.00E+00	9.98E-01	1.00E+00	5.33E-01	1.00E+00	viral genome replication	P
GO:0019098	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	reproductive behavior	P
GO:0019104	11	1.72E-01	1.00E+00	1.69E-01	1.00E+00	1.86E-01	1.00E+00	5.79E-01	1.00E+00	1.53E-01	1.00E+00	5.77E-02	1.00E+00	7.00E-01	1.00E+00	1.00E+00	1.00E+00	DNA N-glycosylase activity	F
GO:0019198	18	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.26E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor protein phosphata	F
GO:0019199	139	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor protein kinase acti	F
GO:0019200	31	6.10E-01	1.00E+00	4.81E-02	1.00E+00	1.32E-01	1.00E+00	9.17E-03	1.12E-01	7.56E-01	1.00E+00	8.85E-02	1.00E+00	9.99E-01	1.00E+00	3.65E-01	1.00E+00	carbohydrate kinase activity	F
GO:0019201	23	5.09E-01	1.00E+00	1.83E-01	1.00E+00	5.34E-02	1.00E+00	1.12E-02	1.27E-01	7.31E-01	1.00E+00	4.58E-01	1.00E+00	9.65E-01	1.00E+00	5.74E-01	1.00E+00	nucleotide kinase activity	F
GO:0019205	52	5.75E-01	1.00E+00	1.22E-01	1.00E+00	6.25E-02	1.00E+00	3.46E-03	5.60E-02	6.48E-01	1.00E+00	3.53E-01	1.00E+00	9.97E-01	1.00E+00	8.81E-01	1.00E+00	nucleobase, nucleoside, nucleotide kinase a	F
GO:0019206	15	9.34E-01	1.00E+00	8.98E-02	1.00E+00	1.63E-01	1.00E+00	1.54E-02	2.81E-01	9.81E-01	1.00E+00	2.11E-01	1.00E+00	9.79E-01	1.00E+00	6.26E-01	1.00E+00	nucleoside kinase activity	F
GO:0019207	101	9.62E-01	1.00E+00	9.97E-01	1.00E+00	6.87E-01	1.00E+00	9.95E-01	1.00E+00	9.38E-01	1.00E+00	9.97E-01	1.00E+00	9.91E-01	1.00E+00	8.84E-01	1.00E+00	kinase regulator activity	F
GO:0019208	58	5.61E-01	1.00E+00	8.90E-01	1.00E+00	2.59E-01	1.00E+00	1.92E-01	1.00E+00	5.02E-01	1.00E+00	9.71E-01	1.00E+00	9.24E-01	1.00E+00	8.79E-01	1.00E+00	phosphatase regulator activity	F
GO:0019209	18	9.45E-01	1.00E+00	9.25E-01	1.00E+00	4.07E-01	1.00E+00	8.47E-01	1.00E+00	9.85E-01	1.00E+00	9.14E-01	1.00E+00	9.17E-01	1.00E+00	9.09E-01	1.00E+00	kinase activator activity	F
GO:0019210	31	7.79E-01	1.00E+00	9.79E-01	1.00E+00	4.03E-01	1.00E+00	8.87E-01	1.00E+00	7.17E-01	1.00E+00	9.71E-01	1.00E+00	9.89E-01	1.00E+00	8.28E-01	1.00E+00	kinase inhibitor activity	F
GO:0019212	30	5.44E-01	1.00E+00	9.10E-01	1.00E+00	2.28E-01	1.00E+00	3.77E-01	1.00E+00	4.83E-01	1.00E+00	9.79E-01	1.00E+00	9.75E-01	1.00E+00	9.09E-01	1.00E+00	phosphatase inhibitor activity	F
GO:0019213	23	4.32E-02	1.00E+00	2.36E-01	1.00E+00	4.57E-02	8.68E-01	6.03E-01	1.00E+00	6.51E-02	1.00E+00	1.44E-01	1.00E+00	3.86E-01	1.00E+00	4.94E-01	1.00E+00	deacetylase activity	F
GO:0019216	53	4.74E-01	1.00E+00	6.44E-01	1.00E+00	1.41E-01	1.00E+00	2.88E-01	1.00E+00	5.09E-01	1.00E+00	5.79E-01	1.00E+00	9.51E-01	1.00E+00	9.97E-01	1.00E+00	regulation of lipid metabolism	P
GO:0019217	24	2.73E-01	1.00E+00	4.16E-01	1.00E+00	1.55E-01	1.00E+00	1.58E-01	1.00E+00	2.86E-01	1.00E+00	3.80E-01	1.00E+00	8.33E-01	1.00E+00	9.76E-01	1.00E+00	regulation of fatty acid metabolism	P
GO:0019218	18	6.52E-01	1.00E+00	7.43E-01	1.00E+00	2.27E-01	1.00E+00	3.86E-01	1.00E+00	7.04E-01	1.00E+00	6.94E-01	1.00E+00	9.10E-01	1.00E+00	9.46E-01	1.00E+00	regulation of steroid metabolism	P
GO:0019219	2681	9.92E-01	1.00E+00	7.48E-05	4.00E-03	2.97E-02	5.65E-01	3.57E-08	0.00E+00	9.93E-01	1.00E+00	3.17E-03	6.40E-02	1.00E+00	1.00E+00	6.77E-01	1.00E+00	regulation of nucleobase, nucleoside, nucle	P
GO:0019220	125	9.43E-01	1.00E+00	9.98E-01	1.00E+00	2.34E-01	1.00E+00	9.97E-01	1.00E+00	9.87E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	9.73E-01	1.00E+00	regulation of phosphate metabolism	P
GO:0019221	45	9.98E-01	1.00E+00	9.92E-01	1.00E+00	8.87E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	cytokine and chemokine mediated signaling	P
GO:0019222	3117	9.70E-01	1.00E+00	9.58E-05	4.00E-03	5.78E-03	9.30E-02	1.14E-08	0.00E+00	9.73E-01	1.00E+00	3.73E-03	7.40E-02	1.00E+00	1.00E+00	7.86E-01	1.00E+00	regulation of metabolism	P
GO:0019226	346	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmission of nerve impulse	P
GO:0019229	20	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	regulation of vasoconstriction	P
GO:0019233	24	9.74E-01	1.00E+00	9.54E-01	1.00E+00	9.87E-01	1.00E+00	3.71E-01	1.00E+00	9.40E-01	1.00E+00	9.65E-01	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	sensory perception of pain	P
GO:0019239	28	4.86E-01	1.00E+00	5.80E-01	1.00E+00	3.41E-01	1.00E+00	4.82E-01	1.00E+00	6.13E-01	1.00E+00	4.06E-01	1.00E+00	4.11E-01	1.00E+00	9.91E-01	1.00E+00	deaminase activity	F
GO:0019290	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	siderophore biosynthesis	P
GO:0019318	173	7.13E-02	1.00E+00	5.35E-02	1.00E+00	1.38E-02	1.92E-01	8.54E-02	1.00E+00	1.07E-01	1.00E+00	6.51E-02	1.00E+00	8.21E-01	1.00E+00	4.17E-01	1.00E+00	hexose metabolism	P
GO:0019319	32	8.70E-01	1.00E+00	7.16E-01	1.00E+00	5.34E-01	1.00E+00	5.44E-01	1.00E+00	7.02E-01	1.00E+00	6.52E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	hexose biosynthesis	P
GO:0019320	81	1.58E-02	3.10E-01	5.16E-03	1.31E-01	7.27E-03	1.57E-01	5.74E-02	1.00E+00	3.26E-02	6.55E-01	9.51E-03	1.43E-01	6.54E-01	1.00E+00	5.97E-02	1.00E+00	hexose catabolism	P
GO:0019321	10	2.82E-01	1.00E+00	2.17E-01	1.00E+00	7.48E-02	1.00E+00	2.00E-01	1.00E+00	4.88E-01	1.00E+00	2.65E-01	1.00E+00	7.61E-01	1.00E+00	3.81E-01	1.00E+00	pentose metabolism	P
GO:0019362	31	5.18E-02	1.00E+00	1.10E-01	1.00E+00	3.33E-02	5.87E-01	1.55E-01	1.00E+00	8.27E-02	1.00E+00	1.21E-01	1.00E+00	2.62E-01	1.00E+00	2.02E-01	1.00E+00	pyridine nucleotide metabolism	P
GO:0019363	13	3.09E-01	1.00E+00	2.50E-01	1.00E+00	3.69E-01	1.00E+00	4.18E-01	1.00E+00	2.62E-01	1.00E+00	2.10E-01	1.00E+00	4.95E-01	1.00E+00	4.53E-01	1.00E+00	pyridine nucleotide biosynthesis	P
GO:0019370	19	7.66E-01	1.00E+00	5.20E-01	1.00E+00	8.86E-01	1.00E+00	7.33E-01	1.00E+00	6.38E-01	1.00E+00	4.86E-01	1.00E+00	6.92E-01	1.00E+00	4.39E-01	1.00E+00	leukotriene biosynthesis	P
GO:0019395	38	7.21E-02	1.00E+00	1.08E-01	1.00E+00	4.12E-02	5.87E-01	4.44E-02	1.00E+00	1.50E-01	1.00E+00	1.74E-01	1.00E+00	4.29E-01	1.00E+00	4.53E-01	1.00E+00	fatty acid oxidation	P
GO:0019438	55	8.56E-01	1.00E+00	2.82E-01	1.00E+00	4.96E-01	1.00E+00	3.04E-01	1.00E+00	9.26E-01	1.00E+00	2.07E-01	1.00E+00	7.51E-01	1.00E+00	9.40E-01	1.00E+00	aromatic compound biosynthesis	P
GO:0019439	19	1.14E-01	1.00E+00	3.48E-01	1.00E+00	8.33E-02	1.00E+00	7.55E-01	1.00E+00	1.31E-01	1.00E+00	3.10E-01	1.00E+00	6.18E-01	1.00E+00	3.62E-01	1.00E+00	aromatic compound catabolism	P
GO:0019538	3650	1.51E-02	3.10E-01	9.81E-04	2.00E-02	1.34E-07	0.00E+00	1.36E-09	0.00E+00	2.02E-01	1.00E+00	5.01E-02	1.00E+00	9.00E-01	1.00E+00	7.71E-01	1.00E+00	protein metabolism	P
GO:0019540	44	8.38E-01	1.00E+00	2.51E-01	1.00E+00	4.51E-01	1.00E+00	4.08E-01	1.00E+00	8.89E-01	1.00E+00	1.50E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	siderophore biosynthesis from catechol	P
GO:0019674	14	1.11E-01	1.00E+00	1.12E-01	1.00E+00	1.10E-01	1.00E+00	2.35E-01	1.00E+00	1.14E-01	1.00E+00	9.16E-02	1.00E+00	2.84E-01	1.00E+00	1.82E-01	1.00E+00	NAD metabolism	P
GO:0019717	53	8.47E-01	1.00E+00	4.69E-01	1.00E+00	8.70E-01	1.00E+00	2.72E-01	1.00E+00	6.10E-01	1.00E+00	5.11E-01	1.00E+00	9.72E-01	1.00E+00	9.76E-01	1.00E+00	synaptosome	C
GO:0019722	47	8.58E-01	1.00E+00	7.24E-01	1.00E+00	5.42E-01	1.00E+00	6.90E-01	1.00E+00	8.83E-01	1.00E+00	5.89E-01	1.00E+00	9.98E-01	1.00E+00	8.45E-01	1.00E+00	calcium-mediated signaling	P
GO:0019724	115	9.95E-01	1.00E+00	9.98E-01	1.00E+00	8.76E-01	1.00E+00	9.39E-01	1.00E+00	9.89E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	B cell mediated immunity	P
GO:0019725	307	3.56E-01	1.00E+00	9.93E-01	1.00E+00	1.70E-02	2.36E-01	9.40E-01	1.00E+00	4.99E-01	1.00E+00	9.67E-01	1.00E+00	9.28E-01	1.00E+00	9.97E-01	1.00E+00	cell homeostasis	P
GO:0019748	96	5.74E-01	1.00E+00	8.43E-02	1.00E+00	1.17E-01	1.00E+00	3.38E-01	1.00E+00	6.66E-01	1.00E+00	5.75E-02	1.00E+00	9.54E-01	1.00E+00	5.73E-01	1.00E+00	secondary metabolism	P
GO:0019751	38	8.42E-01	1.00E+00	3.89E-01	1.00E+00	5.17E-01	1.00E+00	2.36E-01	1.00E+00	9.34E-01	1.00E+00	3.19E-01	1.00E+00	6.49E-01	1.00E+00	9.90E-01	1.00E+00	polyol metabolism	P
GO:0019752	676	2.12E-01	1.00E+00	2.50E-01	1.00E+00	1.68E-04	4.57E-03	1.67E-01	1.00E+00	5.06E-01	1.00E+00	1.95E-01	1.00E+00	9.96E-01	1.00E+00	9.08E-01	1.00E+00	carboxylic acid metabolism	P

GO:0019783	68	1.50E-01	1.00E+00	4.46E-04	1.90E-02	7.22E-03	1.57E-01	4.85E-06	8.32E-04	2.78E-01	1.00E+00	1.07E-02	2.12E-01	8.55E-01	1.00E+00	2.10E-02	1.77E-01	small conjugating protein-specific protease	F
GO:0019787	174	3.58E-02	1.00E+00	5.28E-04	1.90E-02	7.13E-04	1.25E-02	5.64E-06	8.32E-04	1.75E-01	1.00E+00	7.12E-03	1.05E-01	3.39E-01	1.00E+00	1.78E-01	1.00E+00	small conjugating protein ligase activity	F
GO:0019825	36	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen binding	F
GO:0019827	13	9.79E-01	1.00E+00	6.29E-01	1.00E+00	6.48E-01	1.00E+00	9.46E-01	1.00E+00	9.76E-01	1.00E+00	3.90E-01	1.00E+00	1.00E+00	1.00E+00	8.85E-01	1.00E+00	stem cell maintenance	P
GO:0019829	47	4.07E-02	1.00E+00	2.08E-01	1.00E+00	3.96E-02	5.87E-01	8.36E-02	1.00E+00	1.27E-01	1.00E+00	2.75E-01	1.00E+00	3.24E-01	1.00E+00	8.83E-01	1.00E+00	cation-transporting ATPase activity	F
GO:0019835	25	8.72E-01	1.00E+00	8.86E-01	1.00E+00	8.80E-01	1.00E+00	8.20E-01	1.00E+00	8.54E-01	1.00E+00	8.54E-01	1.00E+00	7.78E-01	1.00E+00	8.90E-01	1.00E+00	cytolysis	P
GO:0019838	101	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	growth factor binding	F
GO:0019840	17	6.32E-01	1.00E+00	9.06E-01	1.00E+00	8.81E-01	1.00E+00	9.98E-01	1.00E+00	2.82E-01	1.00E+00	6.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	isoprenoid binding	F
GO:0019841	12	4.38E-01	1.00E+00	6.80E-01	1.00E+00	7.37E-01	1.00E+00	9.54E-01	1.00E+00	1.98E-01	1.00E+00	4.58E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinol binding	F
GO:0019842	149	7.93E-02	1.00E+00	1.87E-01	1.00E+00	3.65E-03	3.50E-02	2.61E-01	1.00E+00	7.86E-02	1.00E+00	1.65E-01	1.00E+00	9.98E-01	1.00E+00	6.14E-01	1.00E+00	vitamin binding	F
GO:0019843	22	2.27E-01	1.00E+00	8.00E-01	1.00E+00	6.19E-01	1.00E+00	1.61E-01	1.00E+00	1.99E-01	1.00E+00	9.02E-01	1.00E+00	3.30E-01	1.00E+00	8.26E-01	1.00E+00	rRNA binding	F
GO:0019861	79	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.92E-01	1.00E+00	9.45E-01	1.00E+00	9.80E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	flagellum	C
GO:0019865	16	7.02E-01	1.00E+00	6.04E-01	1.00E+00	9.95E-01	1.00E+00	6.06E-01	1.00E+00	5.84E-01	1.00E+00	7.54E-01	1.00E+00	3.25E-01	1.00E+00	2.06E-01	1.00E+00	immunoglobulin binding	F
GO:0019866	306	8.80E-04	1.60E-02	5.96E-04	1.90E-02	9.35E-04	1.25E-02	1.49E-03	1.80E-02	6.54E-03	1.48E-01	2.07E-03	5.10E-02	2.03E-01	1.00E+00	2.76E-01	1.00E+00	organelle inner membrane	C
GO:0019867	92	2.38E-01	1.00E+00	4.28E-02	1.00E+00	1.10E-01	1.00E+00	9.68E-02	1.00E+00	6.38E-01	1.00E+00	1.48E-01	1.00E+00	7.77E-02	1.00E+00	1.54E-01	1.00E+00	outer membrane	C
GO:0019882	121	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation	P
GO:0019883	14	9.42E-01	1.00E+00	8.01E-01	1.00E+00	9.68E-01	1.00E+00	9.95E-01	1.00E+00	7.90E-01	1.00E+00	4.86E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation of end	P
GO:0019884	10	9.96E-01	1.00E+00	5.97E-01	1.00E+00	1.00E+00	1.00E+00	6.92E-01	1.00E+00	7.69E-01	1.00E+00	4.06E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019885	12	9.15E-01	1.00E+00	7.40E-01	1.00E+00	8.89E-01	1.00E+00	9.72E-01	1.00E+00	7.45E-01	1.00E+00	4.84E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	antigen processing and presentation of end	P
GO:0019887	83	9.97E-01	1.00E+00	1.00E+00	1.00E+00	8.68E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.83E-01	1.00E+00	protein kinase regulator activity	F
GO:0019888	56	5.06E-01	1.00E+00	8.65E-01	1.00E+00	2.34E-01	1.00E+00	1.91E-01	1.00E+00	4.43E-01	1.00E+00	9.59E-01	1.00E+00	9.16E-01	1.00E+00	8.62E-01	1.00E+00	protein phosphatase regulator activity	F
GO:0019897	42	6.64E-01	1.00E+00	8.01E-01	1.00E+00	5.74E-01	1.00E+00	9.97E-01	1.00E+00	6.14E-01	1.00E+00	6.00E-01	1.00E+00	6.82E-01	1.00E+00	7.18E-01	1.00E+00	extrinsic to plasma membrane	C
GO:0019898	81	6.99E-01	1.00E+00	8.26E-01	1.00E+00	2.61E-01	1.00E+00	8.05E-01	1.00E+00	6.84E-01	1.00E+00	7.25E-01	1.00E+00	9.79E-01	1.00E+00	9.24E-01	1.00E+00	extrinsic to membrane	C
GO:0019899	295	1.31E-01	1.00E+00	2.50E-01	1.00E+00	1.27E-02	1.92E-01	5.92E-02	1.00E+00	2.32E-01	1.00E+00	4.15E-01	1.00E+00	8.89E-01	1.00E+00	5.75E-01	1.00E+00	enzyme binding	F
GO:0019900	104	4.74E-01	1.00E+00	5.17E-01	1.00E+00	2.15E-01	1.00E+00	3.30E-01	1.00E+00	5.07E-01	1.00E+00	4.87E-01	1.00E+00	9.65E-01	1.00E+00	8.61E-01	1.00E+00	kinase binding	F
GO:0019901	87	2.29E-01	1.00E+00	4.07E-01	1.00E+00	1.31E-01	1.00E+00	3.97E-01	1.00E+00	2.64E-01	1.00E+00	3.58E-01	1.00E+00	9.00E-01	1.00E+00	6.82E-01	1.00E+00	protein kinase binding	F
GO:0019902	21	8.90E-01	1.00E+00	6.30E-01	1.00E+00	2.98E-01	1.00E+00	2.75E-01	1.00E+00	9.69E-01	1.00E+00	7.76E-01	1.00E+00	7.89E-01	1.00E+00	5.09E-01	1.00E+00	phosphatase binding	F
GO:0019903	16	9.59E-01	1.00E+00	5.35E-01	1.00E+00	5.60E-01	1.00E+00	3.16E-01	1.00E+00	9.81E-01	1.00E+00	6.55E-01	1.00E+00	8.25E-01	1.00E+00	4.03E-01	1.00E+00	protein phosphatase binding	F
GO:0019904	160	2.86E-01	1.00E+00	5.72E-01	1.00E+00	8.97E-02	1.00E+00	1.63E-01	1.00E+00	3.39E-01	1.00E+00	6.00E-01	1.00E+00	7.67E-01	1.00E+00	8.87E-01	1.00E+00	protein domain specific binding	F
GO:0019905	24	9.91E-01	1.00E+00	1.00E+00	1.00E+00	3.91E-01	1.00E+00	5.74E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	syntaxin binding	F
GO:0019915	12	2.34E-01	1.00E+00	5.58E-01	1.00E+00	1.00E-02	1.57E-01	7.25E-01	1.00E+00	2.69E-01	1.00E+00	4.83E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	sequestering of lipid	P
GO:0019932	263	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	7.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	second-messenger-mediated signaling	P
GO:0019933	96	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cAMP-mediated signaling	P
GO:0019935	125	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	8.30E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cyclic-nucleotide-mediated signaling	P
GO:0019941	221	7.12E-03	1.37E-01	1.61E-05	2.21E-03	2.41E-02	4.97E-01	3.05E-08	0.00E+00	6.11E-02	1.00E+00	9.95E-04	1.02E-02	5.91E-01	1.00E+00	6.07E-02	1.00E+00	modification-dependent protein catabolism	P
GO:0019953	379	9.02E-01	1.00E+00	4.84E-01	1.00E+00	5.59E-01	1.00E+00	2.36E-01	1.00E+00	8.52E-01	1.00E+00	4.63E-01	1.00E+00	9.87E-01	1.00E+00	8.73E-01	1.00E+00	sexual reproduction	P
GO:0019955	137	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.64E-01	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cytokine binding	F
GO:0019956	58	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	7.56E-01	1.00E+00	9.88E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	chemokine binding	F
GO:0019957	40	9.81E-01	1.00E+00	9.82E-01	1.00E+00	9.35E-01	1.00E+00	5.23E-01	1.00E+00	8.82E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	C-C chemokine binding	F
GO:0019958	36	9.99E-01	1.00E+00	9.88E-01	1.00E+00	9.80E-01	1.00E+00	5.54E-01	1.00E+00	9.86E-01	1.00E+00	9.80E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	C-X-C chemokine binding	F
GO:0019959	10	9.99E-01	1.00E+00	4.62E-01	1.00E+00	7.94E-01	1.00E+00	5.66E-01	1.00E+00	1.00E+00	1.00E+00	3.78E-01	1.00E+00	6.06E-01	1.00E+00	9.50E-01	1.00E+00	interleukin-8 binding	F
GO:0019965	67	8.13E-01	1.00E+00	9.96E-01	1.00E+00	7.49E-01	1.00E+00	9.96E-01	1.00E+00	6.88E-01	1.00E+00	9.36E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	interleukin binding	F
GO:0019966	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	interleukin-1 binding	F
GO:0019992	65	2.14E-01	1.00E+00	3.06E-01	1.00E+00	1.91E-01	1.00E+00	1.08E-01	1.00E+00	3.72E-01	1.00E+00	2.92E-01	1.00E+00	2.36E-01	1.00E+00	8.96E-01	1.00E+00	diacylglycerol binding	F
GO:0020037	166	9.72E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.30E-01	1.00E+00	1.00E+00	1.00E+00	heme binding	F
GO:0021510	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	spinal cord development	P
GO:0021515	22	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell differentiation in spinal cord	P
GO:0021516	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	dorsal spinal cord development	P
GO:0021517	13	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.36E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ventral spinal cord development	P
GO:0021522	11	9.89E-01	1.00E+00	1.00E+00	1.00E+00	8.54E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	spinal cord motor neuron differentiation	P
GO:0021536	22	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.38E-01	1.00E+00	9.93E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	diencephalon development	P
GO:0021537	36	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	7.26E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	6.94E-01	1.00E+00	9.97E-01	1.00E+00	telencephalon development	P
GO:0021543	25	9.58E-01	1.00E+00	8.48E-01	1.00E+00	9.52E-01	1.00E+00	4.25E-01	1.00E+00	9.76E-01	1.00E+00	8.86E-01	1.00E+00	6.11E-01	1.00E+00	9.12E-01	1.00E+00	pallium development	P
GO:0021545	10	8.27E-01	1.00E+00	9.88E-01	1.00E+00	9.80E-01	1.00E+00	9.56E-01	1.00E+00	8.07E-01	1.00E+00	9.80E-01	1.00E+00	8.11E-01	1.00E+00	1.00E+00	1.00E+00	cranial nerve development	P
GO:0021549	17	9.22E-01	1.00E+00	1.00E+00	1.00E+00	7.33E-01	1.00E+00	9.39E-01	1.00E+00	9.51E-01	1.00E+00	1.00E+00	1.00E+00	8.72E-01	1.00E+00	9.98E-01	1.00E+00	cerebellum development	P
GO:0021575	12	7.45E-01	1.00E+00	9.75E-01	1.00E+00	5.38E-01	1.00E+00	6.54E-01	1.00E+00	8.33E-01	1.00E+00	9.92E-01	1.00E+00	6.84E-01	1.00E+00	9.24E-01	1.00E+00	hindbrain morphogenesis	P
GO:0021587	11	7.34E-01	1.00E+00	9.69E-01	1.00E+00	5.78E-01	1.00E+00	6.91E-01	1.00E+00	8.02E-01	1.00E+00	9.85E-01	1.00E+00	6.86E-01	1.00E+00	9.46E-01	1.00E+00	cerebellum morphogenesis	P
GO:0021675	15	8.30E-01	1.00E+00	9.96E-01	1.00E+00	7.23E-01	1.00E+00	9.98E-01	1.00E+00	9.42E-01	1.00E+00	9.90E-01	1.00E+00	4.16E-01	1.00E+00	1.00E+00	1.00E+00	nerve development	P
GO:0021695	13	8.11E-01	1.00E+00	9.92E-01	1.00E+00	6.51E-01	1.00E+00	8.05E-01	1.00E+00	8.71E-01	1.00E+00	9.97E-01	1.00E+00	7.21E-01	1.00E+00	9.67E-01	1.00E+00	cerebellar cortex development	P
GO:0021696	11	7.34E-01	1.00E+00	9.69E-01	1.00E+00	5.78E-01	1.00E+00	6.91E-01	1.00E+00	8.02E-01	1.00E+00	9.85E-01	1.00E+00	6.86E-01	1.00E+00	9.46E-01	1.00E+00	cerebellar cortex morphogenesis	P
GO:0021700	84	9.95E-01	1.00E+00	1.00E+00	1.00E+00	3.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	developmental maturation	P
GO:0021761	17	9.87E-01	1.00E+00	8.53E-01	1.00E+00	9.94E-01	1.00E+00	5.31E-01	1.00E+00	9.95E-01	1.00E+00	9.05E-01	1.00E+00	6.93E-01	1.00E+00	8.55E-01	1.00E+00	limbic system development	P
GO:0021766	13	8.64E-01	1.00E+00	5.52E-01	1.00E+00	9.02E-01	1.00E+00	1.88E-01	1.00E+00	9.17E-01	1.00E+00	6.56E-01	1.00E+00	5.42E-01	1.00E+00	6.39E-01	1.00E+00	hippocampus development	P
GO:0021782	13	7.02E-01	1.00E+00	7.70E-01	1.00E+00	2.29E-01	1.00E+00	3.65E-01	1.00E+00	9.86E-01	1.00E+00	9.15E-01	1.00E+00	4.05E-01	1.00E+00	5.51E-01	1.00E+00	glial cell development	P
GO:0021872	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	generation of neurons in the forebrain	P
GO:0021885	10	8.68E-01	1.00E+00	8.51E-01	1.00E+00	8.55E-01	1.00E+00	7.41E-01	1.00E+00	8.70E-01	1.00E+00	7.74E-01	1.00E+00	6.35E-01	1.00E+00	1.00E+00	1.00E+00	forebrain cell migration	P
GO:0021895	10	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cerebral cortex neuron differentiation	P
GO:0021915	48	9.81E-01	1.00E+00	9.86E-01	1.00E+00	9.00E-01	1.00E+00	8.40E-01	1.00E+00	9.53E-01	1.00E+00	9.94E-01	1.00E+00	9.97E-01	1.00E+00	9.18E-01	1.00E+00	neural tube development	P
GO:0021953	26	9.80E-01	1.00E+00	9.91E-01	1.00E+00	8.84E-01	1.00E+00	8.41E-01	1.00E+00	9.98E-01	1.00E+00	9.84E-01	1.00E+00	7.23E-01	1.00E+00	1.00E+00	1.00E+00	central nervous system neuron differentiatic	P
GO:0021954	23	9.99E-01	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	8.37E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	central nervous system neuron developmer	P
GO:0021955	10	9.07E-01	1.00E+00	6.75E-01	1.00E+00	9.67E-01	1.00E+00	6.11E-01	1.00E+00	9.03E-01	1.00E+00	6.04E-01	1.00E+00	7.34E-01	1.00E+00	9.30E-01	1.00E+00	central nervous system neuron axonogenes	P
GO:0021983	18	9.64E-01	1.00E+00	1.00E+00	1.00E+00	6.69E-01	1.00E+00	9.45E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	pituitary gland development	P
GO:0021987	18	6.03E-01	1.00E+00	4.16E-01	1.00E+00	6.88E-01	1.00E+00	1.52E-01	1.00E+00	7.25E-01	1.00E+00	4.55E-01	1.00E+00	2.51E-01	1.00E+00	6.24E-01	1.00E+00	cerebral cortex development	P
GO:0022008	404	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurogenesis	P
GO:0022037	21	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.00E-01	1.00E+00	9.94E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.49E-01	1.00E+00	9.98E-01	1.00E+00	metencephalon development	P

GO:0030001	596	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	metal ion transport	P
GO:0030003	189	6.27E-01	1.00E+00	9.93E-01	1.00E+00	2.11E-02	2.36E-01	9.62E-01	1.00E+00	8.57E-01	1.00E+00	9.63E-01	1.00E+00	9.55E-01	1.00E+00	9.88E-01	1.00E+00	cation homeostasis	P
GO:0030004	18	7.72E-02	1.00E+00	3.02E-01	1.00E+00	4.92E-02	8.68E-01	4.11E-01	1.00E+00	1.26E-01	1.00E+00	2.02E-01	1.00E+00	4.19E-01	1.00E+00	8.10E-01	1.00E+00	monovalent inorganic cation homeostasis	P
GO:0030005	167	7.87E-01	1.00E+00	9.90E-01	1.00E+00	6.20E-02	1.00E+00	9.42E-01	1.00E+00	9.26E-01	1.00E+00	9.71E-01	1.00E+00	9.53E-01	1.00E+00	9.79E-01	1.00E+00	di-, tri-valent inorganic cation homeostasis	P
GO:0030010	11	5.97E-01	1.00E+00	7.17E-01	1.00E+00	3.44E-01	1.00E+00	7.37E-01	1.00E+00	5.98E-01	1.00E+00	7.21E-01	1.00E+00	8.36E-01	1.00E+00	6.04E-01	1.00E+00	establishment of cell polarity	P
GO:0030016	79	8.47E-01	1.00E+00	9.98E-01	1.00E+00	3.28E-01	1.00E+00	9.94E-01	1.00E+00	9.57E-01	1.00E+00	9.95E-01	1.00E+00	9.39E-01	1.00E+00	9.92E-01	1.00E+00	myofibril	C
GO:0030017	74	8.03E-01	1.00E+00	9.98E-01	1.00E+00	3.29E-01	1.00E+00	9.98E-01	1.00E+00	9.36E-01	1.00E+00	9.93E-01	1.00E+00	8.99E-01	1.00E+00	9.87E-01	1.00E+00	sarcomere	C
GO:0030018	26	8.88E-01	1.00E+00	7.70E-01	1.00E+00	9.27E-01	1.00E+00	9.85E-01	1.00E+00	9.68E-01	1.00E+00	6.54E-01	1.00E+00	3.36E-01	1.00E+00	5.20E-01	1.00E+00	Z disc	C
GO:0030027	55	7.52E-01	1.00E+00	4.59E-01	1.00E+00	6.22E-01	1.00E+00	2.95E-01	1.00E+00	5.42E-01	1.00E+00	5.64E-01	1.00E+00	9.99E-01	1.00E+00	4.83E-01	1.00E+00	lamellipodium	C
GO:0030029	255	2.34E-01	1.00E+00	8.27E-01	1.00E+00	4.40E-03	3.50E-02	1.93E-01	1.00E+00	3.57E-01	1.00E+00	9.04E-01	1.00E+00	9.20E-01	1.00E+00	8.86E-01	1.00E+00	actin filament-based process	P
GO:0030030	308	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell projection organization and biogenesis	P
GO:0030031	80	8.65E-01	1.00E+00	3.17E-01	1.00E+00	4.54E-01	1.00E+00	2.38E-01	1.00E+00	7.94E-01	1.00E+00	1.84E-01	1.00E+00	9.92E-01	1.00E+00	9.13E-01	1.00E+00	cell projection biogenesis	P
GO:0030032	13	8.65E-01	1.00E+00	2.74E-01	1.00E+00	7.88E-01	1.00E+00	2.30E-01	1.00E+00	7.57E-01	1.00E+00	3.26E-01	1.00E+00	9.64E-01	1.00E+00	3.06E-01	1.00E+00	lamellipodium biogenesis	P
GO:0030035	18	3.93E-01	1.00E+00	2.02E-01	1.00E+00	3.01E-01	1.00E+00	1.99E-01	1.00E+00	3.48E-01	1.00E+00	9.76E-02	1.00E+00	7.49E-01	1.00E+00	8.78E-01	1.00E+00	microspike biogenesis	P
GO:0030036	229	3.41E-01	1.00E+00	5.04E-01	1.00E+00	1.10E-02	1.57E-01	6.06E-02	1.00E+00	4.55E-01	1.00E+00	6.92E-01	1.00E+00	9.08E-01	1.00E+00	6.70E-01	1.00E+00	actin cytoskeleton organization and biogene	P
GO:0030041	36	1.35E-01	1.00E+00	3.40E-01	1.00E+00	3.95E-01	1.00E+00	1.99E-01	1.00E+00	7.10E-02	1.00E+00	3.49E-01	1.00E+00	6.66E-01	1.00E+00	5.64E-01	1.00E+00	actin filament polymerization	P
GO:0030042	24	2.56E-02	1.00E+00	2.48E-01	1.00E+00	5.90E-03	9.30E-02	6.32E-02	1.00E+00	3.90E-02	1.00E+00	4.16E-01	1.00E+00	8.31E-01	1.00E+00	4.37E-01	1.00E+00	actin filament depolymerization	P
GO:0030048	20	6.35E-01	1.00E+00	9.98E-01	1.00E+00	2.53E-01	1.00E+00	7.71E-01	1.00E+00	7.11E-01	1.00E+00	9.99E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	actin filament-based movement	P
GO:0030054	450	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.57E-01	1.00E+00	7.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	cell junction	C
GO:0030055	47	4.21E-01	1.00E+00	8.93E-01	1.00E+00	1.19E-01	1.00E+00	4.43E-01	1.00E+00	3.56E-01	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	cell-matrix junction	C
GO:0030057	10	9.76E-01	1.00E+00	9.06E-01	1.00E+00	8.93E-01	1.00E+00	7.54E-01	1.00E+00	9.90E-01	1.00E+00	8.68E-01	1.00E+00	8.11E-01	1.00E+00	9.93E-01	1.00E+00	desmosome	C
GO:0030072	35	9.98E-01	1.00E+00	9.89E-01	1.00E+00	9.70E-01	1.00E+00	3.53E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide hormone secretion	P
GO:0030073	29	9.88E-01	1.00E+00	9.83E-01	1.00E+00	9.34E-01	1.00E+00	4.37E-01	1.00E+00	9.84E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	insulin secretion	P
GO:0030097	231	8.82E-01	1.00E+00	9.90E-01	1.00E+00	2.67E-01	1.00E+00	9.14E-01	1.00E+00	9.66E-01	1.00E+00	9.58E-01	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	hemopoiesis	P
GO:0030098	101	6.52E-01	1.00E+00	9.94E-01	1.00E+00	1.44E-01	1.00E+00	9.88E-01	1.00E+00	8.14E-01	1.00E+00	9.86E-01	1.00E+00	8.65E-01	1.00E+00	9.98E-01	1.00E+00	lymphocyte differentiation	P
GO:0030099	106	5.75E-01	1.00E+00	8.91E-01	1.00E+00	1.61E-01	1.00E+00	9.91E-01	1.00E+00	8.08E-01	1.00E+00	6.91E-01	1.00E+00	8.31E-01	1.00E+00	9.50E-01	1.00E+00	myeloid cell differentiation	P
GO:0030100	41	5.08E-01	1.00E+00	9.01E-02	1.00E+00	7.28E-01	1.00E+00	2.37E-01	1.00E+00	2.05E-01	1.00E+00	1.53E-01	1.00E+00	9.98E-01	1.00E+00	8.16E-02	1.00E+00	regulation of endocytosis	P
GO:0030101	20	6.08E-01	1.00E+00	9.92E-01	1.00E+00	8.57E-01	1.00E+00	9.99E-01	1.00E+00	4.25E-01	1.00E+00	9.49E-01	1.00E+00	7.55E-01	1.00E+00	9.96E-01	1.00E+00	natural killer cell activation	P
GO:0030111	32	9.97E-01	1.00E+00	7.87E-01	1.00E+00	8.39E-01	1.00E+00	8.37E-01	1.00E+00	9.99E-01	1.00E+00	7.13E-01	1.00E+00	9.88E-01	1.00E+00	8.91E-01	1.00E+00	regulation of Wnt receptor signaling pathwa	P
GO:0030117	65	2.77E-04	1.10E-02	1.30E-04	4.00E-03	9.31E-05	4.57E-03	8.45E-04	1.03E-02	6.16E-04	4.90E-03	3.11E-04	1.02E-02	4.27E-01	1.00E+00	3.14E-01	1.00E+00	membrane coat	C
GO:0030118	39	7.17E-03	1.37E-01	5.58E-03	1.50E-01	6.10E-04	1.25E-02	1.92E-03	2.70E-02	1.31E-02	3.01E-01	2.35E-02	7.69E-01	7.29E-01	1.00E+00	4.62E-01	1.00E+00	clathrin coat	C
GO:0030119	30	1.69E-02	5.62E-01	1.96E-02	9.24E-01	3.90E-03	3.50E-02	2.96E-03	5.60E-02	3.36E-02	6.55E-01	5.95E-02	1.00E+00	5.77E-01	1.00E+00	7.23E-01	1.00E+00	membrane coat adaptor complex	C
GO:0030120	35	4.20E-04	1.60E-02	5.91E-04	1.90E-02	8.16E-04	1.25E-02	1.05E-02	1.23E-01	6.08E-04	4.90E-03	1.10E-03	1.02E-02	6.48E-01	1.00E+00	1.43E-01	1.00E+00	vesicle coat	C
GO:0030125	19	3.46E-02	1.00E+00	8.53E-02	1.00E+00	9.32E-03	1.57E-01	4.07E-02	1.00E+00	2.95E-02	6.55E-01	1.94E-01	1.00E+00	9.98E-01	1.00E+00	5.73E-01	1.00E+00	clathrin vesicle coat	C
GO:0030130	13	7.45E-02	1.00E+00	4.37E-01	1.00E+00	2.74E-03	1.80E-02	2.29E-01	1.00E+00	1.09E-01	1.00E+00	6.12E-01	1.00E+00	9.45E-01	1.00E+00	7.34E-01	1.00E+00	clathrin coat of trans-Golgi network vesicle	C
GO:0030131	29	1.37E-02	2.72E-01	1.28E-02	3.84E-01	3.84E-03	3.50E-02	2.96E-03	5.60E-02	2.83E-02	6.55E-01	3.83E-02	1.00E+00	5.28E-01	1.00E+00	6.84E-01	1.00E+00	clathrin adaptor complex	C
GO:0030132	10	1.44E-01	1.00E+00	2.16E-01	1.00E+00	3.19E-01	1.00E+00	1.14E-01	1.00E+00	8.80E-02	1.00E+00	4.24E-01	1.00E+00	9.02E-01	1.00E+00	3.15E-01	1.00E+00	clathrin coat of coated pit	C
GO:0030133	50	8.57E-02	1.00E+00	4.66E-01	1.00E+00	5.37E-03	9.30E-02	1.87E-01	1.00E+00	1.42E-01	1.00E+00	5.37E-01	1.00E+00	7.21E-01	1.00E+00	7.48E-01	1.00E+00	transport vesicle	C
GO:0030135	135	5.37E-01	1.00E+00	4.42E-01	1.00E+00	5.04E-02	8.68E-01	6.89E-02	1.00E+00	6.63E-01	1.00E+00	6.48E-01	1.00E+00	9.98E-01	1.00E+00	9.24E-01	1.00E+00	coated vesicle	C
GO:0030136	114	8.82E-01	1.00E+00	8.58E-01	1.00E+00	1.44E-01	1.00E+00	1.84E-01	1.00E+00	9.27E-01	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	clathrin-coated vesicle	C
GO:0030137	12	2.54E-02	1.00E+00	7.19E-04	1.90E-02	1.19E-01	1.00E+00	1.62E-01	1.00E+00	2.78E-02	6.55E-01	9.59E-05	2.29E-03	1.78E-01	1.00E+00	8.30E-02	1.00E+00	COPI-coated vesicle	C
GO:0030139	33	5.88E-01	1.00E+00	3.86E-01	1.00E+00	4.39E-01	1.00E+00	3.95E-01	1.00E+00	5.47E-01	1.00E+00	3.20E-01	1.00E+00	9.81E-01	1.00E+00	6.91E-01	1.00E+00	endocytic vesicle	C
GO:0030140	22	4.36E-01	1.00E+00	6.63E-01	1.00E+00	4.38E-02	7.24E-01	2.63E-01	1.00E+00	4.94E-01	1.00E+00	8.34E-01	1.00E+00	9.99E-01	1.00E+00	7.45E-01	1.00E+00	trans-Golgi network transport vesicle	C
GO:0030141	90	8.05E-01	1.00E+00	9.92E-01	1.00E+00	4.40E-01	1.00E+00	9.90E-01	1.00E+00	7.56E-01	1.00E+00	9.78E-01	1.00E+00	9.76E-01	1.00E+00	9.56E-01	1.00E+00	secretory granule	C
GO:0030145	151	6.98E-01	1.00E+00	1.68E-01	1.00E+00	1.46E-01	1.00E+00	2.49E-02	4.10E-01	6.06E-01	1.00E+00	3.62E-01	1.00E+00	9.99E-01	1.00E+00	7.38E-01	1.00E+00	manganese ion binding	F
GO:0030148	22	5.64E-01	1.00E+00	1.60E-01	1.00E+00	1.56E-01	1.00E+00	6.91E-02	1.00E+00	6.49E-01	1.00E+00	1.36E-01	1.00E+00	6.98E-01	1.00E+00	6.70E-01	1.00E+00	sphingolipid biosynthesis	P
GO:0030149	16	2.39E-01	1.00E+00	8.22E-02	1.00E+00	1.45E-01	1.00E+00	1.74E-01	1.00E+00	1.84E-01	1.00E+00	1.44E-01	1.00E+00	7.01E-01	1.00E+00	3.65E-01	1.00E+00	sphingolipid catabolism	P
GO:0030154	1323	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell differentiation	P
GO:0030155	71	8.63E-01	1.00E+00	9.84E-01	1.00E+00	2.50E-01	1.00E+00	9.59E-01	1.00E+00	8.70E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	regulation of cell adhesion	P
GO:0030159	19	8.71E-01	1.00E+00	8.34E-01	1.00E+00	3.93E-01	1.00E+00	5.23E-01	1.00E+00	9.40E-01	1.00E+00	7.96E-01	1.00E+00	9.50E-01	1.00E+00	9.56E-01	1.00E+00	receptor signaling complex scaffold activity	F
GO:0030162	20	4.60E-01	1.00E+00	8.60E-01	1.00E+00	1.18E-01	1.00E+00	8.90E-01	1.00E+00	5.47E-01	1.00E+00	7.61E-01	1.00E+00	9.96E-01	1.00E+00	9.95E-01	1.00E+00	regulation of proteolysis	P
GO:0030163	283	7.47E-03	1.37E-01	2.42E-05	3.00E-03	2.08E-02	2.36E-01	7.74E-08	0.00E+00	3.83E-02	1.00E+00	8.46E-04	1.02E-02	8.97E-01	1.00E+00	1.15E-01	1.00E+00	protein catabolism	P
GO:0030165	27	8.11E-01	1.00E+00	8.29E-01	1.00E+00	5.17E-01	1.00E+00	8.40E-01	1.00E+00	9.06E-01	1.00E+00	7.31E-01	1.00E+00	7.34E-01	1.00E+00	8.98E-01	1.00E+00	PDZ domain binding	F
GO:0030166	24	9.25E-01	1.00E+00	9.24E-01	1.00E+00	5.17E-01	1.00E+00	5.45E-01	1.00E+00	9.69E-01	1.00E+00	8.46E-01	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	proteoglycan biosynthesis	P
GO:0030168	22	8.64E-01	1.00E+00	8.29E-01	1.00E+00	8.11E-01	1.00E+00	8.04E-01	1.00E+00	6.43E-01	1.00E+00	7.89E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	platelet activation	P
GO:0030169	18	7.37E-01	1.00E+00	5.36E-01	1.00E+00	4.67E-01	1.00E+00	9.00E-01	1.00E+00	7.05E-01	1.00E+00	3.00E-01	1.00E+00	1.00E+00	1.00E+00	9.17E-01	1.00E+00	low-density lipoprotein binding	F
GO:0030170	61	1.57E-01	1.00E+00	5.01E-02	1.00E+00	2.97E-04	6.00E-03	9.00E-02	1.00E+00	5.15E-01	1.00E+00	7.39E-02	1.00E+00	9.53E-01	1.00E+00	7.25E-02	1.00E+00	pyridoxal phosphate binding	F
GO:0030173	40	6.79E-01	1.00E+00	6.72E-01	1.00E+00	4.45E-01	1.00E+00	7.60E-01	1.00E+00	5.95E-01	1.00E+00	5.25E-01	1.00E+00	9.72E-01	1.00E+00	8.38E-01	1.00E+00	integral to Golgi membrane	C
GO:0030175	17	3.77E-01	1.00E+00	6.21E-02	1.00E+00	6.39E-02	1.00E+00	6.54E-02	1.00E+00	5.52E-01	1.00E+00	5.75E-02	1.00E+00	9.63E-01	1.00E+00	3.17E-01	1.00E+00	filopodium	C
GO:0030176	38	5.50E-01	1.00E+00	5.25E-01	1.00E+00	1.02E-01	1.00E+00	1.66E-01	1.00E+00	6.32E-01	1.00E+00	7.92E-01	1.00E+00	9.66E-01	1.00E+00	2.21E-01	1.00E+00	integral to endoplasmic reticulum membran	C
GO:0030178	20	9.84E-01	1.00E+00	7.81E-01	1.00E+00	9.56E-01	1.00E+00	7.95E-01	1.00E+00	9.84E-01	1.00E+00	7.34E-01	1.00E+00	9.70E-01	1.00E+00	7.88E-01	1.00E+00	negative regulation of Wnt receptor signalin	P
GO:0030182	332	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron differentiation	P
GO:0030183	51	7.94E-01	1.00E+00	1.00E+00	1.00E+00	2.21E-01	1.00E+00	9.73E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	6.21E-01	1.00E+00	9.99E-01	1.00E+00	B cell differentiation	P
GO:0030193	19	2.72E-01	1.00E+00	6.34E-01	1.00E+00	4.23E-01	1.00E+00	7.33E-01	1.00E+00	1.35E-01	1.00E+00	5.40E-01	1.00E+00	8.14E-01	1.00E+00	6.79E-01	1.00E+00	regulation of blood coagulation	P
GO:0030195	15	2.95E-01	1.00E+00	8.22E-01	1.00E+00	4.69E-01	1.00E+00	9.78E-01	1.00E+00	1.17E-01	1.00E+00	6.50E-01	1.00E+00	9.85E-01	1.00E+00	7.67E-01	1.00E+00	negative regulation of blood coagulation	P
GO:0030198	82	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular matrix organization and biogen	P
GO:0030199	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	collagen fibril organization	P
GO:0030201	13	9.99E-01	1.00E+00	9.51E-01	1.00E+00	6.21E-01	1.00E+00	9.46E-01	1.00E+00	9.83E-01	1.00E+00	6.23E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	heparan sulfate proteoglycan metabolism	P
GO:0030203	45	3.59E-01	1.00E+00	6.01E-01	1.00E+00	2.37E-01	1.00E+00	4.83E-01	1.00E+00	4.00E-01	1.00E+00	6.07E-01	1.00E+00	5.30E-01	1.00E+00	6.08E-01	1.00E+00	glycosaminoglycan metabolism	P
GO:0030216	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	keratinocyte differentiation	P
GO:0030217	62	4.58E-01	1.00E+00	9.17E-01	1.00E+00	3.37E-01	1.00E+00	7.09E-01	1.00E+00	3.93E-01	1.00E+00	9.14E-01	1.00E+00	9.44E-01	1.00E+00	9.66E-01	1.00E+00	T cell differentiation	P
GO:0030218	44	2.57E-01	1.00E+00	7.03E-01	1.00E+00	6.64E-02	1.00E+00	8.07E-01	1.00E+00	7.40E-01	1.00E+00	5.88E-01	1.00E+00	2.50E-01	1.00E+00	8.56E-01	1.00E+00	erythrocyte differentiation	P
GO:0030225	15	4.42E-01	1.00E+00	7.47E-01	1.00E+00	1.99E-01	1.00E+00	6.11E-01	1.00E+00	9.50E-01	1.00E+00	6.55E-01	1.00E+00	4.54E-01	1.00E+00	9.41E-01	1.00E+00	macrophage differentiation	P
GO:0030228	13	8.26E-01	1.00E+00	3.56E-01	1.00E+00	5.38E-01	1.00E+00	7.39E-01	1.00E+00	7.83E-01	1.00E+00	2.11E-01	1.00E+00	9.97E-01	1.00E+00	7.58E-01	1.00E+00	lipoprotein receptor activity	F
GO:0030234	889	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.42E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	enzyme regulator activity	F

GO:0030239	16	2.87E-01	1.00E+00	1.00E+00	1.00E+00	1.46E-01	1.00E+00	9.96E-01	1.00E+00	3.19E-01	1.00E+00	9.99E-01	1.00E+00	6.78E-01	1.00E+00	1.00E+00	1.00E+00	myofibril assembly	P
GO:0030246	322	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.83E-01	1.00E+00	carbohydrate binding	F
GO:0030247	116	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.80E-01	1.00E+00	polysaccharide binding	F
GO:0030258	37	4.17E-01	1.00E+00	2.54E-01	1.00E+00	1.20E-01	1.00E+00	9.89E-02	1.00E+00	5.65E-01	1.00E+00	4.88E-01	1.00E+00	5.58E-01	1.00E+00	1.79E-01	1.00E+00	lipid modification	P
GO:0030260	10	7.82E-01	1.00E+00	8.27E-01	1.00E+00	7.34E-01	1.00E+00	6.61E-01	1.00E+00	4.94E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	6.05E-01	1.00E+00	entry into host cell	P
GO:0030261	21	1.85E-01	1.00E+00	9.95E-02	1.00E+00	3.96E-01	1.00E+00	7.82E-02	1.00E+00	3.07E-01	1.00E+00	2.22E-01	1.00E+00	7.99E-02	1.00E+00	2.05E-01	1.00E+00	chromosome condensation	P
GO:0030262	21	1.67E-01	1.00E+00	7.70E-02	1.00E+00	3.61E-01	1.00E+00	2.08E-01	1.00E+00	2.83E-01	1.00E+00	1.60E-01	1.00E+00	8.68E-02	1.00E+00	2.16E-01	1.00E+00	apoptotic nuclear changes	P
GO:0030278	33	7.56E-01	1.00E+00	7.93E-01	1.00E+00	6.78E-01	1.00E+00	9.96E-01	1.00E+00	6.34E-01	1.00E+00	4.82E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	regulation of ossification	P
GO:0030279	10	4.60E-01	1.00E+00	9.55E-01	1.00E+00	3.56E-01	1.00E+00	9.98E-01	1.00E+00	4.52E-01	1.00E+00	8.17E-01	1.00E+00	7.14E-01	1.00E+00	9.93E-01	1.00E+00	negative regulation of ossification	P
GO:0030282	38	8.65E-01	1.00E+00	9.45E-01	1.00E+00	8.44E-01	1.00E+00	9.84E-01	1.00E+00	7.30E-01	1.00E+00	7.97E-01	1.00E+00	9.78E-01	1.00E+00	9.95E-01	1.00E+00	bone mineralization	P
GO:0030286	33	3.72E-01	1.00E+00	6.32E-01	1.00E+00	1.31E-01	1.00E+00	1.34E-01	1.00E+00	4.20E-01	1.00E+00	8.79E-01	1.00E+00	6.20E-01	1.00E+00	3.20E-01	1.00E+00	dynein complex	C
GO:0030288	27	9.51E-01	1.00E+00	9.56E-01	1.00E+00	4.73E-01	1.00E+00	5.91E-01	1.00E+00	9.64E-01	1.00E+00	9.59E-01	1.00E+00	9.71E-01	1.00E+00	9.37E-01	1.00E+00	periplasmic space (sensu Proteobacteria)	C
GO:0030295	12	9.33E-01	1.00E+00	9.72E-01	1.00E+00	9.69E-01	1.00E+00	8.76E-01	1.00E+00	9.19E-01	1.00E+00	9.59E-01	1.00E+00	9.06E-01	1.00E+00	9.90E-01	1.00E+00	protein kinase activator activity	F
GO:0030301	16	7.96E-01	1.00E+00	3.61E-01	1.00E+00	2.15E-01	1.00E+00	3.95E-01	1.00E+00	8.73E-01	1.00E+00	3.30E-01	1.00E+00	9.95E-01	1.00E+00	6.13E-01	1.00E+00	cholesterol transport	P
GO:0030308	64	5.31E-01	1.00E+00	9.85E-01	1.00E+00	1.90E-01	1.00E+00	5.73E-01	1.00E+00	5.89E-01	1.00E+00	9.88E-01	1.00E+00	9.75E-01	1.00E+00	9.99E-01	1.00E+00	negative regulation of cell growth	P
GO:0030312	33	9.91E-01	1.00E+00	9.95E-01	1.00E+00	6.38E-01	1.00E+00	7.60E-01	1.00E+00	9.90E-01	1.00E+00	9.94E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	external encapsulating structure	C
GO:0030313	28	9.55E-01	1.00E+00	9.63E-01	1.00E+00	4.62E-01	1.00E+00	6.39E-01	1.00E+00	9.66E-01	1.00E+00	9.61E-01	1.00E+00	9.82E-01	1.00E+00	9.40E-01	1.00E+00	cell envelope	C
GO:0030315	12	9.42E-01	1.00E+00	8.88E-01	1.00E+00	7.18E-01	1.00E+00	9.51E-01	1.00E+00	9.45E-01	1.00E+00	8.52E-01	1.00E+00	1.00E+00	1.00E+00	6.99E-01	1.00E+00	T-tubule	C
GO:0030316	19	9.95E-01	1.00E+00	9.36E-01	1.00E+00	9.98E-01	1.00E+00	9.72E-01	1.00E+00	9.69E-01	1.00E+00	8.47E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	osteoclast differentiation	P
GO:0030317	24	8.61E-01	1.00E+00	9.97E-01	1.00E+00	7.02E-01	1.00E+00	1.00E+00	1.00E+00	7.88E-01	1.00E+00	9.27E-01	1.00E+00	9.22E-01	1.00E+00	9.97E-01	1.00E+00	sperm motility	P
GO:0030318	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	melanocyte differentiation	P
GO:0030323	74	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	respiratory tube development	P
GO:0030324	71	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	lung development	P
GO:0030326	70	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic limb morphogenesis	P
GO:0030330	17	3.25E-01	1.00E+00	2.62E-01	1.00E+00	6.62E-01	1.00E+00	4.20E-01	1.00E+00	2.12E-01	1.00E+00	2.35E-01	1.00E+00	6.66E-01	1.00E+00	5.45E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0030334	86	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.38E-01	1.00E+00	6.67E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of cell migration	P
GO:0030335	35	9.92E-01	1.00E+00	9.71E-01	1.00E+00	9.75E-01	1.00E+00	4.00E-01	1.00E+00	9.73E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of cell migration	P
GO:0030336	26	8.66E-01	1.00E+00	8.71E-01	1.00E+00	1.68E-01	1.00E+00	9.27E-01	1.00E+00	9.32E-01	1.00E+00	8.47E-01	1.00E+00	9.98E-01	1.00E+00	9.37E-01	1.00E+00	negative regulation of cell migration	P
GO:0030374	34	9.77E-01	1.00E+00	7.88E-01	1.00E+00	7.36E-01	1.00E+00	7.64E-01	1.00E+00	9.73E-01	1.00E+00	7.04E-01	1.00E+00	9.95E-01	1.00E+00	9.69E-01	1.00E+00	ligand-dependent nuclear receptor transcrip	F
GO:0030375	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	thyroid hormone receptor coactivator activit	F
GO:0030384	63	2.10E-01	1.00E+00	7.70E-02	1.00E+00	1.26E-01	1.00E+00	8.15E-02	1.00E+00	1.84E-01	1.00E+00	2.12E-01	1.00E+00	6.69E-01	1.00E+00	1.61E-01	1.00E+00	phosphoinositide metabolism	P
GO:0030414	182	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	protease inhibitor activity	F
GO:0030424	67	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	axon	C
GO:0030425	69	9.99E-01	1.00E+00	9.92E-01	1.00E+00	3.13E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	dendrite	C
GO:0030426	28	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.92E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.95E-01	1.00E+00	7.07E-01	1.00E+00	growth cone	C
GO:0030427	29	9.98E-01	1.00E+00	9.73E-01	1.00E+00	9.68E-01	1.00E+00	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.69E-01	1.00E+00	9.82E-01	1.00E+00	7.07E-01	1.00E+00	site of polarized growth	C
GO:0030433	18	6.95E-01	1.00E+00	3.71E-01	1.00E+00	8.95E-01	1.00E+00	1.83E-01	1.00E+00	5.06E-01	1.00E+00	4.33E-01	1.00E+00	8.18E-01	1.00E+00	6.68E-01	1.00E+00	ER-associated protein catabolism	P
GO:0030496	12	3.82E-01	1.00E+00	3.86E-01	1.00E+00	4.55E-01	1.00E+00	5.09E-01	1.00E+00	4.27E-01	1.00E+00	3.16E-01	1.00E+00	3.90E-01	1.00E+00	8.31E-01	1.00E+00	midbody	C
GO:0030500	22	7.10E-01	1.00E+00	8.47E-01	1.00E+00	7.98E-01	1.00E+00	8.81E-01	1.00E+00	6.62E-01	1.00E+00	7.46E-01	1.00E+00	5.76E-01	1.00E+00	9.70E-01	1.00E+00	regulation of bone mineralization	P
GO:0030501	13	7.93E-01	1.00E+00	9.46E-01	1.00E+00	8.36E-01	1.00E+00	7.52E-01	1.00E+00	6.94E-01	1.00E+00	9.53E-01	1.00E+00	9.76E-01	1.00E+00	9.93E-01	1.00E+00	positive regulation of bone mineralization	P
GO:0030509	50	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.80E-01	1.00E+00	6.02E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	BMP signaling pathway	P
GO:0030510	17	9.83E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	9.83E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of BMP signaling pathway	P
GO:0030514	11	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.76E-01	1.00E+00	9.96E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	negative regulation of BMP signaling pathw	P
GO:0030516	15	6.38E-01	1.00E+00	9.73E-01	1.00E+00	2.11E-01	1.00E+00	9.31E-01	1.00E+00	8.16E-01	1.00E+00	9.86E-01	1.00E+00	8.99E-01	1.00E+00	9.61E-01	1.00E+00	regulation of axon extension	P
GO:0030518	52	5.82E-01	1.00E+00	4.61E-02	1.00E+00	7.46E-02	1.00E+00	1.01E-02	1.23E-01	8.12E-01	1.00E+00	9.28E-02	1.00E+00	8.46E-01	1.00E+00	7.17E-01	1.00E+00	steroid hormone receptor signaling pathway	P
GO:0030521	37	3.43E-01	1.00E+00	7.20E-02	1.00E+00	1.21E-01	1.00E+00	3.93E-02	1.00E+00	5.30E-01	1.00E+00	1.10E-01	1.00E+00	4.30E-01	1.00E+00	4.48E-01	1.00E+00	androgen receptor signaling pathway	P
GO:0030522	62	7.52E-01	1.00E+00	1.90E-01	1.00E+00	1.74E-01	1.00E+00	3.78E-02	1.00E+00	8.64E-01	1.00E+00	2.64E-01	1.00E+00	9.68E-01	1.00E+00	8.52E-01	1.00E+00	intracellular receptor-mediated signaling pa	P
GO:0030528	1517	1.00E+00	1.00E+00	9.82E-01	1.00E+00	7.38E-01	1.00E+00	1.32E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	transcription regulator activity	F
GO:0030529	535	5.51E-03	1.37E-01	2.00E-04	8.26E-03	1.93E-01	1.00E+00	5.97E-04	7.17E-03	1.68E-02	3.81E-01	3.84E-03	7.40E-02	1.58E-01	1.00E+00	2.17E-01	1.00E+00	ribonucleoprotein complex	C
GO:0030530	16	9.52E-01	1.00E+00	8.14E-01	1.00E+00	8.59E-01	1.00E+00	9.73E-01	1.00E+00	7.93E-01	1.00E+00	7.84E-01	1.00E+00	1.00E+00	1.00E+00	3.49E-01	1.00E+00	heterogeneous nuclear ribonucleoprotein c	C
GO:0030532	24	8.28E-04	1.60E-02	7.97E-03	3.40E-01	2.66E-03	1.80E-02	1.49E-02	2.81E-01	3.55E-02	6.55E-01	1.84E-02	5.65E-01	3.66E-02	9.62E-01	1.89E-01	1.00E+00	small nuclear ribonucleoprotein complex	C
GO:0030534	67	8.94E-01	1.00E+00	9.80E-01	1.00E+00	2.76E-01	1.00E+00	8.78E-01	1.00E+00	9.82E-01	1.00E+00	9.54E-01	1.00E+00	9.47E-01	1.00E+00	9.99E-01	1.00E+00	adult behavior	P
GO:0030539	12	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	male genitalia development	P
GO:0030545	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.93E-01	1.00E+00	receptor regulator activity	F
GO:0030547	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.56E-01	1.00E+00	receptor inhibitor activity	F
GO:0030551	29	9.02E-01	1.00E+00	9.51E-01	1.00E+00	9.54E-01	1.00E+00	9.49E-01	1.00E+00	9.41E-01	1.00E+00	9.32E-01	1.00E+00	4.86E-01	1.00E+00	7.77E-01	1.00E+00	cyclic nucleotide binding	F
GO:0030552	20	9.25E-01	1.00E+00	6.79E-01	1.00E+00	7.06E-01	1.00E+00	6.51E-01	1.00E+00	9.62E-01	1.00E+00	6.07E-01	1.00E+00	8.74E-01	1.00E+00	7.64E-01	1.00E+00	cAMP binding	F
GO:0030554	1684	6.35E-04	1.60E-02	3.11E-06	1.41E-03	1.78E-09	0.00E+00	6.29E-08	0.00E+00	3.02E-02	6.55E-01	1.10E-04	2.29E-03	8.89E-01	1.00E+00	7.60E-01	1.00E+00	adenyl nucleotide binding	F
GO:0030574	20	9.76E-01	1.00E+00	9.94E-01	1.00E+00	6.73E-01	1.00E+00	9.52E-01	1.00E+00	9.56E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	collagen catabolism	P
GO:0030593	15	8.20E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	8.18E-01	1.00E+00	4.58E-01	1.00E+00	9.92E-01	1.00E+00	9.90E-01	1.00E+00	5.64E-01	1.00E+00	neutrophil chemotaxis	P
GO:0030594	240	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter receptor activity	F
GO:0030595	28	9.37E-01	1.00E+00	8.96E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	6.52E-01	1.00E+00	7.30E-01	1.00E+00	1.00E+00	1.00E+00	7.43E-01	1.00E+00	leukocyte chemotaxis	P
GO:0030641	14	5.57E-02	1.00E+00	2.23E-01	1.00E+00	5.46E-02	1.00E+00	3.71E-01	1.00E+00	9.38E-02	1.00E+00	1.69E-01	1.00E+00	3.20E-01	1.00E+00	7.02E-01	1.00E+00	hydrogen ion homeostasis	P
GO:0030658	20	5.40E-03	1.37E-01	5.95E-02	1.00E+00	3.80E-04	7.18E-03	4.22E-02	1.00E+00	1.40E-02	3.01E-01	1.16E-01	1.00E+00	6.72E-01	1.00E+00	4.14E-01	1.00E+00	transport vesicle membrane	C
GO:0030659	109	1.83E-01	1.00E+00	1.82E-01	1.00E+00	2.93E-02	5.65E-01	7.15E-02	1.00E+00	1.14E-01	1.00E+00	2.67E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	cytoplasmic vesicle membrane	C
GO:0030660	22	5.55E-03	1.37E-01	6.29E-02	1.00E+00	1.40E-03	1.60E-02	7.04E-02	1.00E+00	1.19E-02	3.01E-01	1.77E-01	1.00E+00	8.14E-01	1.00E+00	1.80E-01	1.00E+00	Golgi-associated vesicle membrane	C
GO:0030662	38	5.10E-04	1.60E-02	8.60E-04	2.00E-02	6.76E-04	1.25E-02	7.42E-03	8.10E-02	6.74E-04	4.90E-03	1.18E-03	1.02E-02	6.04E-01	1.00E+00	8.06E-02	1.00E+00	coated vesicle membrane	C
GO:0030665	22	3.32E-02	1.00E+00	6.37E-02	1.00E+00	7.83E-03	1.57E-01	2.82E-02	5.42E-01	2.78E-02	6.55E-01	1.22E-01	1.00E+00	9.92E-01	1.00E+00	3.26E-01	1.00E+00	clathrin coated vesicle membrane	C
GO:0030666	11	3.97E-01	1.00E+00	2.66E-01	1.00E+00	4.89E-01	1.00E+00	1.41E-01	1.00E+00	3.39E-01	1.00E+00	3.58E-01	1.00E+00	9.14E-01	1.00E+00	3.29E-01	1.00E+00	endocytic vesicle membrane	C
GO:0030667	17	6.43E-01	1.00E+00	9.61E-01	1.00E+00	4.64E-01	1.00E+00	8.97E-01	1.00E+00	4.45E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	secretory granule membrane	C
GO:0030672	10	9.58E-01	1.00E+00	9.99E-01	1.00E+00	5.94E-01	1.00E+00	1.00E+00	1.00E+00	9.02E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synaptic vesicle membrane	C
GO:0030674	81	6.65E-01	1.00E+00	7.56E-01	1.00E+00	5.20E-02	1.00E+00	1.56E-01	1.00E+00	8.33E-01	1.00E+00	8.97E-01	1.00E+00	9.93E-01	1.00E+00	6.47E-01	1.00E+00	protein binding, bridging	F
GO:0030693	21	9.95E-01	1.00E+00	6.01E-01	1.00E+00	5.47E-01	1.00E+00	1.63E-01	1.00E+00	9.98E-01	1.00E+00	8.56E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	caspase activity	F
GO:0030695	416	9.41E-01	1.00E+00	9.99E-01	1.00E+00	6.55E-02	1.00E+00	4.15E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	GTPase regulator activity	F
GO:0030705	135	4.33E-01	1.00E+00	7.15E-01	1.00E+00	3.96E-03	3.50E-02	8.97E-02	1.00E+00	7.93E-01	1.00E+00	8.93E-01	1.00E+00	8.32E-01	1.00E+00	7.69E-01	1.00E+00	cytoskeleton-dependent intracellular transp	P

GO:0030742	10	3.91E-01	1.00E+00	1.42E-01	1.00E+00	5.84E-01	1.00E+00	4.72E-01	1.00E+00	2.07E-01	1.00E+00	9.29E-02	1.00E+00	9.70E-01	1.00E+00	6.66E-01	1.00E+00	GTP-dependent protein binding	F
GO:0030799	13	8.16E-01	1.00E+00	8.45E-01	1.00E+00	3.82E-01	1.00E+00	8.62E-01	1.00E+00	6.79E-01	1.00E+00	7.38E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	regulation of cyclic nucleotide metabolism	P
GO:0030832	56	5.34E-02	1.00E+00	2.74E-01	1.00E+00	4.22E-02	5.87E-01	8.13E-02	1.00E+00	3.33E-02	6.55E-01	3.21E-01	1.00E+00	9.07E-01	1.00E+00	6.77E-01	1.00E+00	regulation of actin filament length	P
GO:0030833	26	8.21E-02	1.00E+00	1.66E-01	1.00E+00	3.01E-01	1.00E+00	1.79E-01	1.00E+00	4.13E-02	1.00E+00	1.29E-01	1.00E+00	6.64E-01	1.00E+00	5.48E-01	1.00E+00	regulation of actin filament polymerization	P
GO:0030834	24	2.56E-02	1.00E+00	2.48E-01	1.00E+00	5.90E-03	9.30E-02	6.32E-02	1.00E+00	3.90E-02	1.00E+00	4.16E-01	1.00E+00	8.31E-01	1.00E+00	4.37E-01	1.00E+00	regulation of actin filament depolymerizatio	P
GO:0030835	22	1.36E-02	2.72E-01	1.35E-01	1.00E+00	5.96E-03	9.30E-02	5.50E-02	1.00E+00	1.95E-02	3.81E-01	2.61E-01	1.00E+00	7.58E-01	1.00E+00	2.64E-01	1.00E+00	negative regulation of actin filament depoly	P
GO:0030855	50	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	epithelial cell differentiation	P
GO:0030856	11	8.38E-01	1.00E+00	1.00E+00	1.00E+00	5.56E-01	1.00E+00	1.00E+00	1.00E+00	7.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	regulation of epithelial cell differentiation	P
GO:0030863	32	4.27E-01	1.00E+00	6.42E-01	1.00E+00	9.13E-02	1.00E+00	2.76E-01	1.00E+00	5.61E-01	1.00E+00	7.54E-01	1.00E+00	8.62E-01	1.00E+00	6.19E-01	1.00E+00	cortical cytoskeleton	C
GO:0030864	22	2.85E-01	1.00E+00	5.69E-01	1.00E+00	5.42E-02	1.00E+00	2.61E-01	1.00E+00	4.36E-01	1.00E+00	6.66E-01	1.00E+00	5.72E-01	1.00E+00	5.82E-01	1.00E+00	cortical actin cytoskeleton	C
GO:0030865	11	3.23E-01	1.00E+00	1.74E-01	1.00E+00	2.14E-01	1.00E+00	3.92E-01	1.00E+00	4.76E-01	1.00E+00	2.24E-01	1.00E+00	2.69E-01	1.00E+00	1.56E-01	1.00E+00	cortical cytoskeleton organization and biogε	P
GO:0030866	10	3.47E-01	1.00E+00	2.17E-01	1.00E+00	2.53E-01	1.00E+00	4.73E-01	1.00E+00	5.09E-01	1.00E+00	2.74E-01	1.00E+00	2.48E-01	1.00E+00	1.55E-01	1.00E+00	cortical actin cytoskeleton organization and	P
GO:0030867	11	2.41E-01	1.00E+00	2.67E-01	1.00E+00	2.78E-01	1.00E+00	4.66E-01	1.00E+00	1.73E-01	1.00E+00	2.68E-01	1.00E+00	7.32E-01	1.00E+00	2.54E-01	1.00E+00	rough endoplasmic reticulum membrane	C
GO:0030879	28	9.59E-01	1.00E+00	9.99E-01	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	8.55E-01	1.00E+00	9.78E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	mammary gland development	P
GO:0030880	26	3.41E-02	1.00E+00	2.94E-02	1.00E+00	9.97E-02	1.00E+00	8.93E-01	1.00E+00	1.05E-01	1.00E+00	5.56E-03	7.40E-02	6.13E-01	1.00E+00	3.22E-01	1.00E+00	RNA polymerase complex	C
GO:0030888	17	8.58E-01	1.00E+00	9.16E-01	1.00E+00	7.92E-01	1.00E+00	5.01E-01	1.00E+00	7.18E-01	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	3.70E-01	1.00E+00	regulation of B cell proliferation	P
GO:0030890	14	8.22E-01	1.00E+00	8.67E-01	1.00E+00	8.62E-01	1.00E+00	4.93E-01	1.00E+00	6.68E-01	1.00E+00	9.06E-01	1.00E+00	1.00E+00	1.00E+00	5.39E-01	1.00E+00	positive regulation of B cell proliferation	P
GO:0030894	11	8.93E-02	1.00E+00	3.22E-02	1.00E+00	1.09E-02	1.57E-01	1.01E-01	1.00E+00	1.12E-01	1.00E+00	4.70E-02	1.00E+00	8.55E-01	1.00E+00	1.96E-01	1.00E+00	replisome	C
GO:0030900	106	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	forebrain development	P
GO:0030901	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	midbrain development	P
GO:0030902	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hindbrain development	P
GO:0030955	119	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	potassium ion binding	F
GO:0030968	17	8.59E-01	1.00E+00	9.75E-01	1.00E+00	7.85E-01	1.00E+00	3.61E-01	1.00E+00	6.38E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	unfolded protein response	P
GO:0030983	23	2.98E-07	1.25E-04	7.32E-06	1.41E-03	3.19E-02	5.87E-01	1.11E-01	1.00E+00	1.50E-06	5.00E-04	5.67E-07	2.22E-04	8.94E-01	1.00E+00	5.75E-02	1.00E+00	mismatched DNA binding	F
GO:0031012	351	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular matrix	C
GO:0031016	20	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	pancreas development	P
GO:0031018	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endocrine pancreas development	P
GO:0031023	18	1.02E-01	1.00E+00	9.99E-03	3.84E-01	4.95E-02	8.68E-01	3.14E-02	5.42E-01	1.78E-01	1.00E+00	3.24E-02	1.00E+00	4.89E-01	1.00E+00	4.19E-02	8.10E-01	microtubule organizing center organization	P
GO:0031032	12	5.94E-01	1.00E+00	3.49E-01	1.00E+00	4.25E-01	1.00E+00	6.12E-01	1.00E+00	6.85E-01	1.00E+00	2.52E-01	1.00E+00	5.05E-01	1.00E+00	6.62E-01	1.00E+00	actomyosin structure organization and biog	P
GO:0031047	14	5.76E-01	1.00E+00	1.02E-01	1.00E+00	5.11E-01	1.00E+00	1.03E-01	1.00E+00	5.18E-01	1.00E+00	1.30E-01	1.00E+00	8.07E-01	1.00E+00	1.27E-01	1.00E+00	RNA-mediated gene silencing	P
GO:0031069	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.49E-01	1.00E+00	hair follicle morphogenesis	P
GO:0031072	66	4.42E-01	1.00E+00	4.53E-02	1.00E+00	3.59E-01	1.00E+00	1.04E-01	1.00E+00	4.73E-01	1.00E+00	4.12E-02	1.00E+00	7.82E-01	1.00E+00	5.41E-01	1.00E+00	heat shock protein binding	F
GO:0031090	1525	1.48E-03	4.90E-02	1.59E-05	2.21E-03	1.13E-09	0.00E+00	5.06E-09	0.00E+00	2.41E-02	6.55E-01	1.37E-03	1.70E-02	8.93E-01	1.00E+00	7.68E-01	1.00E+00	organelle membrane	C
GO:0031091	45	8.45E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	7.35E-01	1.00E+00	9.84E-01	1.00E+00	8.42E-01	1.00E+00	1.00E+00	1.00E+00	platelet alpha granule	C
GO:0031092	10	7.34E-01	1.00E+00	9.85E-01	1.00E+00	5.36E-01	1.00E+00	9.54E-01	1.00E+00	6.19E-01	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	platelet alpha granule membrane	C
GO:0031093	33	7.34E-01	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	6.43E-01	1.00E+00	9.53E-01	1.00E+00	6.47E-01	1.00E+00	9.99E-01	1.00E+00	platelet alpha granule lumen	C
GO:0031098	83	9.43E-01	1.00E+00	9.67E-01	1.00E+00	8.06E-01	1.00E+00	8.88E-01	1.00E+00	9.18E-01	1.00E+00	9.67E-01	1.00E+00	9.79E-01	1.00E+00	8.35E-01	1.00E+00	stress-activated protein kinase signaling pa	P
GO:0031099	26	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.00E-01	1.00E+00	9.98E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	8.08E-01	1.00E+00	regeneration	P
GO:0031105	12	2.38E-01	1.00E+00	4.13E-01	1.00E+00	2.91E-01	1.00E+00	8.91E-01	1.00E+00	2.33E-01	1.00E+00	3.21E-01	1.00E+00	2.31E-01	1.00E+00	2.52E-01	1.00E+00	septin complex	C
GO:0031109	32	9.43E-01	1.00E+00	8.35E-01	1.00E+00	4.31E-01	1.00E+00	4.63E-01	1.00E+00	9.67E-01	1.00E+00	8.61E-01	1.00E+00	9.97E-01	1.00E+00	8.72E-01	1.00E+00	microtubule polymerization or depolymeriza	P
GO:0031110	29	8.30E-01	1.00E+00	7.50E-01	1.00E+00	3.06E-01	1.00E+00	4.34E-01	1.00E+00	8.89E-01	1.00E+00	7.77E-01	1.00E+00	9.84E-01	1.00E+00	8.19E-01	1.00E+00	regulation of microtubule polymerization or	P
GO:0031111	18	4.38E-01	1.00E+00	8.58E-02	1.00E+00	2.46E-01	1.00E+00	1.37E-01	1.00E+00	4.36E-01	1.00E+00	8.67E-02	1.00E+00	8.98E-01	1.00E+00	4.36E-01	1.00E+00	negative regulation of microtubule polymeri	P
GO:0031112	12	9.24E-01	1.00E+00	1.00E+00	1.00E+00	4.33E-01	1.00E+00	9.96E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031113	13	9.44E-01	1.00E+00	9.97E-01	1.00E+00	4.15E-01	1.00E+00	6.03E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	9.68E-01	1.00E+00	regulation of microtubule polymerization	P
GO:0031114	16	3.10E-01	1.00E+00	1.66E-01	1.00E+00	1.68E-01	1.00E+00	3.34E-01	1.00E+00	3.35E-01	1.00E+00	1.21E-01	1.00E+00	7.80E-01	1.00E+00	4.91E-01	1.00E+00	regulation of microtubule depolymerization	P
GO:0031116	11	9.06E-01	1.00E+00	1.00E+00	1.00E+00	3.25E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031123	15	6.40E-03	1.37E-01	2.04E-02	9.24E-01	2.19E-04	6.00E-03	3.11E-02	5.42E-01	1.81E-02	3.81E-01	4.52E-02	1.00E+00	5.77E-01	1.00E+00	6.72E-02	1.00E+00	RNA 3'-end processing	P
GO:0031124	13	1.44E-02	2.72E-01	4.45E-02	1.00E+00	1.03E-03	1.25E-02	7.91E-02	1.00E+00	2.88E-02	6.55E-01	7.85E-02	1.00E+00	5.52E-01	1.00E+00	6.24E-02	1.00E+00	mRNA 3'-end processing	P
GO:0031128	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	induction	P
GO:0031145	69	4.85E-02	1.00E+00	4.07E-02	1.00E+00	1.69E-01	1.00E+00	4.70E-03	6.84E-02	5.45E-02	1.00E+00	9.47E-02	1.00E+00	3.72E-01	1.00E+00	3.90E-01	1.00E+00	anaphase-promoting complex-dependent pı	P
GO:0031175	215	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurite development	P
GO:0031177	18	4.55E-02	1.00E+00	6.01E-01	1.00E+00	3.28E-01	1.00E+00	6.10E-01	1.00E+00	2.95E-02	6.55E-01	5.72E-01	1.00E+00	3.18E-01	1.00E+00	8.24E-01	1.00E+00	phosphopantetheine binding	F
GO:0031201	11	9.22E-01	1.00E+00	5.23E-01	1.00E+00	7.13E-01	1.00E+00	4.88E-01	1.00E+00	9.54E-01	1.00E+00	5.82E-01	1.00E+00	9.66E-01	1.00E+00	3.24E-01	1.00E+00	SNARE complex	C
GO:0031202	25	7.42E-04	1.60E-02	5.55E-03	1.50E-01	2.18E-03	1.80E-02	3.29E-02	5.42E-01	2.70E-03	4.90E-02	6.00E-03	1.05E-01	1.63E-01	1.00E+00	5.13E-01	1.00E+00	RNA splicing factor activity, transesterificatic	F
GO:0031214	141	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.80E-01	1.00E+00	9.61E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	biomineral formation	P
GO:0031224	5122	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	intrinsic to membrane	C
GO:0031225	127	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	anchored to membrane	C
GO:0031226	1204	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	intrinsic to plasma membrane	C
GO:0031227	47	6.27E-01	1.00E+00	8.01E-01	1.00E+00	1.65E-01	1.00E+00	2.97E-01	1.00E+00	6.68E-01	1.00E+00	9.41E-01	1.00E+00	9.64E-01	1.00E+00	3.65E-01	1.00E+00	intrinsic to endoplasmic reticulum membran	C
GO:0031228	43	6.58E-01	1.00E+00	5.62E-01	1.00E+00	4.77E-01	1.00E+00	8.85E-01	1.00E+00	5.31E-01	1.00E+00	3.50E-01	1.00E+00	9.89E-01	1.00E+00	8.11E-01	1.00E+00	intrinsic to Golgi membrane	C
GO:0031231	12	1.21E-01	1.00E+00	5.75E-01	1.00E+00	1.18E-01	1.00E+00	7.26E-01	1.00E+00	1.88E-01	1.00E+00	4.40E-01	1.00E+00	7.75E-01	1.00E+00	5.68E-01	1.00E+00	intrinsic to peroxisomal membrane	C
GO:0031252	90	8.90E-01	1.00E+00	5.68E-01	1.00E+00	5.38E-01	1.00E+00	1.87E-01	1.00E+00	7.48E-01	1.00E+00	6.63E-01	1.00E+00	1.00E+00	1.00E+00	7.72E-01	1.00E+00	leading edge	C
GO:0031253	14	2.84E-01	1.00E+00	6.41E-01	1.00E+00	4.41E-01	1.00E+00	3.30E-01	1.00E+00	2.27E-01	1.00E+00	7.00E-01	1.00E+00	7.55E-01	1.00E+00	7.95E-01	1.00E+00	cell projection membrane	C
GO:0031267	75	6.00E-01	1.00E+00	2.80E-01	1.00E+00	5.33E-01	1.00E+00	1.70E-01	1.00E+00	5.41E-01	1.00E+00	3.84E-01	1.00E+00	6.65E-01	1.00E+00	3.67E-01	1.00E+00	small GTPase binding	F
GO:0031279	44	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.98E-01	1.00E+00	5.75E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	regulation of cyclase activity	P
GO:0031280	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of cyclase activity	P
GO:0031281	25	9.64E-01	1.00E+00	8.96E-01	1.00E+00	9.29E-01	1.00E+00	3.09E-01	1.00E+00	9.61E-01	1.00E+00	9.91E-01	1.00E+00	6.28E-01	1.00E+00	9.68E-01	1.00E+00	positive regulation of cyclase activity	P
GO:0031290	10	9.89E-01	1.00E+00	9.82E-01	1.00E+00	9.82E-01	1.00E+00	9.51E-01	1.00E+00	9.92E-01	1.00E+00	9.85E-01	1.00E+00	9.67E-01	1.00E+00	9.83E-01	1.00E+00	retinal ganglion cell axon guidance	P
GO:0031300	114	5.38E-01	1.00E+00	5.63E-01	1.00E+00	5.38E-02	1.00E+00	4.05E-01	1.00E+00	5.73E-01	1.00E+00	6.07E-01	1.00E+00	9.98E-01	1.00E+00	5.94E-01	1.00E+00	intrinsic to organelle membrane	C
GO:0031301	100	5.33E-01	1.00E+00	4.80E-01	1.00E+00	2.78E-02	4.97E-01	1.88E-01	1.00E+00	6.32E-01	1.00E+00	6.62E-01	1.00E+00	9.99E-01	1.00E+00	4.49E-01	1.00E+00	integral to organelle membrane	C
GO:0031323	2947	9.94E-01	1.00E+00	1.95E-04	8.26E-03	1.42E-02	1.92E-01	5.70E-08	0.00E+00	9.95E-01	1.00E+00	4.58E-03	7.40E-02	1.00E+00	1.00E+00	8.03E-01	1.00E+00	regulation of cellular metabolism	P
GO:0031324	454	8.27E-01	1.00E+00	4.42E-01	1.00E+00	2.31E-01	1.00E+00	1.86E-02	4.10E-01	7.52E-01	1.00E+00	6.97E-01	1.00E+00	1.00E+00	1.00E+00	7.97E-01	1.00E+00	negative regulation of cellular metabolism	P
GO:0031325	516	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.03E-01	1.00E+00	9.27E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of cellular metabolism	P
GO:0031326	212	4.42E-01	1.00E+00	1.75E-01	1.00E+00	7.07E-02	1.00E+00	3.70E-02	1.00E+00	5.72E-01	1.00E+00	1.56E-01	1.00E+00	9.78E-01	1.00E+00	9.55E-01	1.00E+00	regulation of cellular biosynthesis	P
GO:0031327	49	3.40E-01	1.00E+00	2.95E-01	1.00E+00	3.18E-01	1.00E+00	8.07E-02	1.00E+00	4.16E-01	1.00E+00	4.79E-01	1.00E+00	4.08E-01	1.00E+00	3.37E-01	1.00E+00	negative regulation of cellular biosynthesis	P

GO:0031328	79	8.34E-01	1.00E+00	8.20E-01	1.00E+00	2.86E-01	1.00E+00	4.30E-01	1.00E+00	7.67E-01	1.00E+00	6.95E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	positive regulation of cellular biosynthesis	P
GO:0031341	12	4.11E-01	1.00E+00	9.29E-01	1.00E+00	8.91E-01	1.00E+00	9.40E-01	1.00E+00	2.78E-01	1.00E+00	8.73E-01	1.00E+00	7.07E-01	1.00E+00	9.32E-01	1.00E+00	regulation of cell killing	P
GO:0031365	11	5.98E-01	1.00E+00	2.54E-02	1.00E+00	3.51E-02	5.87E-01	5.08E-04	7.17E-03	9.12E-01	1.00E+00	1.33E-01	1.00E+00	9.76E-01	1.00E+00	4.26E-01	1.00E+00	N-terminal protein amino acid modification	P
GO:0031396	12	4.57E-01	1.00E+00	8.67E-01	1.00E+00	2.10E-01	1.00E+00	9.92E-01	1.00E+00	5.76E-01	1.00E+00	7.94E-01	1.00E+00	7.42E-01	1.00E+00	7.08E-01	1.00E+00	regulation of protein ubiquitination	P
GO:0031399	14	4.99E-01	1.00E+00	8.99E-01	1.00E+00	1.98E-01	1.00E+00	9.94E-01	1.00E+00	6.19E-01	1.00E+00	8.47E-01	1.00E+00	7.99E-01	1.00E+00	6.90E-01	1.00E+00	regulation of protein modification	P
GO:0031402	113	9.91E-01	1.00E+00	1.00E+00	1.00E+00	4.71E-01	1.00E+00	9.64E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	sodium ion binding	F
GO:0031404	69	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.10E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	chloride ion binding	F
GO:0031406	12	5.08E-01	1.00E+00	1.43E-01	1.00E+00	7.15E-01	1.00E+00	4.19E-01	1.00E+00	4.65E-01	1.00E+00	1.53E-01	1.00E+00	4.08E-01	1.00E+00	1.48E-01	1.00E+00	carboxylic acid binding	F
GO:0031410	494	7.82E-01	1.00E+00	5.29E-01	1.00E+00	2.57E-01	1.00E+00	9.06E-02	1.00E+00	6.50E-01	1.00E+00	6.20E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	cytoplasmic vesicle	C
GO:0031418	20	4.12E-01	1.00E+00	7.67E-01	1.00E+00	3.84E-01	1.00E+00	6.43E-01	1.00E+00	3.25E-01	1.00E+00	6.07E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	L-ascorbic acid binding	F
GO:0031420	215	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	alkali metal ion binding	F
GO:0031424	42	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	9.86E-01	1.00E+00	8.56E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	keratinization	P
GO:0031461	13	2.10E-01	1.00E+00	6.17E-02	1.00E+00	2.02E-01	1.00E+00	1.38E-01	1.00E+00	4.04E-01	1.00E+00	1.56E-01	1.00E+00	2.01E-02	2.56E-01	1.71E-01	1.00E+00	cullin-RING ubiquitin ligase complex	C
GO:0031497	117	2.16E-01	1.00E+00	4.27E-01	1.00E+00	3.24E-01	1.00E+00	4.25E-01	1.00E+00	1.58E-01	1.00E+00	2.67E-01	1.00E+00	9.53E-01	1.00E+00	9.98E-01	1.00E+00	chromatin assembly	P
GO:0031507	14	6.00E-02	1.00E+00	9.01E-02	1.00E+00	1.31E-01	1.00E+00	2.13E-01	1.00E+00	5.47E-02	1.00E+00	3.86E-02	1.00E+00	4.70E-01	1.00E+00	8.09E-01	1.00E+00	heterochromatin formation	P
GO:0031513	18	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.88E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	nonmotile primary cilium	C
GO:0031519	12	4.80E-01	1.00E+00	1.35E-01	1.00E+00	1.26E-01	1.00E+00	1.55E-01	1.00E+00	6.71E-01	1.00E+00	1.71E-01	1.00E+00	8.35E-01	1.00E+00	8.47E-02	1.00E+00	PcG protein complex	C
GO:0031526	11	3.70E-01	1.00E+00	6.50E-01	1.00E+00	7.77E-01	1.00E+00	4.57E-01	1.00E+00	2.33E-01	1.00E+00	6.23E-01	1.00E+00	7.69E-01	1.00E+00	9.05E-01	1.00E+00	brush border membrane	C
GO:0031532	12	6.77E-01	1.00E+00	2.74E-01	1.00E+00	5.38E-01	1.00E+00	8.78E-02	1.00E+00	9.97E-01	1.00E+00	4.15E-01	1.00E+00	2.42E-01	1.00E+00	7.53E-01	1.00E+00	actin cytoskeleton reorganization	P
GO:0031570	36	7.61E-02	1.00E+00	1.81E-02	9.24E-01	9.98E-03	1.57E-01	1.23E-02	1.57E-01	1.50E-01	1.00E+00	5.05E-02	1.00E+00	3.34E-01	1.00E+00	2.04E-01	1.00E+00	DNA integrity checkpoint	P
GO:0031589	121	8.47E-01	1.00E+00	9.08E-01	1.00E+00	2.90E-01	1.00E+00	7.35E-01	1.00E+00	7.99E-01	1.00E+00	8.43E-01	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	cell-substrate adhesion	P
GO:0031594	15	9.98E-01	1.00E+00	9.59E-01	1.00E+00	8.40E-01	1.00E+00	3.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.69E-01	1.00E+00	7.94E-01	1.00E+00	neuromuscular junction	C
GO:0031625	13	6.33E-01	1.00E+00	2.16E-01	1.00E+00	2.06E-01	1.00E+00	2.44E-01	1.00E+00	9.57E-01	1.00E+00	3.40E-01	1.00E+00	4.43E-01	1.00E+00	3.40E-01	1.00E+00	ubiquitin protein ligase binding	F
GO:0031644	75	1.00E+00	1.00E+00	9.55E-01	1.00E+00	8.81E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	6.44E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	regulation of neurophysiological process	P
GO:0031645	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.17E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of neurophysiological pr	P
GO:0031646	23	1.00E+00	1.00E+00	8.39E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	5.19E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	positive regulation of neurophysiological pro	P
GO:0031647	29	6.64E-01	1.00E+00	4.17E-01	1.00E+00	5.31E-01	1.00E+00	2.09E-01	1.00E+00	6.41E-01	1.00E+00	4.71E-01	1.00E+00	6.82E-01	1.00E+00	5.64E-01	1.00E+00	regulation of protein stability	P
GO:0031663	10	4.72E-01	1.00E+00	5.42E-01	1.00E+00	4.02E-01	1.00E+00	6.54E-01	1.00E+00	4.48E-01	1.00E+00	4.51E-01	1.00E+00	9.92E-01	1.00E+00	8.72E-01	1.00E+00	lipopolysaccharide-mediated signaling path	P
GO:0031667	91	8.77E-01	1.00E+00	8.28E-01	1.00E+00	2.40E-01	1.00E+00	9.02E-01	1.00E+00	9.30E-01	1.00E+00	7.66E-01	1.00E+00	9.30E-01	1.00E+00	6.20E-01	1.00E+00	response to nutrient levels	P
GO:0031668	15	4.83E-01	1.00E+00	6.43E-01	1.00E+00	6.61E-01	1.00E+00	5.74E-01	1.00E+00	4.94E-01	1.00E+00	7.91E-01	1.00E+00	4.44E-01	1.00E+00	1.51E-01	1.00E+00	cellular response to extracellular stimulus	P
GO:0031669	13	3.27E-01	1.00E+00	6.02E-01	1.00E+00	4.98E-01	1.00E+00	8.68E-01	1.00E+00	3.66E-01	1.00E+00	6.12E-01	1.00E+00	3.11E-01	1.00E+00	2.06E-01	1.00E+00	cellular response to nutrient levels	P
GO:0031672	23	2.70E-01	1.00E+00	9.97E-01	1.00E+00	1.48E-01	1.00E+00	9.54E-01	1.00E+00	3.36E-01	1.00E+00	9.88E-01	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	A band	C
GO:0031901	22	5.57E-01	1.00E+00	9.41E-02	1.00E+00	3.80E-01	1.00E+00	4.77E-02	1.00E+00	5.77E-01	1.00E+00	1.80E-01	1.00E+00	8.19E-01	1.00E+00	3.33E-01	1.00E+00	early endosome membrane	C
GO:0031902	37	1.78E-01	1.00E+00	2.20E-01	1.00E+00	4.76E-01	1.00E+00	1.78E-02	4.10E-01	9.21E-02	1.00E+00	2.57E-01	1.00E+00	9.66E-01	1.00E+00	9.34E-01	1.00E+00	late endosome membrane	C
GO:0031903	42	3.11E-02	1.00E+00	3.47E-01	1.00E+00	9.70E-02	1.00E+00	8.05E-02	1.00E+00	7.29E-02	1.00E+00	5.60E-01	1.00E+00	4.37E-01	1.00E+00	4.44E-01	1.00E+00	microbody membrane	C
GO:0031941	14	2.18E-01	1.00E+00	6.23E-01	1.00E+00	1.17E-01	1.00E+00	2.58E-01	1.00E+00	3.00E-01	1.00E+00	6.40E-01	1.00E+00	4.15E-01	1.00E+00	9.63E-01	1.00E+00	filamentous actin	C
GO:0031965	161	9.48E-04	1.60E-02	3.88E-07	1.00E-03	8.46E-06	9.71E-04	5.09E-06	8.32E-04	2.19E-03	4.30E-02	8.54E-06	2.29E-03	6.73E-01	1.00E+00	1.31E-02	1.38E-01	nuclear membrane	C
GO:0031966	376	6.03E-04	1.60E-02	1.94E-04	8.26E-03	3.01E-04	6.00E-03	9.65E-04	1.11E-02	1.12E-02	3.01E-01	7.31E-04	1.02E-02	1.55E-01	1.00E+00	3.04E-01	1.00E+00	mitochondrial membrane	C
GO:0031967	586	1.11E-05	5.00E-03	9.34E-09	1.00E-03	2.20E-08	0.00E+00	1.32E-07	0.00E+00	1.28E-03	4.30E-02	6.71E-07	2.22E-04	2.10E-01	1.00E+00	6.50E-02	1.00E+00	organelle envelope	C
GO:0031968	88	2.32E-01	1.00E+00	4.02E-02	1.00E+00	1.22E-01	1.00E+00	8.59E-02	1.00E+00	6.51E-01	1.00E+00	1.50E-01	1.00E+00	5.49E-02	1.00E+00	1.41E-01	1.00E+00	organelle outer membrane	C
GO:0031970	33	9.15E-01	1.00E+00	4.08E-01	1.00E+00	5.31E-01	1.00E+00	6.72E-02	1.00E+00	9.77E-01	1.00E+00	4.90E-01	1.00E+00	8.88E-01	1.00E+00	9.48E-01	1.00E+00	organelle envelope lumen	C
GO:0031974	1243	3.11E-06	2.60E-03	6.58E-13	0.00E+00	3.59E-08	0.00E+00	1.84E-10	0.00E+00	4.31E-04	4.00E-03	6.31E-09	1.05E-04	4.61E-01	1.00E+00	1.29E-01	1.00E+00	membrane-enclosed lumen	C
GO:0031975	613	4.03E-05	5.00E-03	8.86E-08	1.00E-03	2.97E-08	0.00E+00	7.17E-07	0.00E+00	4.10E-03	6.24E-02	2.98E-06	2.29E-03	2.35E-01	1.00E+00	9.48E-02	1.00E+00	envelope	C
GO:0031980	195	2.12E-03	4.90E-02	1.06E-03	2.00E-02	9.60E-02	1.00E+00	2.75E-03	5.60E-02	2.36E-03	4.30E-02	1.01E-02	2.12E-01	2.77E-01	1.00E+00	6.44E-01	1.00E+00	mitochondrial lumen	C
GO:0031981	899	1.59E-05	5.00E-03	4.03E-13	0.00E+00	3.60E-08	0.00E+00	3.43E-09	0.00E+00	1.61E-03	4.30E-02	4.72E-09	1.05E-04	5.09E-01	1.00E+00	1.89E-02	1.77E-01	nuclear lumen	C
GO:0031982	510	8.45E-01	1.00E+00	5.69E-01	1.00E+00	2.49E-01	1.00E+00	9.15E-02	1.00E+00	7.38E-01	1.00E+00	6.42E-01	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	vesicle	C
GO:0031988	422	7.00E-01	1.00E+00	5.10E-01	1.00E+00	1.53E-01	1.00E+00	1.34E-01	1.00E+00	5.92E-01	1.00E+00	5.52E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	membrane-bound vesicle	C
GO:0032011	16	8.17E-01	1.00E+00	9.25E-01	1.00E+00	3.62E-01	1.00E+00	4.51E-01	1.00E+00	9.37E-01	1.00E+00	9.85E-01	1.00E+00	7.84E-01	1.00E+00	6.35E-01	1.00E+00	ARF protein signal transduction	P
GO:0032012	16	8.17E-01	1.00E+00	9.25E-01	1.00E+00	3.62E-01	1.00E+00	4.51E-01	1.00E+00	9.37E-01	1.00E+00	9.85E-01	1.00E+00	7.84E-01	1.00E+00	6.35E-01	1.00E+00	regulation of ARF protein signal transductio	P
GO:0032039	13	1.83E-01	1.00E+00	1.11E-01	1.00E+00	5.21E-02	1.00E+00	3.70E-02	1.00E+00	5.83E-01	1.00E+00	1.33E-01	1.00E+00	1.76E-01	1.00E+00	7.87E-01	1.00E+00	integrator complex	C
GO:0032094	10	9.28E-01	1.00E+00	9.64E-01	1.00E+00	3.93E-01	1.00E+00	6.53E-01	1.00E+00	9.83E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.02E-01	1.00E+00	response to food	P
GO:0032147	64	9.70E-01	1.00E+00	9.90E-01	1.00E+00	9.84E-01	1.00E+00	7.39E-01	1.00E+00	9.55E-01	1.00E+00	9.83E-01	1.00E+00	7.29E-01	1.00E+00	9.93E-01	1.00E+00	activation of protein kinase activity	P
GO:0032156	12	2.38E-01	1.00E+00	4.13E-01	1.00E+00	2.91E-01	1.00E+00	8.91E-01	1.00E+00	2.33E-01	1.00E+00	3.21E-01	1.00E+00	2.31E-01	1.00E+00	2.52E-01	1.00E+00	septin cytoskeleton	C
GO:0032182	13	2.95E-02	1.00E+00	6.46E-02	1.00E+00	3.55E-03	3.50E-02	1.80E-01	1.00E+00	1.52E-01	1.00E+00	1.26E-01	1.00E+00	9.30E-01	1.00E+00	2.97E-01	1.00E+00	small conjugating protein binding	F
GO:0032200	28	2.57E-01	1.00E+00	9.08E-02	1.00E+00	2.01E-01	1.00E+00	9.74E-02	1.00E+00	2.18E-01	1.00E+00	3.05E-01	1.00E+00	7.83E-01	1.00E+00	7.58E-02	1.00E+00	telomere organization and biogenesis	P
GO:0032259	69	3.29E-01	1.00E+00	1.45E-02	3.84E-01	7.66E-02	1.00E+00	1.78E-03	2.70E-02	3.79E-01	1.00E+00	1.16E-01	1.00E+00	9.41E-01	1.00E+00	1.71E-02	1.77E-01	methylation	P
GO:0032312	31	2.07E-02	1.00E+00	6.04E-01	1.00E+00	3.44E-02	5.87E-01	1.45E-01	1.00E+00	1.51E-01	1.00E+00	8.05E-01	1.00E+00	1.57E-02	2.07E-01	4.58E-01	1.00E+00	regulation of ARF GTPase activity	P
GO:0032313	59	9.93E-01	1.00E+00	9.98E-01	1.00E+00	7.98E-01	1.00E+00	9.13E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.59E-01	1.00E+00	regulation of Rab GTPase activity	P
GO:0032318	104	6.63E-01	1.00E+00	9.81E-01	1.00E+00	2.88E-01	1.00E+00	5.78E-01	1.00E+00	8.53E-01	1.00E+00	9.93E-01	1.00E+00	3.27E-01	1.00E+00	9.61E-01	1.00E+00	regulation of Ras GTPase activity	P
GO:0032319	12	2.46E-01	1.00E+00	1.49E-01	1.00E+00	3.45E-01	1.00E+00	1.92E-01	1.00E+00	3.03E-01	1.00E+00	9.27E-02	1.00E+00	1.70E-01	1.00E+00	7.71E-01	1.00E+00	regulation of Rho GTPase activity	P
GO:0032392	12	1.79E-01	1.00E+00	6.00E-02	1.00E+00	8.98E-02	1.00E+00	5.83E-01	1.00E+00	6.99E-01	1.00E+00	1.96E-01	1.00E+00	1.38E-01	1.00E+00	1.00E-01	1.00E+00	DNA geometric change	P
GO:0032393	24	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	MHC class I receptor activity	F
GO:0032395	23	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	MHC class II receptor activity	F
GO:0032403	110	9.91E-01	1.00E+00	9.04E-01	1.00E+00	7.25E-01	1.00E+00	6.15E-01	1.00E+00	9.81E-01	1.00E+00	9.57E-01	1.00E+00	9.93E-01	1.00E+00	8.23E-01	1.00E+00	protein complex binding	F
GO:0032432	19	8.85E-01	1.00E+00	4.85E-01	1.00E+00	7.34E-01	1.00E+00	2.96E-01	1.00E+00	9.65E-01	1.00E+00	4.01E-01	1.00E+00	5.53E-01	1.00E+00	8.87E-01	1.00E+00	actin filament bundle	C
GO:0035004	12	1.60E-01	1.00E+00	2.28E-01	1.00E+00	4.39E-02	7.24E-01	1.84E-01	1.00E+00	2.54E-01	1.00E+00	2.35E-01	1.00E+00	8.72E-01	1.00E+00	8.06E-01	1.00E+00	phosphoinositide 3-kinase activity	F
GO:0035014	10	9.43E-02	1.00E+00	9.13E-02	1.00E+00	2.32E-01	1.00E+00	4.12E-01	1.00E+00	5.20E-02	1.00E+00	1.23E-01	1.00E+00	4.65E-01	1.00E+00	1.74E-01	1.00E+00	phosphoinositide 3-kinase regulator activity	F
GO:0035023	78	9.91E-01	1.00E+00	9.25E-01	1.00E+00	6.51E-01	1.00E+00	2.90E-01	1.00E+00	9.89E-01	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of Rho protein signal transductio	P
GO:0035036	16	1.92E-01	1.00E+00	7.89E-02	1.00E+00	3.00E-01	1.00E+00	6.77E-02	1.00E+00	2.55E-01	1.00E+00	7.21E-02	1.00E+00	1.92E-01	1.00E+00	9.01E-01	1.00E+00	sperm-egg recognition	P
GO:0035051	15	6.85E-01	1.00E+00	9.28E-01	1.00E+00	5.20E-01	1.00E+00	5.31E-01	1.00E+00	6.47E-01	1.00E+00	9.67E-01	1.00E+00	9.62E-01	1.00E+00	9.98E-01	1.00E+00	cardiac cell differentiation	P
GO:0035088	12	6.22E-01	1.00E+00	7.00E-01	1.00E+00	2.68E-01	1.00E+00	3.56E-01	1.00E+00	5.95E-01	1.00E+00	8.41E-01	1.00E+00	9.46E-01	1.00E+00	3.98E-01	1.00E+00	establishment and/or maintenance of apical	P
GO:0035091	84	9.76E-02	1.00E+00	9.41E-03	3.84E-01	3.17E-03	3.50E-02	3.54E-04	7.00E-03	1.94E-01	1.00E+00	4.23E-02	1.00E+00	6.89E-01	1.00E+00	2.73E-01	1.00E+00	phosphoinositide binding	F
GO:0035094	11	8.20E-01	1.00E+00	4.01E-01	1.00E+00	5.66E-01	1.00E+00	7.16E-01	1.00E+00	9.33E-01	1.00E+00	2.95E-01	1.00E+00	4.66E-01	1.00E+00	4.57E-01	1.00E+00	response to nicotine	P
GO:0035107	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	appendage morphogenesis	P
GO:0035108	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	limb morphogenesis	P

GO:0035113	70	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic appendage morphogenesis	P
GO:0035115	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic forelimb morphogenesis	P
GO:0035116	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic hindlimb morphogenesis	P
GO:0035136	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	forelimb morphogenesis	P
GO:0035137	20	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.93E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hindlimb morphogenesis	P
GO:0035239	94	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tube morphogenesis	P
GO:0035240	66	9.97E-01	1.00E+00	9.90E-01	1.00E+00	9.28E-01	1.00E+00	9.63E-01	1.00E+00	9.99E-01	1.00E+00	9.65E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	dopamine binding	F
GO:0035249	19	9.62E-01	1.00E+00	1.00E+00	1.00E+00	7.71E-01	1.00E+00	9.84E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	synaptic transmission, glutamatergic	P
GO:0035250	19	1.00E+00	1.00E+00	8.40E-01	1.00E+00	9.92E-01	1.00E+00	1.86E-01	1.00E+00	9.91E-01	1.00E+00	9.29E-01	1.00E+00	1.00E+00	1.00E+00	8.33E-01	1.00E+00	1.00E+00	UDP-galactosyltransferase activity	F
GO:0035257	75	8.34E-01	1.00E+00	2.22E-01	1.00E+00	2.33E-01	1.00E+00	2.25E-02	4.10E-01	8.79E-01	1.00E+00	3.01E-01	1.00E+00	9.98E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	nuclear hormone receptor binding	F
GO:0035258	35	6.69E-01	1.00E+00	1.85E-01	1.00E+00	1.76E-01	1.00E+00	1.78E-02	4.10E-01	7.87E-01	1.00E+00	4.38E-01	1.00E+00	9.26E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	steroid hormone receptor binding	F
GO:0035264	51	8.48E-01	1.00E+00	8.60E-01	1.00E+00	3.69E-01	1.00E+00	4.93E-01	1.00E+00	9.14E-01	1.00E+00	8.89E-01	1.00E+00	9.44E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	body growth	P
GO:0035265	18	9.98E-01	1.00E+00	8.65E-01	1.00E+00	9.98E-01	1.00E+00	2.12E-01	1.00E+00	9.96E-01	1.00E+00	9.89E-01	1.00E+00	8.80E-01	1.00E+00	6.89E-01	1.00E+00	1.00E+00	organ growth	P
GO:0035270	43	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endocrine system development	P
GO:0035272	15	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.08E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	exocrine system development	P
GO:0035282	40	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	segmentation	P
GO:0035295	161	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	tube development	P
GO:0035315	18	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hair cell differentiation	P
GO:0040007	341	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	6.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	growth	P
GO:0040008	234	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.77E-01	1.00E+00	8.53E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of growth	P
GO:0040011	508	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	locomotion	P
GO:0040012	102	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.80E-01	1.00E+00	7.01E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of locomotion	P
GO:0040013	33	9.87E-01	1.00E+00	9.67E-01	1.00E+00	3.07E-01	1.00E+00	9.77E-01	1.00E+00	9.95E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	negative regulation of locomotion	P
GO:0040014	41	9.55E-01	1.00E+00	9.53E-01	1.00E+00	4.91E-01	1.00E+00	6.05E-01	1.00E+00	9.81E-01	1.00E+00	9.48E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	regulation of body size	P
GO:0040017	40	9.89E-01	1.00E+00	9.59E-01	1.00E+00	9.81E-01	1.00E+00	3.46E-01	1.00E+00	9.79E-01	1.00E+00	9.46E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of locomotion	P
GO:0040018	18	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	9.88E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	positive regulation of body size	P
GO:0040029	57	3.84E-01	1.00E+00	5.06E-01	1.00E+00	2.86E-01	1.00E+00	2.43E-01	1.00E+00	3.51E-01	1.00E+00	5.64E-01	1.00E+00	7.34E-01	1.00E+00	9.19E-01	1.00E+00	1.00E+00	regulation of gene expression, epigenetic	P
GO:0042033	14	5.44E-01	1.00E+00	4.54E-01	1.00E+00	4.71E-01	1.00E+00	5.35E-01	1.00E+00	4.82E-01	1.00E+00	4.85E-01	1.00E+00	1.00E+00	1.00E+00	2.54E-01	1.00E+00	1.00E+00	chemokine biosynthesis	P
GO:0042035	73	7.18E-01	1.00E+00	9.82E-01	1.00E+00	2.69E-01	1.00E+00	9.93E-01	1.00E+00	7.48E-01	1.00E+00	9.06E-01	1.00E+00	9.57E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	regulation of cytokine biosynthesis	P
GO:0042036	18	6.98E-01	1.00E+00	9.96E-01	1.00E+00	5.83E-01	1.00E+00	8.97E-01	1.00E+00	7.72E-01	1.00E+00	1.00E+00	1.00E+00	4.40E-01	1.00E+00	6.45E-01	1.00E+00	1.00E+00	negative regulation of cytokine biosynthesis	P
GO:0042044	11	9.92E-01	1.00E+00	8.42E-01	1.00E+00	9.93E-01	1.00E+00	9.59E-01	1.00E+00	8.95E-01	1.00E+00	5.71E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	fluid transport	P
GO:0042054	37	1.31E-02	2.72E-01	6.42E-03	1.50E-01	1.27E-03	1.25E-02	1.10E-02	1.27E-01	3.28E-02	6.55E-01	4.29E-02	1.00E+00	7.37E-01	1.00E+00	5.51E-03	6.60E-02	1.00E+00	histone methyltransferase activity	F
GO:0042060	192	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	wound healing	P
GO:0042063	44	9.84E-01	1.00E+00	1.00E+00	1.00E+00	7.30E-01	1.00E+00	9.92E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	gliogenesis	P
GO:0042088	13	7.98E-02	1.00E+00	3.87E-01	1.00E+00	5.26E-02	1.00E+00	7.19E-01	1.00E+00	6.91E-02	1.00E+00	1.83E-01	1.00E+00	8.95E-01	1.00E+00	9.30E-01	1.00E+00	1.00E+00	T-helper 1 type immune response	P
GO:0042089	84	6.39E-01	1.00E+00	9.97E-01	1.00E+00	3.38E-01	1.00E+00	9.98E-01	1.00E+00	7.21E-01	1.00E+00	9.69E-01	1.00E+00	9.59E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	cytokine biosynthesis	P
GO:0042092	11	4.39E-01	1.00E+00	8.72E-01	1.00E+00	7.07E-01	1.00E+00	5.76E-01	1.00E+00	3.37E-01	1.00E+00	8.31E-01	1.00E+00	9.20E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	T-helper 2 type immune response	P
GO:0042093	13	3.45E-01	1.00E+00	6.14E-01	1.00E+00	2.36E-01	1.00E+00	7.79E-01	1.00E+00	2.80E-01	1.00E+00	4.28E-01	1.00E+00	9.35E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	T-helper cell differentiation	P
GO:0042094	18	4.05E-01	1.00E+00	9.93E-01	1.00E+00	1.63E-01	1.00E+00	9.79E-01	1.00E+00	3.36E-01	1.00E+00	9.78E-01	1.00E+00	9.82E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	interleukin-2 biosynthesis	P
GO:0042095	14	1.93E-01	1.00E+00	8.57E-01	1.00E+00	8.42E-02	1.00E+00	9.84E-01	1.00E+00	3.13E-01	1.00E+00	5.04E-01	1.00E+00	5.05E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	interferon-gamma biosynthesis	P
GO:0042098	54	3.47E-01	1.00E+00	9.84E-01	1.00E+00	2.63E-01	1.00E+00	9.24E-01	1.00E+00	2.90E-01	1.00E+00	9.44E-01	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	T cell proliferation	P
GO:0042100	24	9.54E-01	1.00E+00	9.36E-01	1.00E+00	7.82E-01	1.00E+00	7.42E-01	1.00E+00	9.26E-01	1.00E+00	9.24E-01	1.00E+00	9.01E-01	1.00E+00	7.90E-01	1.00E+00	1.00E+00	B cell proliferation	P
GO:0042101	13	5.68E-02	1.00E+00	9.90E-01	1.00E+00	1.57E-02	1.92E-01	7.77E-01	1.00E+00	5.81E-01	1.00E+00	9.95E-01	1.00E+00	6.04E-01	1.00E+00	6.26E-01	1.00E+00	1.00E+00	T cell receptor complex	C
GO:0042102	31	4.03E-01	1.00E+00	9.93E-01	1.00E+00	2.73E-01	1.00E+00	9.16E-01	1.00E+00	3.61E-01	1.00E+00	9.90E-01	1.00E+00	9.95E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	positive regulation of T cell proliferation	P
GO:0042107	85	6.63E-01	1.00E+00	9.98E-01	1.00E+00	3.58E-01	1.00E+00	9.99E-01	1.00E+00	7.36E-01	1.00E+00	9.75E-01	1.00E+00	9.64E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	cytokine metabolism	P
GO:0042108	49	7.16E-01	1.00E+00	8.49E-01	1.00E+00	2.97E-01	1.00E+00	9.46E-01	1.00E+00	6.77E-01	1.00E+00	6.32E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	1.00E+00	positive regulation of cytokine biosynthesis	P
GO:0042110	135	4.11E-01	1.00E+00	9.92E-01	1.00E+00	1.16E-01	1.00E+00	7.26E-01	1.00E+00	4.11E-01	1.00E+00	9.84E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	T cell activation	P
GO:0042113	98	5.73E-01	1.00E+00	9.08E-01	1.00E+00	3.31E-01	1.00E+00	8.82E-01	1.00E+00	6.08E-01	1.00E+00	8.58E-01	1.00E+00	7.55E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	B cell activation	P
GO:0042116	12	3.86E-01	1.00E+00	3.48E-01	1.00E+00	6.26E-01	1.00E+00	8.34E-01	1.00E+00	2.57E-01	1.00E+00	1.73E-01	1.00E+00	8.39E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	macrophage activation	P
GO:0042127	582	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	regulation of cell proliferation	P
GO:0042129	43	4.48E-01	1.00E+00	1.00E+00	1.00E+00	1.38E-01	1.00E+00	9.93E-01	1.00E+00	4.46E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	regulation of T cell proliferation	P
GO:0042130	15	9.08E-01	1.00E+00	1.00E+00	1.00E+00	4.68E-01	1.00E+00	1.00E+00	1.00E+00	9.12E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	negative regulation of T cell proliferation	P
GO:0042133	39	9.46E-01	1.00E+00	9.92E-01	1.00E+00	3.52E-01	1.00E+00	4.82E-01	1.00E+00	9.82E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter metabolism	P
GO:0042135	10	6.42E-01	1.00E+00	9.42E-01	1.00E+00	1.14E-01	1.00E+00	6.68E-01	1.00E+00	9.22E-01	1.00E+00	9.73E-01	1.00E+00	8.50E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	neurotransmitter catabolism	P
GO:0042136	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter biosynthesis	P
GO:0042147	10	5.32E-01	1.00E+00	2.60E-01	1.00E+00	2.65E-01	1.00E+00	3.02E-01	1.00E+00	7.44E-01	1.00E+00	1.96E-01	1.00E+00	5.74E-01	1.00E+00	4.47E-01	1.00E+00	1.00E+00	retrograde transport, endosome to Golgi	P
GO:0042157	75	6.16E-01	1.00E+00	1.85E-01	1.00E+00	2.06E-01	1.00E+00	8.06E-02	1.00E+00	6.34E-01	1.00E+00	4.34E-01	1.00E+00	9.71E-01	1.00E+00	3.88E-01	1.00E+00	1.00E+00	lipoprotein metabolism	P
GO:0042158	57	7.46E-01	1.00E+00	1.52E-01	1.00E+00	2.67E-01	1.00E+00	7.58E-02	1.00E+00	7.40E-01	1.00E+00	3.48E-01	1.00E+00	9.89E-01	1.00E+00	5.42E-01	1.00E+00	1.00E+00	lipoprotein biosynthesis	P
GO:0042162	10	5.89E-01	1.00E+00	1.64E-01	1.00E+00	4.27E-01	1.00E+00	1.15E-01	1.00E+00	6.01E-01	1.00E+00	3.74E-01	1.00E+00	6.81E-01	1.00E+00	2.82E-01	1.00E+00	1.00E+00	telomeric DNA binding	F
GO:0042165	244	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter binding	F
GO:0042166	31	5.50E-01	1.00E+00	8.64E-01	1.00E+00	2.43E-01	1.00E+00	6.14E-01	1.00E+00	6.52E-01	1.00E+00	7.64E-01	1.00E+00	7.64E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	acetylcholine binding	F
GO:0042168	19	3.21E-01	1.00E+00	1.42E-01	1.00E+00	1.78E-01	1.00E+00	4.20E-01	1.00E+00	3.82E-01	1.00E+00	1.08E-01	1.00E+00	6.25E-01	1.00E+00	4.01E-01	1.00E+00	1.00E+00	heme metabolism	P
GO:0042169	19	1.16E-01	1.00E+00	1.16E-01	1.00E+00	4.72E-02	8.68E-01	3.22E-02	5.42E-01	1.62E-01	1.00E+00	1.85E-01	1.00E+00	6.33E-01	1.00E+00	4.13E-01	1.00E+00	1.00E+00	SH2 domain binding	F
GO:0042175	521	5.36E-01	1.00E+00	3.16E-01	1.00E+00	1.16E-03	1.25E-02	3.09E-03	5.60E-02	7.66E-01	1.00E+00	7.31E-01	1.00E+00	9.99E-01	1.00E+00	8.20E-01	1.00E+00	1.00E+00	nuclear envelope-endoplasmic reticulum ne	C
GO:0042176	24	8.37E-01	1.00E+00	9.46E-01	1.00E+00	5.81E-01	1.00E+00	7.30E-01	1.00E+00	8.21E-01	1.00E+00	9.60E-01	1.00E+00	8.81E-01	1.00E+00	9.22E-01	1.00E+00	1.00E+00	regulation of protein catabolism	P
GO:0042219	17	8.73E-02	1.00E+00	2.42E-01	1.00E+00	6.80E-02	1.00E+00	3.10E-01	1.00E+00	9.57E-02	1.00E+00	2.11E-01	1.00E+00	8.65E-01	1.00E+00	4.89E-01	1.00E+00	1.00E+00	amino acid derivative catabolism	P
GO:0042221	764	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.58E-01	1.00E+00	8.49E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to chemical stimulus	P
GO:0042226	13	6.57E-01	1.00E+00	9.94E-01	1.00E+00	4.89E-01	1.00E+00	1.00E+00	1.00E+00	6.06E-01	1.00E+00	9.88E-01	1.00E+00	9.25E-01	1.00E+00	9.15E-01	1.00E+00	1.00E+00	interleukin-6 biosynthesis	P
GO:0042228	10	9.90E-01	1.00E+00	9.31E-01	1.00E+00	6.96E-01	1.00E+00	3.75E-01	1.00E+00	8.34E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	6.06E-01	1.00E+00	1.00E+00	interleukin-8 biosynthesis	P
GO:0042246	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.25E-01	1.00E+00	1.00E+00	tissue regeneration	P
GO:0042254	98	4.20E-02	1.00E+00	8.85E-03	3.84E-01	7.54E-03	1.57E-01	2.39E-02	4.10E-01	1.12E-01	1.00E+00	2.54E-02	7.69E-01	4.28E-01	1.00E+00	7.10E-01	1.00E+00	1.00E+00	ribosome biogenesis and assembly	P
GO:0042267	18	5.97E-01	1.00E+00	9.71E-01	1.00E+00	6.93E-01	1.00E+00	9.98E-01	1.00E+00	4.13E-01	1.00E+00	9.52E-01	1.00E+00	9.02E-01	1.00E+00	7.59E-01	1.00E+00	1.00E+00	natural killer cell mediated cytotoxicity	P
GO:0042277	336	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide binding	F
GO:0042278	10	4.02E-01	1.00E+00	5.46E-02	1.00E+00	1.95E-02	2.36E-01	8.68E-03	1.12E-01	9.54E-01	1.00E+00	9.94E-02	1.00E+00	6.61E-01	1.00E+00	3.71E-01	1.00E+00	1.00E+00	purine nucleoside metabolism	P
GO:0042287	36	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.43E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.35E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	MHC protein binding	F

GO:0042288	23	9.83E-01	1.00E+00	9.37E-01	1.00E+00	7.61E-01	1.00E+00	9.91E-01	1.00E+00	9.74E-01	1.00E+00	7.85E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	MHC class I protein binding	F
GO:0042303	31	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	molting cycle	P
GO:0042306	35	5.69E-01	1.00E+00	1.91E-01	1.00E+00	4.18E-01	1.00E+00	2.75E-01	1.00E+00	5.88E-01	1.00E+00	1.59E-01	1.00E+00	7.51E-01	1.00E+00	4.67E-01	1.00E+00	regulation of protein import into nucleus	P
GO:0042307	17	3.56E-01	1.00E+00	1.07E-01	1.00E+00	3.41E-01	1.00E+00	9.49E-02	1.00E+00	4.14E-01	1.00E+00	1.19E-01	1.00E+00	3.44E-01	1.00E+00	3.51E-01	1.00E+00	positive regulation of protein import into nuc	P
GO:0042308	15	9.96E-01	1.00E+00	9.90E-01	1.00E+00	9.03E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.79E-01	1.00E+00	9.95E-01	1.00E+00	9.62E-01	1.00E+00	negative regulation of protein import into nu	P
GO:0042309	194	9.97E-01	1.00E+00	9.96E-01	1.00E+00	5.05E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	homoiothermy	P
GO:0042310	27	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	vasoconstriction	P
GO:0042311	28	9.53E-01	1.00E+00	9.33E-01	1.00E+00	3.85E-01	1.00E+00	9.98E-01	1.00E+00	9.73E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	vasodilation	P
GO:0042312	13	1.00E+00	1.00E+00	9.11E-01	1.00E+00	8.37E-01	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	8.70E-01	1.00E+00	9.99E-01	1.00E+00	9.17E-01	1.00E+00	regulation of vasodilation	P
GO:0042325	117	9.82E-01	1.00E+00	1.00E+00	1.00E+00	3.43E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.96E-01	1.00E+00	regulation of phosphorylation	P
GO:0042326	17	7.10E-01	1.00E+00	8.00E-01	1.00E+00	1.63E-01	1.00E+00	6.34E-01	1.00E+00	9.91E-01	1.00E+00	8.17E-01	1.00E+00	4.96E-01	1.00E+00	7.07E-01	1.00E+00	negative regulation of phosphorylation	P
GO:0042327	36	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.61E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of phosphorylation	P
GO:0042330	195	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	6.07E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	taxis	P
GO:0042345	18	4.63E-01	1.00E+00	7.32E-02	1.00E+00	4.67E-01	1.00E+00	6.74E-02	1.00E+00	4.14E-01	1.00E+00	8.75E-02	1.00E+00	7.30E-01	1.00E+00	2.79E-01	1.00E+00	regulation of NF-kappaB import into nucleus	P
GO:0042346	10	2.49E-01	1.00E+00	7.95E-02	1.00E+00	3.12E-01	1.00E+00	7.02E-02	1.00E+00	2.49E-01	1.00E+00	9.94E-02	1.00E+00	3.62E-01	1.00E+00	2.95E-01	1.00E+00	positive regulation of NF-kappaB import into	P
GO:0042348	18	4.63E-01	1.00E+00	7.32E-02	1.00E+00	4.67E-01	1.00E+00	6.74E-02	1.00E+00	4.14E-01	1.00E+00	8.75E-02	1.00E+00	7.30E-01	1.00E+00	2.79E-01	1.00E+00	NF-kappaB import into nucleus	P
GO:0042354	10	5.56E-01	1.00E+00	5.15E-02	1.00E+00	8.95E-01	1.00E+00	1.30E-01	1.00E+00	4.31E-01	1.00E+00	5.61E-02	1.00E+00	5.73E-01	1.00E+00	1.55E-01	1.00E+00	L-fucose metabolism	P
GO:0042364	24	2.55E-01	1.00E+00	3.11E-01	1.00E+00	7.53E-02	1.00E+00	1.44E-01	1.00E+00	2.73E-01	1.00E+00	3.63E-01	1.00E+00	7.51E-01	1.00E+00	7.64E-01	1.00E+00	water-soluble vitamin biosynthesis	P
GO:0042375	11	1.22E-03	3.76E-02	8.29E-04	2.00E-02	2.48E-02	4.97E-01	3.04E-03	5.60E-02	1.26E-02	3.01E-01	2.09E-03	5.10E-02	4.22E-01	1.00E+00	1.83E-01	1.00E+00	quinone cofactor metabolism	P
GO:0042379	58	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.19E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	chemokine receptor binding	F
GO:0042383	19	8.20E-01	1.00E+00	2.04E-01	1.00E+00	8.80E-01	1.00E+00	4.74E-01	1.00E+00	8.24E-01	1.00E+00	2.07E-01	1.00E+00	4.50E-01	1.00E+00	8.78E-02	1.00E+00	sarcolemma	C
GO:0042384	22	9.53E-01	1.00E+00	8.00E-01	1.00E+00	9.47E-01	1.00E+00	5.93E-01	1.00E+00	9.69E-01	1.00E+00	8.00E-01	1.00E+00	7.10E-01	1.00E+00	8.08E-01	1.00E+00	cilium biogenesis	P
GO:0042391	44	2.79E-01	1.00E+00	8.22E-01	1.00E+00	3.05E-02	5.65E-01	6.91E-01	1.00E+00	5.69E-01	1.00E+00	8.44E-01	1.00E+00	4.74E-01	1.00E+00	6.86E-01	1.00E+00	regulation of membrane potential	P
GO:0042393	16	4.27E-02	1.00E+00	8.77E-03	3.84E-01	1.04E-01	1.00E+00	7.08E-04	8.43E-03	2.47E-02	6.55E-01	2.80E-02	1.00E+00	2.43E-01	1.00E+00	6.45E-01	1.00E+00	histone binding	F
GO:0042398	39	4.96E-01	1.00E+00	6.68E-01	1.00E+00	2.23E-01	1.00E+00	9.24E-01	1.00E+00	6.24E-01	1.00E+00	4.08E-01	1.00E+00	4.46E-01	1.00E+00	9.66E-01	1.00E+00	amino acid derivative biosynthesis	P
GO:0042401	31	8.39E-01	1.00E+00	7.36E-01	1.00E+00	7.17E-01	1.00E+00	9.90E-01	1.00E+00	9.02E-01	1.00E+00	4.16E-01	1.00E+00	4.39E-01	1.00E+00	9.84E-01	1.00E+00	biogenic amine biosynthesis	P
GO:0042402	14	1.48E-01	1.00E+00	5.27E-01	1.00E+00	1.31E-01	1.00E+00	5.95E-01	1.00E+00	1.55E-01	1.00E+00	4.37E-01	1.00E+00	7.58E-01	1.00E+00	6.31E-01	1.00E+00	biogenic amine catabolism	P
GO:0042403	10	6.86E-01	1.00E+00	1.00E+00	1.00E+00	5.81E-01	1.00E+00	5.92E-01	1.00E+00	6.09E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	thyroid hormone metabolism	P
GO:0042417	18	9.72E-01	1.00E+00	9.96E-01	1.00E+00	6.10E-01	1.00E+00	9.07E-01	1.00E+00	9.85E-01	1.00E+00	9.89E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	dopamine metabolism	P
GO:0042423	12	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	catecholamine biosynthesis	P
GO:0042430	11	1.30E-01	1.00E+00	1.59E-01	1.00E+00	4.53E-01	1.00E+00	5.92E-01	1.00E+00	9.58E-02	1.00E+00	1.66E-01	1.00E+00	1.89E-01	1.00E+00	2.14E-01	1.00E+00	indole and derivative metabolism	P
GO:0042434	11	1.30E-01	1.00E+00	1.59E-01	1.00E+00	4.53E-01	1.00E+00	5.92E-01	1.00E+00	9.58E-02	1.00E+00	1.66E-01	1.00E+00	1.89E-01	1.00E+00	2.14E-01	1.00E+00	indole derivative metabolism	P
GO:0042440	43	1.49E-01	1.00E+00	4.79E-02	1.00E+00	4.43E-02	7.24E-01	1.89E-01	1.00E+00	1.69E-01	1.00E+00	5.13E-02	1.00E+00	7.91E-01	1.00E+00	1.72E-01	1.00E+00	pigment metabolism	P
GO:0042445	105	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.42E-01	1.00E+00	7.04E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hormone metabolism	P
GO:0042446	48	9.29E-01	1.00E+00	9.98E-01	1.00E+00	6.47E-01	1.00E+00	5.49E-01	1.00E+00	9.02E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	hormone biosynthesis	P
GO:0042461	11	9.91E-01	1.00E+00	9.05E-01	1.00E+00	8.36E-01	1.00E+00	9.61E-01	1.00E+00	9.96E-01	1.00E+00	9.52E-01	1.00E+00	9.98E-01	1.00E+00	2.59E-01	1.00E+00	photoreceptor cell development	P
GO:0042470	84	4.74E-02	1.00E+00	3.20E-04	8.26E-03	1.52E-01	1.00E+00	2.33E-02	4.10E-01	2.28E-02	4.78E-01	4.10E-04	1.02E-02	5.10E-01	1.00E+00	4.69E-02	8.10E-01	melanosome	C
GO:0042471	50	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ear morphogenesis	P
GO:0042472	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inner ear morphogenesis	P
GO:0042474	10	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	middle ear morphogenesis	P
GO:0042475	35	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	odontogenesis (sensu Vertebrata)	P
GO:0042476	42	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	odontogenesis	P
GO:0042490	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mechanoreceptor differentiation	P
GO:0042491	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	auditory receptor cell differentiation	P
GO:0042493	125	5.20E-01	1.00E+00	9.93E-01	1.00E+00	1.13E-01	1.00E+00	6.79E-01	1.00E+00	6.72E-01	1.00E+00	9.95E-01	1.00E+00	8.11E-01	1.00E+00	1.00E+00	1.00E+00	response to drug	P
GO:0042503	10	9.98E-01	1.00E+00	9.39E-01	1.00E+00	7.87E-01	1.00E+00	7.60E-01	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	tyrosine phosphorylation of Stat3 protein	P
GO:0042506	10	9.10E-01	1.00E+00	9.29E-01	1.00E+00	3.10E-01	1.00E+00	8.84E-01	1.00E+00	9.97E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tyrosine phosphorylation of Stat5 protein	P
GO:0042509	20	9.88E-01	1.00E+00	9.07E-01	1.00E+00	3.20E-01	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	6.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of tyrosine phosphorylation of ST	P
GO:0042531	13	9.78E-01	1.00E+00	9.47E-01	1.00E+00	3.31E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of tyrosine phosphorylati	P
GO:0042542	29	3.33E-01	1.00E+00	6.25E-01	1.00E+00	6.35E-01	1.00E+00	9.08E-01	1.00E+00	3.81E-01	1.00E+00	4.55E-01	1.00E+00	1.88E-01	1.00E+00	6.74E-01	1.00E+00	response to hydrogen peroxide	P
GO:0042551	19	9.96E-01	1.00E+00	1.00E+00	1.00E+00	7.47E-01	1.00E+00	5.15E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	neuron maturation	P
GO:0042552	31	5.72E-01	1.00E+00	7.48E-01	1.00E+00	1.53E-01	1.00E+00	2.20E-01	1.00E+00	7.52E-01	1.00E+00	7.26E-01	1.00E+00	7.57E-01	1.00E+00	9.60E-01	1.00E+00	myelination	P
GO:0042558	14	6.36E-01	1.00E+00	1.04E-01	1.00E+00	4.13E-01	1.00E+00	2.35E-01	1.00E+00	8.34E-01	1.00E+00	2.00E-01	1.00E+00	1.95E-01	1.00E+00	9.41E-02	1.00E+00	pteridine and derivative metabolism	P
GO:0042559	11	6.88E-01	1.00E+00	3.43E-01	1.00E+00	6.19E-01	1.00E+00	2.94E-01	1.00E+00	8.21E-01	1.00E+00	7.05E-01	1.00E+00	2.61E-01	1.00E+00	2.43E-01	1.00E+00	pteridine and derivative biosynthesis	P
GO:0042562	27	9.35E-01	1.00E+00	5.64E-01	1.00E+00	3.38E-01	1.00E+00	2.46E-01	1.00E+00	9.34E-01	1.00E+00	6.83E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	hormone binding	F
GO:0042577	14	3.20E-01	1.00E+00	8.07E-01	1.00E+00	1.30E-01	1.00E+00	1.00E+00	1.00E+00	5.66E-01	1.00E+00	6.86E-01	1.00E+00	8.20E-01	1.00E+00	5.26E-01	1.00E+00	lipid phosphatase activity	F
GO:0042578	351	3.35E-01	1.00E+00	3.68E-01	1.00E+00	2.62E-03	1.80E-02	7.29E-03	8.10E-02	7.83E-01	1.00E+00	7.05E-01	1.00E+00	7.86E-01	1.00E+00	7.78E-01	1.00E+00	phosphoric ester hydrolase activity	F
GO:0042579	98	5.33E-03	1.37E-01	7.61E-02	1.00E+00	8.51E-03	1.57E-01	3.07E-03	5.60E-02	4.87E-02	1.00E+00	2.53E-01	1.00E+00	4.22E-01	1.00E+00	7.32E-01	1.00E+00	microbody	C
GO:0042592	636	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.43E-01	1.00E+00	9.63E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	homeostasis	P
GO:0042593	35	8.51E-01	1.00E+00	7.37E-01	1.00E+00	7.90E-01	1.00E+00	4.92E-01	1.00E+00	6.54E-01	1.00E+00	7.83E-01	1.00E+00	1.00E+00	1.00E+00	8.29E-01	1.00E+00	glucose homeostasis	P
GO:0042594	16	2.90E-01	1.00E+00	8.23E-01	1.00E+00	2.03E-01	1.00E+00	9.13E-01	1.00E+00	3.98E-01	1.00E+00	7.83E-01	1.00E+00	4.35E-01	1.00E+00	4.10E-01	1.00E+00	response to starvation	P
GO:0042596	13	8.01E-01	1.00E+00	9.99E-01	1.00E+00	7.56E-01	1.00E+00	9.89E-01	1.00E+00	7.21E-01	1.00E+00	1.00E+00	1.00E+00	8.41E-01	1.00E+00	9.95E-01	1.00E+00	fear response	P
GO:0042597	28	8.59E-01	1.00E+00	9.17E-01	1.00E+00	4.46E-01	1.00E+00	5.15E-01	1.00E+00	9.07E-01	1.00E+00	9.23E-01	1.00E+00	7.66E-01	1.00E+00	9.19E-01	1.00E+00	periplasmic space	C
GO:0042598	188	9.99E-01	1.00E+00	9.57E-01	1.00E+00	7.03E-01	1.00E+00	2.08E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	9.92E-01	1.00E+00	vesicular fraction	C
GO:0042605	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	peptide antigen binding	F
GO:0042611	87	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	MHC protein complex	C
GO:0042612	47	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	MHC class I protein complex	C
GO:0042613	40	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	MHC class II protein complex	C
GO:0042623	288	1.53E-01	1.00E+00	8.27E-02	1.00E+00	8.87E-03	1.57E-01	1.18E-03	1.30E-02	3.76E-01	1.00E+00	1.49E-01	1.00E+00	6.96E-01	1.00E+00	9.81E-01	1.00E+00	ATPase activity, coupled	F
GO:0042625	89	1.47E-01	1.00E+00	3.55E-01	1.00E+00	2.15E-02	2.63E-01	1.84E-01	1.00E+00	3.40E-01	1.00E+00	3.09E-01	1.00E+00	6.21E-01	1.00E+00	9.89E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042626	138	3.83E-01	1.00E+00	8.30E-01	1.00E+00	2.26E-02	2.63E-01	2.77E-01	1.00E+00	5.85E-01	1.00E+00	7.90E-01	1.00E+00	9.02E-01	1.00E+00	1.00E+00	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042627	12	4.79E-01	1.00E+00	6.98E-01	1.00E+00	3.46E-01	1.00E+00	9.62E-01	1.00E+00	4.62E-01	1.00E+00	6.28E-01	1.00E+00	8.78E-01	1.00E+00	5.66E-01	1.00E+00	chylomicron	C
GO:0042632	29	9.96E-01	1.00E+00	6.74E-01	1.00E+00	3.04E-01	1.00E+00	2.60E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	cholesterol homeostasis	P
GO:0042633	31	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	hair cycle	P
GO:0042692	75	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	muscle cell differentiation	P

GO:0042698	35	6.07E-01	1.00E+00	9.50E-01	1.00E+00	3.52E-01	1.00E+00	8.74E-01	1.00E+00	9.43E-01	1.00E+00	9.15E-01	1.00E+00	1.84E-01	1.00E+00	9.70E-01	1.00E+00	menstrual cycle	P
GO:0042730	12	2.33E-01	1.00E+00	7.67E-01	1.00E+00	3.84E-01	1.00E+00	9.09E-01	1.00E+00	8.55E-02	1.00E+00	6.44E-01	1.00E+00	9.57E-01	1.00E+00	7.06E-01	1.00E+00	fibrinolysis	P
GO:0042733	16	8.97E-01	1.00E+00	9.97E-01	1.00E+00	6.70E-01	1.00E+00	7.88E-01	1.00E+00	8.75E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	embryonic digit morphogenesis	P
GO:0042734	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	presynaptic membrane	C
GO:0042742	108	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	defense response to bacterium	P
GO:0042743	21	3.85E-01	1.00E+00	9.21E-01	1.00E+00	6.25E-01	1.00E+00	9.91E-01	1.00E+00	5.15E-01	1.00E+00	8.94E-01	1.00E+00	8.46E-02	1.00E+00	7.55E-01	1.00E+00	hydrogen peroxide metabolism	P
GO:0042744	16	4.57E-01	1.00E+00	9.53E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	4.73E-01	1.00E+00	9.08E-01	1.00E+00	1.40E-01	1.00E+00	8.01E-01	1.00E+00	hydrogen peroxide catabolism	P
GO:0042770	54	1.37E-01	1.00E+00	2.48E-03	5.10E-02	7.22E-02	1.00E+00	1.91E-03	2.70E-02	1.30E-01	1.00E+00	7.51E-03	1.05E-01	6.99E-01	1.00E+00	2.16E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0042773	51	2.64E-03	4.90E-02	2.97E-03	5.10E-02	2.18E-01	1.00E+00	3.86E-02	1.00E+00	7.12E-04	4.90E-03	6.12E-03	1.05E-01	1.69E-01	1.00E+00	8.38E-02	1.00E+00	ATP synthesis coupled electron transport	P
GO:0042775	47	1.95E-03	4.90E-02	1.89E-03	3.90E-02	2.13E-01	1.00E+00	2.54E-02	4.10E-01	6.30E-04	4.90E-03	3.85E-03	7.40E-02	1.39E-01	1.00E+00	9.87E-02	1.00E+00	ATP synthesis coupled electron transport (s	P
GO:0042802	459	2.86E-01	1.00E+00	4.73E-01	1.00E+00	9.87E-02	1.00E+00	1.09E-01	1.00E+00	5.02E-01	1.00E+00	5.48E-01	1.00E+00	3.80E-01	1.00E+00	9.81E-01	1.00E+00	identical protein binding	F
GO:0042803	219	5.85E-01	1.00E+00	3.41E-01	1.00E+00	1.64E-01	1.00E+00	1.75E-01	1.00E+00	7.80E-01	1.00E+00	4.53E-01	1.00E+00	4.87E-01	1.00E+00	7.70E-01	1.00E+00	protein homodimerization activity	F
GO:0042809	26	8.99E-01	1.00E+00	7.19E-01	1.00E+00	6.17E-01	1.00E+00	8.82E-01	1.00E+00	8.88E-01	1.00E+00	5.11E-01	1.00E+00	9.57E-01	1.00E+00	9.67E-01	1.00E+00	vitamin D receptor binding	F
GO:0042824	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.29E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	MHC class I peptide loading complex	C
GO:0042825	13	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.87E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.02E-01	1.00E+00	TAP complex	C
GO:0042826	11	3.58E-01	1.00E+00	3.77E-01	1.00E+00	9.08E-02	1.00E+00	3.23E-01	1.00E+00	6.88E-01	1.00E+00	3.22E-01	1.00E+00	9.96E-01	1.00E+00	9.76E-01	1.00E+00	histone deacetylase binding	F
GO:0042895	27	9.52E-01	1.00E+00	9.51E-01	1.00E+00	9.24E-01	1.00E+00	9.04E-01	1.00E+00	8.77E-01	1.00E+00	8.79E-01	1.00E+00	8.86E-01	1.00E+00	9.99E-01	1.00E+00	antibiotic transporter activity	F
GO:0042923	127	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	7.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuropeptide binding	F
GO:0042974	22	1.00E+00	1.00E+00	9.88E-01	1.00E+00	7.50E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	retinoic acid receptor binding	F
GO:0042981	604	9.64E-01	1.00E+00	8.11E-01	1.00E+00	9.84E-02	1.00E+00	2.14E-01	1.00E+00	9.96E-01	1.00E+00	8.65E-01	1.00E+00	9.98E-01	1.00E+00	9.80E-01	1.00E+00	regulation of apoptosis	P
GO:0042982	12	3.55E-01	1.00E+00	6.88E-01	1.00E+00	6.76E-02	1.00E+00	5.08E-01	1.00E+00	4.96E-01	1.00E+00	7.03E-01	1.00E+00	1.00E+00	1.00E+00	6.74E-01	1.00E+00	amyloid precursor protein metabolism	P
GO:0042990	29	6.90E-01	1.00E+00	1.72E-01	1.00E+00	6.39E-01	1.00E+00	1.55E-01	1.00E+00	6.35E-01	1.00E+00	1.79E-01	1.00E+00	8.50E-01	1.00E+00	3.94E-01	1.00E+00	regulation of transcription factor import into	P
GO:0042991	29	6.90E-01	1.00E+00	1.72E-01	1.00E+00	6.39E-01	1.00E+00	1.55E-01	1.00E+00	6.35E-01	1.00E+00	1.79E-01	1.00E+00	8.50E-01	1.00E+00	3.94E-01	1.00E+00	transcription factor import into nucleus	P
GO:0042992	13	9.95E-01	1.00E+00	9.90E-01	1.00E+00	9.60E-01	1.00E+00	9.87E-01	1.00E+00	9.93E-01	1.00E+00	9.87E-01	1.00E+00	9.88E-01	1.00E+00	9.36E-01	1.00E+00	negative regulation of transcription factor im	P
GO:0042993	13	2.91E-01	1.00E+00	6.70E-02	1.00E+00	3.21E-01	1.00E+00	6.52E-02	1.00E+00	2.91E-01	1.00E+00	8.14E-02	1.00E+00	4.55E-01	1.00E+00	2.92E-01	1.00E+00	positive regulation of transcription factor imp	P
GO:0042994	10	9.93E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	9.39E-01	1.00E+00	cytoplasmic sequestering of transcription fa	P
GO:0042995	485	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.98E-01	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell projection	C
GO:0043005	149	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.38E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron projection	C
GO:0043009	186	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.18E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.53E-01	1.00E+00	embryonic development (sensu Vertebrata)	P
GO:0043010	54	9.78E-01	1.00E+00	9.78E-01	1.00E+00	3.55E-01	1.00E+00	9.75E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.31E-01	1.00E+00	6.36E-01	1.00E+00	eye development (sensu Vertebrata)	P
GO:0043021	19	3.71E-01	1.00E+00	5.22E-03	1.31E-01	5.54E-01	1.00E+00	2.75E-02	4.10E-01	5.45E-01	1.00E+00	1.01E-02	2.12E-01	2.49E-01	1.00E+00	3.70E-01	1.00E+00	ribonucleoprotein binding	F
GO:0043025	76	9.89E-01	1.00E+00	9.70E-01	1.00E+00	3.56E-01	1.00E+00	4.20E-01	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	6.73E-01	1.00E+00	cell soma	C
GO:0043028	21	3.74E-02	1.00E+00	6.56E-03	1.50E-01	1.27E-01	1.00E+00	9.88E-03	1.23E-01	7.69E-02	1.00E+00	1.73E-02	5.65E-01	2.94E-02	2.56E-01	2.29E-01	1.00E+00	caspase regulator activity	F
GO:0043029	15	2.28E-01	1.00E+00	2.11E-01	1.00E+00	3.08E-01	1.00E+00	2.42E-01	1.00E+00	2.24E-01	1.00E+00	1.77E-01	1.00E+00	5.61E-01	1.00E+00	9.10E-01	1.00E+00	T cell homeostasis	P
GO:0043037	257	2.41E-02	1.00E+00	7.39E-05	4.00E-03	7.84E-02	1.00E+00	1.71E-02	4.10E-01	9.14E-02	1.00E+00	2.03E-04	2.90E-03	4.58E-01	1.00E+00	3.68E-02	5.54E-01	translation	P
GO:0043038	75	3.76E-03	1.37E-01	3.98E-03	6.30E-02	2.71E-02	4.97E-01	1.90E-01	1.00E+00	5.46E-03	1.35E-01	7.13E-03	1.05E-01	1.08E-01	1.00E+00	2.80E-02	2.52E-01	amino acid activation	P
GO:0043039	75	3.76E-03	1.37E-01	3.98E-03	6.30E-02	2.71E-02	4.97E-01	1.90E-01	1.00E+00	5.46E-03	1.35E-01	7.13E-03	1.05E-01	1.08E-01	1.00E+00	2.80E-02	2.52E-01	tRNA aminoacylation	P
GO:0043043	10	1.37E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.36E-01	1.00E+00	7.13E-02	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide biosynthesis	P
GO:0043062	82	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular structure organization and bioc	P
GO:0043064	14	4.77E-01	1.00E+00	2.93E-01	1.00E+00	3.84E-01	1.00E+00	3.31E-01	1.00E+00	5.41E-01	1.00E+00	1.95E-01	1.00E+00	4.50E-01	1.00E+00	7.44E-01	1.00E+00	flagellum organization and biogenesis	P
GO:0043065	291	7.91E-01	1.00E+00	2.80E-01	1.00E+00	7.15E-02	1.00E+00	3.13E-02	5.42E-01	9.67E-01	1.00E+00	4.96E-01	1.00E+00	8.28E-01	1.00E+00	9.18E-01	1.00E+00	positive regulation of apoptosis	P
GO:0043066	269	9.77E-01	1.00E+00	9.88E-01	1.00E+00	3.77E-01	1.00E+00	8.48E-01	1.00E+00	9.96E-01	1.00E+00	9.90E-01	1.00E+00	9.88E-01	1.00E+00	9.62E-01	1.00E+00	negative regulation of apoptosis	P
GO:0043067	611	9.66E-01	1.00E+00	8.43E-01	1.00E+00	9.80E-02	1.00E+00	2.30E-01	1.00E+00	9.96E-01	1.00E+00	8.91E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	regulation of programmed cell death	P
GO:0043068	294	7.54E-01	1.00E+00	3.01E-01	1.00E+00	5.64E-02	1.00E+00	3.34E-02	5.42E-01	9.57E-01	1.00E+00	5.17E-01	1.00E+00	8.27E-01	1.00E+00	9.23E-01	1.00E+00	positive regulation of programmed cell deat	P
GO:0043069	273	9.85E-01	1.00E+00	9.92E-01	1.00E+00	4.31E-01	1.00E+00	8.69E-01	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	9.91E-01	1.00E+00	9.66E-01	1.00E+00	negative regulation of programmed cell dea	P
GO:0043085	327	4.71E-01	1.00E+00	3.22E-01	1.00E+00	7.85E-01	1.00E+00	4.75E-03	6.84E-02	2.92E-01	1.00E+00	6.12E-01	1.00E+00	8.20E-01	1.00E+00	8.70E-01	1.00E+00	positive regulation of enzyme activity	P
GO:0043086	171	5.81E-01	1.00E+00	5.32E-01	1.00E+00	3.48E-01	1.00E+00	5.83E-02	1.00E+00	4.24E-01	1.00E+00	6.17E-01	1.00E+00	9.89E-01	1.00E+00	9.50E-01	1.00E+00	negative regulation of enzyme activity	P
GO:0043087	120	6.55E-01	1.00E+00	9.74E-01	1.00E+00	3.00E-01	1.00E+00	6.23E-01	1.00E+00	8.35E-01	1.00E+00	9.89E-01	1.00E+00	3.73E-01	1.00E+00	9.01E-01	1.00E+00	regulation of GTPase activity	P
GO:0043112	21	2.84E-01	1.00E+00	5.24E-01	1.00E+00	5.24E-01	1.00E+00	1.02E-01	1.00E+00	1.57E-01	1.00E+00	6.78E-01	1.00E+00	7.57E-01	1.00E+00	9.16E-01	1.00E+00	receptor metabolism	P
GO:0043118	1205	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.83E-01	1.00E+00	2.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of physiological process	P
GO:0043119	1160	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	7.07E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of physiological process	P
GO:0043122	107	7.35E-01	1.00E+00	2.79E-01	1.00E+00	7.45E-02	1.00E+00	4.28E-01	1.00E+00	8.05E-01	1.00E+00	2.26E-01	1.00E+00	9.95E-01	1.00E+00	6.84E-01	1.00E+00	regulation of I-kappaB kinase/NF-kappaB c	P
GO:0043123	100	8.88E-01	1.00E+00	3.32E-01	1.00E+00	7.52E-02	1.00E+00	4.47E-01	1.00E+00	9.56E-01	1.00E+00	2.71E-01	1.00E+00	9.97E-01	1.00E+00	7.22E-01	1.00E+00	positive regulation of I-kappaB kinase/NF-k	P
GO:0043130	13	2.95E-02	1.00E+00	6.46E-02	1.00E+00	3.55E-03	3.50E-02	1.80E-01	1.00E+00	1.52E-01	1.00E+00	1.26E-01	1.00E+00	9.30E-01	1.00E+00	2.97E-01	1.00E+00	ubiquitin binding	F
GO:0043149	10	2.74E-01	1.00E+00	4.05E-01	1.00E+00	4.93E-02	8.68E-01	2.49E-01	1.00E+00	4.15E-01	1.00E+00	4.60E-01	1.00E+00	7.40E-01	1.00E+00	4.35E-01	1.00E+00	stress fiber formation	P
GO:0043154	12	3.13E-01	1.00E+00	1.04E-01	1.00E+00	2.93E-01	1.00E+00	1.19E-01	1.00E+00	6.41E-01	1.00E+00	8.60E-02	1.00E+00	1.28E-01	1.00E+00	5.72E-01	1.00E+00	negative regulation of caspase activity	P
GO:0043161	99	9.47E-02	1.00E+00	7.35E-02	1.00E+00	1.35E-01	1.00E+00	4.29E-03	6.84E-02	1.10E-01	1.00E+00	2.06E-01	1.00E+00	5.61E-01	1.00E+00	4.07E-01	1.00E+00	proteasomal ubiquitin-dependent protein ca	P
GO:0043167	4347	1.00E+00	1.00E+00	7.77E-01	1.00E+00	2.17E-03	1.80E-02	4.86E-03	6.84E-02	1.00E+00	1.00E+00	9.18E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	ion binding	F
GO:0043168	69	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.10E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	anion binding	F
GO:0043169	3959	1.00E+00	1.00E+00	7.71E-01	1.00E+00	1.26E-02	1.92E-01	6.26E-03	8.10E-02	1.00E+00	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	cation binding	F
GO:0043170	5007	3.83E-06	2.60E-03	2.07E-12	0.00E+00	4.01E-17	0.00E+00	1.35E-19	0.00E+00	8.32E-03	2.02E-01	2.61E-06	1.67E-03	9.19E-01	1.00E+00	3.71E-01	1.00E+00	macromolecule metabolism	P
GO:0043176	52	9.04E-01	1.00E+00	8.68E-01	1.00E+00	3.79E-01	1.00E+00	3.29E-01	1.00E+00	9.40E-01	1.00E+00	9.41E-01	1.00E+00	9.35E-01	1.00E+00	9.11E-01	1.00E+00	amine binding	F
GO:0043193	20	9.20E-01	1.00E+00	9.47E-01	1.00E+00	3.14E-01	1.00E+00	5.82E-01	1.00E+00	9.84E-01	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	positive regulation of gene-specific transcrip	P
GO:0043197	15	9.61E-01	1.00E+00	9.87E-01	1.00E+00	6.66E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	8.98E-01	1.00E+00	9.54E-01	1.00E+00	9.72E-01	1.00E+00	dendritic spine	C
GO:0043226	8345	2.22E-02	1.00E+00	1.27E-14	0.00E+00	7.98E-14	0.00E+00	1.14E-21	0.00E+00	3.64E-01	1.00E+00	4.04E-08	1.05E-04	9.96E-01	1.00E+00	5.93E-01	1.00E+00	organelle	C
GO:0043227	7429	7.43E-03	1.37E-01	1.41E-19	0.00E+00	7.65E-15	0.00E+00	8.17E-27	0.00E+00	2.22E-01	1.00E+00	5.35E-11	1.05E-04	9.97E-01	1.00E+00	4.76E-01	1.00E+00	membrane-bound organelle	C
GO:0043228	1943	7.79E-02	1.00E+00	2.49E-02	1.00E+00	5.68E-03	9.30E-02	1.09E-03	1.30E-02	1.61E-01	1.00E+00	8.00E-02	1.00E+00	8.11E-01	1.00E+00	6.89E-01	1.00E+00	non-membrane-bound organelle	C
GO:0043229	8340	2.09E-02	1.00E+00	1.09E-14	0.00E+00	7.22E-14	0.00E+00	9.00E-22	0.00E+00	3.58E-01	1.00E+00	3.89E-08	1.05E-04	9.96E-01	1.00E+00	5.88E-01	1.00E+00	intracellular organelle	C
GO:0043231	7427	7.36E-03	1.37E-01	1.46E-19	0.00E+00	8.56E-15	0.00E+00	8.93E-27	0.00E+00	2.20E-01	1.00E+00	5.41E-11	1.05E-04	9.97E-01	1.00E+00	4.74E-01	1.00E+00	intracellular membrane-bound organelle	C
GO:0043232	1943	7.79E-02	1.00E+00	2.49E-02	1.00E+00	5.68E-03	9.30E-02	1.09E-03	1.30E-02	1.61E-01	1.00E+00	8.00E-02	1.00E+00	8.11E-01	1.00E+00	6.89E-01	1.00E+00	intracellular non-membrane-bound organell	C
GO:0043233	1243	3.11E-06	2.60E-03	6.58E-13	0.00E+00	3.59E-08	0.00E+00	1.84E-10	0.00E+00	4.31E-04	4.00E-03	6.31E-09	1.05E-04	4.61E-01	1.00E+00	1.29E-01	1.00E+00	organelle lumen	C
GO:0043234	2521	5.60E-03	1.37E-01	1.22E-03	3.90E-02	1.01E-07	0.00E+00	1.77E-07	0.00E+00	7.91E-02	1.00E+00	3.06E-02	1.00E+00	8.46E-01	1.00E+00	7.28E-01	1.00E+00	protein complex	C
GO:0043235	92	4.16E-01	1.00E+00	9.32E-01	1.00E+00	9.34E-03	1.57E-01	3.74E-01	1.00E+00	8.43E-01	1.00E+00	9.45E-01	1.00E+00	5.79E-01	1.00E+00	9.91E-01	1.00E+00	receptor complex	C
GO:0043269	31	7.15E-01	1.00E+00	7.28E-01	1.00E+00	6.20E-01	1.00E+00	1.66E-01	1.00E+00	5.81E-01	1.00E+00	9.05E-01	1.00E+00	9.96E-01	1.00E+00	9.77E-01	1.00E+00	regulation of ion transport	P
GO:0043279	11	7.57E-01	1.00E+00	9.90E-01	1.00E+00	4.19E-01	1.00E+00	9.82E-01	1.00E+00	7.04E-01	1.00E+00	9.53E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to alkaloid	P

GO:0043280	50	1.00E-01	1.00E+00	5.21E-02	1.00E+00	5.39E-01	1.00E+00	2.23E-02	4.10E-01	6.68E-02	1.00E+00	8.46E-02	1.00E+00	3.91E-01	1.00E+00	2.21E-01	1.00E+00	positive regulation of caspase activity	P
GO:0043281	65	6.98E-02	1.00E+00	1.27E-02	3.84E-01	4.12E-01	1.00E+00	5.48E-03	8.10E-02	8.51E-02	1.00E+00	2.44E-02	7.69E-01	1.66E-01	1.00E+00	1.81E-01	1.00E+00	regulation of caspase activity	P
GO:0043283	3228	3.54E-07	1.25E-04	6.40E-17	0.00E+00	3.38E-19	0.00E+00	1.96E-20	0.00E+00	1.35E-03	4.30E-02	1.16E-09	1.05E-04	9.98E-01	1.00E+00	7.22E-02	1.00E+00	biopolymer metabolism	P
GO:0043284	47	4.67E-01	1.00E+00	8.08E-01	1.00E+00	8.89E-02	1.00E+00	4.33E-01	1.00E+00	6.00E-01	1.00E+00	7.41E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	biopolymer biosynthesis	P
GO:0043285	365	4.43E-03	1.37E-01	1.55E-05	2.21E-03	5.62E-03	9.30E-02	3.73E-09	0.00E+00	5.98E-02	1.00E+00	1.10E-03	1.02E-02	7.29E-01	1.00E+00	1.35E-01	1.00E+00	biopolymer catabolism	P
GO:0043292	85	5.68E-01	1.00E+00	1.00E+00	1.00E+00	1.73E-01	1.00E+00	9.99E-01	1.00E+00	7.29E-01	1.00E+00	9.99E-01	1.00E+00	8.87E-01	1.00E+00	9.98E-01	1.00E+00	contractile fiber	C
GO:0043296	98	2.89E-01	1.00E+00	7.65E-01	1.00E+00	2.59E-01	1.00E+00	4.13E-01	1.00E+00	2.24E-01	1.00E+00	5.89E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	apical junction complex	C
GO:0043299	12	5.60E-02	1.00E+00	2.07E-01	1.00E+00	6.38E-02	1.00E+00	6.59E-01	1.00E+00	1.14E-01	1.00E+00	1.56E-01	1.00E+00	1.58E-01	1.00E+00	2.56E-01	1.00E+00	leukocyte degranulation	P
GO:0043331	12	6.04E-01	1.00E+00	7.28E-01	1.00E+00	7.10E-01	1.00E+00	6.85E-01	1.00E+00	4.82E-01	1.00E+00	6.92E-01	1.00E+00	9.72E-01	1.00E+00	8.94E-01	1.00E+00	response to dsRNA	P
GO:0043367	18	6.16E-01	1.00E+00	9.30E-01	1.00E+00	5.44E-01	1.00E+00	9.76E-01	1.00E+00	4.89E-01	1.00E+00	8.24E-01	1.00E+00	9.75E-01	1.00E+00	9.97E-01	1.00E+00	CD4-positive, alpha beta T cell differentiatic	P
GO:0043393	14	2.58E-01	1.00E+00	3.14E-01	1.00E+00	5.22E-01	1.00E+00	3.57E-01	1.00E+00	3.33E-01	1.00E+00	2.56E-01	1.00E+00	1.70E-01	1.00E+00	6.98E-01	1.00E+00	regulation of protein binding	P
GO:0043405	115	9.96E-01	1.00E+00	9.87E-01	1.00E+00	9.12E-01	1.00E+00	7.50E-01	1.00E+00	9.80E-01	1.00E+00	9.81E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	regulation of MAPK activity	P
GO:0043406	81	9.35E-01	1.00E+00	9.02E-01	1.00E+00	9.95E-01	1.00E+00	4.85E-01	1.00E+00	7.53E-01	1.00E+00	9.23E-01	1.00E+00	9.07E-01	1.00E+00	9.34E-01	1.00E+00	positive regulation of MAPK activity	P
GO:0043407	31	9.97E-01	1.00E+00	9.96E-01	1.00E+00	3.10E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of MAPK activity	P
GO:0043408	25	9.01E-01	1.00E+00	9.44E-01	1.00E+00	8.53E-01	1.00E+00	2.09E-01	1.00E+00	8.03E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of MAPKKK cascade	P
GO:0043410	16	9.22E-01	1.00E+00	8.70E-01	1.00E+00	1.00E+00	1.00E+00	2.21E-01	1.00E+00	8.14E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of MAPKKK cascade	P
GO:0043412	1953	1.03E-02	1.77E-01	4.76E-06	1.41E-03	8.32E-09	0.00E+00	1.75E-12	0.00E+00	1.43E-01	1.00E+00	3.95E-03	7.40E-02	1.00E+00	1.00E+00	4.43E-01	1.00E+00	biopolymer modification	P
GO:0043413	118	6.44E-01	1.00E+00	1.75E-01	1.00E+00	1.28E-01	1.00E+00	6.77E-02	1.00E+00	7.91E-01	1.00E+00	2.23E-01	1.00E+00	8.73E-01	1.00E+00	8.15E-01	1.00E+00	biopolymer glycosylation	P
GO:0043414	50	1.72E-01	1.00E+00	7.30E-03	3.40E-01	5.57E-02	1.00E+00	5.77E-04	7.17E-03	2.24E-01	1.00E+00	9.13E-02	1.00E+00	7.08E-01	1.00E+00	8.27E-03	6.60E-02	biopolymer methylation	P
GO:0043433	21	9.08E-01	1.00E+00	2.75E-01	1.00E+00	6.68E-01	1.00E+00	3.62E-01	1.00E+00	8.93E-01	1.00E+00	3.42E-01	1.00E+00	9.46E-01	1.00E+00	1.04E-01	1.00E+00	negative regulation of transcription factor ac	P
GO:0043434	22	2.46E-01	1.00E+00	7.41E-01	1.00E+00	2.47E-02	4.97E-01	3.29E-01	1.00E+00	5.82E-01	1.00E+00	8.88E-01	1.00E+00	6.57E-01	1.00E+00	3.98E-01	1.00E+00	response to peptide hormone stimulus	P
GO:0043449	30	7.03E-01	1.00E+00	5.68E-01	1.00E+00	8.49E-01	1.00E+00	8.23E-01	1.00E+00	5.07E-01	1.00E+00	5.87E-01	1.00E+00	8.88E-01	1.00E+00	2.78E-01	1.00E+00	alkene metabolism	P
GO:0043450	22	6.67E-01	1.00E+00	5.61E-01	1.00E+00	8.99E-01	1.00E+00	8.48E-01	1.00E+00	4.46E-01	1.00E+00	6.08E-01	1.00E+00	7.87E-01	1.00E+00	2.47E-01	1.00E+00	alkene biosynthesis	P
GO:0043473	38	9.73E-01	1.00E+00	7.10E-01	1.00E+00	5.36E-01	1.00E+00	5.63E-01	1.00E+00	9.96E-01	1.00E+00	6.52E-01	1.00E+00	9.65E-01	1.00E+00	9.16E-01	1.00E+00	pigmentation	P
GO:0043487	15	6.86E-01	1.00E+00	3.56E-01	1.00E+00	5.71E-01	1.00E+00	3.23E-01	1.00E+00	7.29E-01	1.00E+00	3.26E-01	1.00E+00	9.52E-01	1.00E+00	5.64E-01	1.00E+00	regulation of RNA stability	P
GO:0043488	14	6.78E-01	1.00E+00	3.50E-01	1.00E+00	6.18E-01	1.00E+00	2.50E-01	1.00E+00	6.89E-01	1.00E+00	3.56E-01	1.00E+00	9.42E-01	1.00E+00	5.40E-01	1.00E+00	regulation of mRNA stability	P
GO:0043492	140	4.03E-01	1.00E+00	7.97E-01	1.00E+00	2.34E-02	4.97E-01	2.07E-01	1.00E+00	6.08E-01	1.00E+00	7.73E-01	1.00E+00	9.04E-01	1.00E+00	9.99E-01	1.00E+00	ATPase activity, coupled to movement of su	F
GO:0043498	14	8.22E-01	1.00E+00	2.93E-01	1.00E+00	9.97E-01	1.00E+00	4.88E-01	1.00E+00	6.02E-01	1.00E+00	2.54E-01	1.00E+00	7.88E-01	1.00E+00	5.75E-01	1.00E+00	cell surface binding	F
GO:0043506	29	9.62E-01	1.00E+00	8.64E-01	1.00E+00	9.64E-01	1.00E+00	3.99E-01	1.00E+00	9.29E-01	1.00E+00	9.19E-01	1.00E+00	9.88E-01	1.00E+00	9.57E-01	1.00E+00	regulation of JNK activity	P
GO:0043507	27	9.58E-01	1.00E+00	8.69E-01	1.00E+00	9.80E-01	1.00E+00	4.70E-01	1.00E+00	9.13E-01	1.00E+00	9.12E-01	1.00E+00	9.89E-01	1.00E+00	9.49E-01	1.00E+00	positive regulation of JNK activity	P
GO:0043523	54	7.95E-01	1.00E+00	4.60E-01	1.00E+00	8.19E-01	1.00E+00	6.59E-01	1.00E+00	7.98E-01	1.00E+00	3.31E-01	1.00E+00	7.18E-01	1.00E+00	8.13E-01	1.00E+00	regulation of neuron apoptosis	P
GO:0043524	29	5.68E-01	1.00E+00	3.09E-01	1.00E+00	4.21E-01	1.00E+00	1.77E-01	1.00E+00	7.10E-01	1.00E+00	2.75E-01	1.00E+00	4.77E-01	1.00E+00	7.38E-01	1.00E+00	negative regulation of neuron apoptosis	P
GO:0043525	17	6.94E-01	1.00E+00	4.16E-01	1.00E+00	9.80E-01	1.00E+00	8.42E-01	1.00E+00	6.23E-01	1.00E+00	2.75E-01	1.00E+00	4.82E-01	1.00E+00	8.96E-01	1.00E+00	positive regulation of neuron apoptosis	P
GO:0043531	12	1.93E-01	1.00E+00	3.56E-01	1.00E+00	9.97E-02	1.00E+00	3.15E-01	1.00E+00	4.33E-01	1.00E+00	3.78E-01	1.00E+00	2.47E-01	1.00E+00	6.73E-01	1.00E+00	ADP binding	F
GO:0043542	20	9.56E-01	1.00E+00	7.02E-01	1.00E+00	3.90E-01	1.00E+00	5.75E-01	1.00E+00	9.99E-01	1.00E+00	7.08E-01	1.00E+00	9.57E-01	1.00E+00	6.39E-01	1.00E+00	endothelial cell migration	P
GO:0043543	32	9.59E-02	1.00E+00	1.48E-02	3.84E-01	9.14E-03	1.57E-01	5.90E-03	8.10E-02	1.69E-01	1.00E+00	4.14E-02	1.00E+00	7.10E-01	1.00E+00	2.14E-01	1.00E+00	protein amino acid acylation	P
GO:0043549	251	9.94E-01	1.00E+00	9.88E-01	1.00E+00	9.45E-01	1.00E+00	3.78E-01	1.00E+00	9.75E-01	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	regulation of kinase activity	P
GO:0043565	551	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sequence-specific DNA binding	F
GO:0043566	105	2.40E-02	1.00E+00	3.22E-03	6.30E-02	1.57E-01	1.00E+00	8.15E-02	1.00E+00	9.62E-03	2.02E-01	3.03E-03	6.40E-02	8.85E-01	1.00E+00	2.43E-01	1.00E+00	structure-specific DNA binding	F
GO:0043574	14	4.08E-01	1.00E+00	9.18E-01	1.00E+00	8.23E-02	1.00E+00	2.31E-01	1.00E+00	6.23E-01	1.00E+00	9.97E-01	1.00E+00	7.84E-01	1.00E+00	4.60E-01	1.00E+00	peroxisomal transport	P
GO:0043583	62	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ear development	P
GO:0043588	11	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	8.98E-01	1.00E+00	skin development	P
GO:0043596	13	1.03E-01	1.00E+00	4.85E-02	1.00E+00	5.82E-03	9.30E-02	1.72E-01	1.00E+00	1.30E-01	1.00E+00	6.93E-02	1.00E+00	9.59E-01	1.00E+00	1.64E-01	1.00E+00	replication fork (sensu Eukaryota)	C
GO:0043601	11	8.93E-02	1.00E+00	3.22E-02	1.00E+00	1.09E-02	1.57E-01	1.01E-01	1.00E+00	1.12E-01	1.00E+00	4.70E-02	1.00E+00	8.55E-01	1.00E+00	1.96E-01	1.00E+00	replisome (sensu Eukaryota)	C
GO:0043621	10	6.07E-01	1.00E+00	9.84E-01	1.00E+00	7.77E-02	1.00E+00	9.82E-01	1.00E+00	9.29E-01	1.00E+00	9.02E-01	1.00E+00	6.83E-01	1.00E+00	9.04E-01	1.00E+00	protein self-association	F
GO:0043627	30	9.68E-01	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	8.68E-01	1.00E+00	9.52E-01	1.00E+00	9.99E-01	1.00E+00	6.88E-01	1.00E+00	9.54E-01	1.00E+00	response to estrogen stimulus	P
GO:0043631	11	2.75E-03	4.90E-02	3.49E-02	1.00E+00	9.95E-07	8.48E-04	6.41E-02	1.00E+00	2.11E-02	3.81E-01	5.93E-02	1.00E+00	9.93E-01	1.00E+00	7.34E-02	1.00E+00	RNA polyadenylation	P
GO:0043632	221	7.12E-03	1.37E-01	1.61E-05	2.21E-03	2.41E-02	4.97E-01	3.05E-08	0.00E+00	6.11E-02	1.00E+00	9.95E-04	1.02E-02	5.91E-01	1.00E+00	6.07E-02	1.00E+00	modification-dependent macromolecule cata	P
GO:0043648	11	4.51E-01	1.00E+00	2.47E-01	1.00E+00	2.68E-01	1.00E+00	1.49E-01	1.00E+00	4.25E-01	1.00E+00	2.64E-01	1.00E+00	9.73E-01	1.00E+00	9.34E-01	1.00E+00	dicarboxylic acid metabolism	P
GO:0043681	13	5.90E-01	1.00E+00	6.60E-01	1.00E+00	6.51E-01	1.00E+00	5.22E-01	1.00E+00	7.03E-01	1.00E+00	5.91E-01	1.00E+00	3.66E-01	1.00E+00	7.14E-01	1.00E+00	protein import into mitochondrion	P
GO:0044237	8004	3.55E-02	1.00E+00	1.87E-09	1.00E-03	1.82E-15	0.00E+00	2.73E-20	0.00E+00	4.08E-01	1.00E+00	1.57E-04	2.29E-03	9.99E-01	1.00E+00	8.11E-01	1.00E+00	cellular metabolism	P
GO:0044238	7984	6.40E-02	1.00E+00	2.27E-09	1.00E-03	2.04E-14	0.00E+00	3.46E-20	0.00E+00	5.53E-01	1.00E+00	1.93E-04	2.90E-03	9.99E-01	1.00E+00	7.90E-01	1.00E+00	primary metabolism	P
GO:0044241	10	1.53E-01	1.00E+00	2.23E-01	1.00E+00	2.57E-01	1.00E+00	2.14E-01	1.00E+00	1.49E-01	1.00E+00	3.30E-01	1.00E+00	4.68E-01	1.00E+00	1.11E-01	1.00E+00	lipid digestion	P
GO:0044242	53	4.64E-01	1.00E+00	1.43E-01	1.00E+00	5.60E-02	1.00E+00	4.76E-01	1.00E+00	5.52E-01	1.00E+00	9.67E-02	1.00E+00	9.55E-01	1.00E+00	7.48E-01	1.00E+00	cellular lipid catabolism	P
GO:0044247	15	9.77E-01	1.00E+00	9.80E-01	1.00E+00	4.54E-01	1.00E+00	7.36E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.67E-01	1.00E+00	8.51E-01	1.00E+00	cellular polysaccharide catabolism	P
GO:0044248	660	1.49E-03	4.90E-02	7.37E-05	4.00E-03	1.86E-04	4.57E-03	2.63E-06	0.00E+00	6.86E-02	1.00E+00	1.55E-03	3.00E-02	7.04E-01	1.00E+00	3.03E-01	1.00E+00	cellular catabolism	P
GO:0044249	1371	1.61E-02	3.10E-01	1.54E-02	3.84E-01	1.75E-03	1.60E-02	5.78E-04	7.17E-03	5.69E-02	1.00E+00	6.58E-02	1.00E+00	7.73E-01	1.00E+00	6.32E-01	1.00E+00	cellular biosynthesis	P
GO:0044255	681	6.78E-01	1.00E+00	6.13E-01	1.00E+00	2.68E-03	1.80E-02	1.25E-02	1.57E-01	8.45E-01	1.00E+00	7.80E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	cellular lipid metabolism	P
GO:0044257	246	2.78E-02	1.00E+00	2.06E-04	8.26E-03	3.21E-02	5.87E-01	5.93E-07	0.00E+00	1.70E-01	1.00E+00	4.33E-03	7.40E-02	8.22E-01	1.00E+00	1.31E-01	1.00E+00	cellular protein catabolism	P
GO:0044260	3366	8.67E-03	1.56E-01	5.23E-03	1.31E-01	4.57E-08	0.00E+00	6.68E-09	0.00E+00	1.70E-01	1.00E+00	1.55E-01	1.00E+00	8.91E-01	1.00E+00	7.42E-01	1.00E+00	cellular macromolecule metabolism	P
GO:0044262	389	1.87E-01	1.00E+00	2.01E-01	1.00E+00	7.02E-03	1.57E-01	7.50E-02	1.00E+00	3.08E-01	1.00E+00	1.72E-01	1.00E+00	9.72E-01	1.00E+00	9.54E-01	1.00E+00	cellular carbohydrate metabolism	P
GO:0044264	85	8.82E-01	1.00E+00	9.91E-01	1.00E+00	2.15E-01	1.00E+00	8.06E-01	1.00E+00	9.48E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cellular polysaccharide metabolism	P
GO:0044265	407	2.75E-03	4.90E-02	1.79E-05	2.21E-03	4.00E-03	3.50E-02	3.17E-07	0.00E+00	4.99E-02	1.00E+00	9.33E-04	1.02E-02	7.66E-01	1.00E+00	8.07E-02	1.00E+00	cellular macromolecule catabolism	P
GO:0044267	3309	6.98E-03	1.37E-01	2.57E-03	5.10E-02	9.55E-08	0.00E+00	3.96E-09	0.00E+00	1.42E-01	1.00E+00	1.05E-01	1.00E+00	8.70E-01	1.00E+00	7.08E-01	1.00E+00	cellular protein metabolism	P
GO:0044270	74	1.66E-01	1.00E+00	3.36E-01	1.00E+00	6.18E-02	1.00E+00	2.41E-01	1.00E+00	2.00E-01	1.00E+00	3.69E-01	1.00E+00	7.46E-01	1.00E+00	5.53E-01	1.00E+00	nitrogen compound catabolism	P
GO:0044271	128	7.85E-01	1.00E+00	7.23E-01	1.00E+00	1.83E-01	1.00E+00	5.27E-01	1.00E+00	9.40E-01	1.00E+00	4.75E-01	1.00E+00	8.57E-01	1.00E+00	1.00E+00	1.00E+00	nitrogen compound biosynthesis	P
GO:0044272	44	5.24E-01	1.00E+00	6.92E-01	1.00E+00	6.94E-02	1.00E+00	4.42E-01	1.00E+00	7.44E-01	1.00E+00	6.42E-01	1.00E+00	9.29E-01	1.00E+00	9.30E-01	1.00E+00	sulfur compound biosynthesis	P
GO:0044275	113	2.12E-02	1.00E+00	2.67E-02	1.00E+00	7.23E-03	1.57E-01	7.73E-02	1.00E+00	6.48E-02	1.00E+00	5.20E-02	1.00E+00	4.74E-01	1.00E+00	1.12E-01	1.00E+00	cellular carbohydrate catabolism	P
GO:0044403	58	5.06E-01	1.00E+00	9.51E-01	1.00E+00	1.54E-01	1.00E+00	9.07E-01	1.00E+00	5.57E-01	1.00E+00	9.63E-01	1.00E+00	7.86E-01	1.00E+00	5.13E-01	1.00E+00	symbiosis, encompassing mutualism throug	P
GO:0044409	10	7.82E-01	1.00E+00	8.27E-01	1.00E+00	7.34E-01	1.00E+00	6.61E-01	1.00E+00	4.94E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	6.05E-01	1.00E+00	entry into host	P
GO:0044419	264	2.24E-01	1.00E+00	2.06E-02	9.24E-01	5.28E-03	9.30E-02	2.74E-02	4.10E-01	5.47E-01	1.00E+00	7.17E-02	1.00E+00	7.09E-01	1.00E+00	1.57E-01	1.00E+00	interspecies interaction between organisms	P
GO:0044420	115	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular matrix part	C
GO:0044421	818	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	extracellular region part	C
GO:0044422	3737	2.33E-06	2.60E-03	1.86E-11	0.00E+00	1.93E-16	0.00E+00	4.07E-15	0.00E+00	1.20E-03	4.30E-02	1.50E-07	2.22E-04	9.64E-01	1.00E+00	7.10E-01	1.00E+00	organelle part	C
GO:0044423	15	1.00E+00	1.00E+00	9.63E-01	1.00E+00	5.58E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	2.44E-01	1.00E+00	virion part	C

GO:0044424	10057	8.56E-02	1.00E+00	3.27E-10	0.00E+00	1.42E-15	0.00E+00	3.27E-21	0.00E+00	6.33E-01	1.00E+00	5.92E-05	2.29E-03	9.99E-01	1.00E+00	8.27E-01	1.00E+00	intracellular part	C
GO:0044425	5808	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.50E-01	1.00E+00	9.36E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	membrane part	C
GO:0044427	365	3.06E-02	1.00E+00	1.70E-03	3.90E-02	1.08E-02	1.57E-01	1.18E-03	1.30E-02	3.92E-02	1.00E+00	5.40E-03	7.40E-02	9.27E-01	1.00E+00	3.76E-01	1.00E+00	chromosomal part	C
GO:0044428	1259	1.53E-07	1.25E-04	2.51E-18	0.00E+00	1.03E-12	0.00E+00	4.31E-13	0.00E+00	7.31E-05	2.00E-03	7.18E-13	1.05E-04	6.92E-01	1.00E+00	5.35E-03	6.60E-02	nuclear part	C
GO:0044429	542	8.05E-06	5.00E-03	1.05E-06	1.00E-03	4.06E-05	4.57E-03	5.55E-06	8.32E-04	3.76E-04	4.00E-03	4.47E-05	2.29E-03	1.16E-01	1.00E+00	3.32E-01	1.00E+00	mitochondrial part	C
GO:0044430	681	5.60E-01	1.00E+00	6.53E-01	1.00E+00	2.32E-03	1.80E-02	3.12E-01	1.00E+00	9.05E-01	1.00E+00	6.03E-01	1.00E+00	9.80E-01	1.00E+00	9.46E-01	1.00E+00	cytoskeletal part	C
GO:0044431	406	4.80E-01	1.00E+00	1.78E-01	1.00E+00	1.38E-04	4.57E-03	4.02E-03	6.84E-02	7.64E-01	1.00E+00	3.37E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	Golgi apparatus part	C
GO:0044432	573	2.98E-01	1.00E+00	1.11E-01	1.00E+00	3.15E-04	7.18E-03	1.57E-03	1.80E-02	5.59E-01	1.00E+00	3.77E-01	1.00E+00	9.93E-01	1.00E+00	7.38E-01	1.00E+00	endoplasmic reticulum part	C
GO:0044433	152	3.27E-01	1.00E+00	7.10E-01	1.00E+00	1.09E-01	1.00E+00	3.64E-01	1.00E+00	2.02E-01	1.00E+00	6.64E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	cytoplasmic vesicle part	C
GO:0044437	78	2.93E-01	1.00E+00	1.41E-01	1.00E+00	2.36E-01	1.00E+00	8.88E-03	1.12E-01	1.74E-01	1.00E+00	2.20E-01	1.00E+00	9.93E-01	1.00E+00	8.54E-01	1.00E+00	vacuolar part	C
GO:0044438	47	2.37E-02	1.00E+00	4.30E-01	1.00E+00	6.50E-02	1.00E+00	1.24E-01	1.00E+00	6.27E-02	1.00E+00	5.58E-01	1.00E+00	6.14E-01	1.00E+00	6.07E-01	1.00E+00	microbody part	C
GO:0044439	47	2.37E-02	1.00E+00	4.30E-01	1.00E+00	6.50E-02	1.00E+00	1.24E-01	1.00E+00	6.27E-02	1.00E+00	5.58E-01	1.00E+00	6.14E-01	1.00E+00	6.07E-01	1.00E+00	peroxisomal part	C
GO:0044440	115	3.19E-02	1.00E+00	1.08E-02	3.84E-01	3.01E-02	5.65E-01	1.98E-04	7.00E-03	3.50E-02	6.55E-01	4.00E-02	1.00E+00	7.91E-01	1.00E+00	3.78E-01	1.00E+00	endosomal part	C
GO:0044441	10	2.81E-02	1.00E+00	4.82E-02	1.00E+00	3.68E-02	5.87E-01	8.24E-02	1.00E+00	4.48E-02	1.00E+00	2.51E-02	7.69E-01	6.77E-01	1.00E+00	4.16E-01	1.00E+00	cilium part	C
GO:0044444	4137	2.22E-05	5.00E-03	3.00E-08	1.00E-03	5.23E-14	0.00E+00	1.08E-15	0.00E+00	1.36E-02	3.01E-01	9.72E-05	2.29E-03	8.41E-01	1.00E+00	7.61E-01	1.00E+00	cytoplasmic part	C
GO:0044445	77	7.32E-01	1.00E+00	6.09E-01	1.00E+00	5.79E-01	1.00E+00	9.42E-01	1.00E+00	8.27E-01	1.00E+00	4.31E-01	1.00E+00	6.36E-01	1.00E+00	7.89E-01	1.00E+00	cytosolic part	C
GO:0044446	3737	2.33E-06	2.60E-03	1.86E-11	0.00E+00	1.93E-16	0.00E+00	4.07E-15	0.00E+00	1.20E-03	4.30E-02	1.50E-07	2.22E-04	9.64E-01	1.00E+00	7.10E-01	1.00E+00	intracellular organelle part	C
GO:0044447	16	5.47E-01	1.00E+00	2.77E-01	1.00E+00	3.55E-01	1.00E+00	1.89E-01	1.00E+00	5.52E-01	1.00E+00	2.78E-01	1.00E+00	8.92E-01	1.00E+00	7.10E-01	1.00E+00	axoneme part	C
GO:0044448	57	3.63E-01	1.00E+00	6.06E-01	1.00E+00	4.18E-02	5.87E-01	4.00E-01	1.00E+00	4.63E-01	1.00E+00	6.54E-01	1.00E+00	8.83E-01	1.00E+00	6.09E-01	1.00E+00	cell cortex part	C
GO:0044449	81	5.45E-01	1.00E+00	9.99E-01	1.00E+00	1.63E-01	1.00E+00	9.98E-01	1.00E+00	7.46E-01	1.00E+00	9.97E-01	1.00E+00	8.32E-01	1.00E+00	9.96E-01	1.00E+00	contractile fiber part	C
GO:0044450	28	9.74E-03	1.77E-01	9.02E-03	3.84E-01	3.04E-03	3.50E-02	3.08E-02	5.42E-01	8.16E-02	1.00E+00	3.90E-02	1.00E+00	1.06E-01	1.00E+00	4.86E-02	8.10E-01	microtubule organizing center part	C
GO:0044451	460	2.09E-03	4.90E-02	3.31E-06	1.41E-03	2.04E-05	1.00E-03	2.98E-04	7.00E-03	2.10E-02	3.81E-01	1.11E-05	2.29E-03	7.17E-01	1.00E+00	1.32E-01	1.00E+00	nucleoplasm part	C
GO:0044452	42	2.39E-01	1.00E+00	5.21E-02	1.00E+00	4.13E-01	1.00E+00	5.29E-02	1.00E+00	2.28E-01	1.00E+00	2.54E-01	1.00E+00	6.57E-01	1.00E+00	7.68E-01	1.00E+00	nucleolar part	C
GO:0044453	107	1.91E-03	4.90E-02	3.02E-07	1.00E-03	1.92E-05	9.71E-04	1.17E-05	2.00E-03	9.71E-03	2.02E-01	1.26E-05	2.29E-03	2.28E-01	1.00E+00	5.69E-03	6.60E-02	nuclear membrane part	C
GO:0044454	82	2.06E-02	1.00E+00	2.27E-03	5.10E-02	3.04E-02	5.65E-01	1.16E-02	1.27E-01	2.11E-02	3.81E-01	8.48E-03	1.05E-01	6.51E-01	1.00E+00	2.93E-02	2.52E-01	nuclear chromosome part	C
GO:0044455	110	2.85E-03	4.90E-02	1.50E-03	3.90E-02	1.27E-02	1.92E-01	6.76E-03	8.10E-02	1.72E-02	3.81E-01	8.05E-03	1.05E-01	1.17E-01	1.00E+00	1.56E-01	1.00E+00	mitochondrial membrane part	C
GO:0044456	145	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	synapse part	C
GO:0044459	1890	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	plasma membrane part	C
GO:0044460	15	9.93E-01	1.00E+00	9.20E-01	1.00E+00	7.69E-01	1.00E+00	9.51E-01	1.00E+00	9.59E-01	1.00E+00	8.11E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	flagellar part	C
GO:0044461	12	9.58E-01	1.00E+00	8.24E-01	1.00E+00	5.72E-01	1.00E+00	8.82E-01	1.00E+00	8.69E-01	1.00E+00	6.43E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	flagellar part (sensu Bacteria)	C
GO:0044462	29	9.63E-01	1.00E+00	9.76E-01	1.00E+00	4.51E-01	1.00E+00	6.84E-01	1.00E+00	9.72E-01	1.00E+00	9.74E-01	1.00E+00	9.89E-01	1.00E+00	9.57E-01	1.00E+00	external encapsulating structure part	C
GO:0044463	92	9.87E-01	1.00E+00	9.53E-01	1.00E+00	5.06E-01	1.00E+00	8.27E-01	1.00E+00	9.91E-01	1.00E+00	8.94E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	cell projection part	C
GO:0044464	14224	1.00E+00	1.00E+00	9.52E-01	1.00E+00	1.20E-05	9.71E-04	1.45E-07	0.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell part	C
GO:0045005	31	1.16E-07	1.25E-04	5.77E-07	1.00E-03	5.89E-03	9.30E-02	9.30E-02	1.00E+00	9.44E-06	5.00E-04	1.14E-08	1.05E-04	5.45E-01	1.00E+00	9.09E-02	1.00E+00	maintenance of fidelity during DNA-dependi	P
GO:0045026	13	4.58E-01	1.00E+00	9.97E-01	1.00E+00	3.04E-01	1.00E+00	9.92E-01	1.00E+00	3.54E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	plasma membrane fusion	P
GO:0045028	100	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.44E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	purinergic nucleotide receptor activity, G-pr	F
GO:0045045	237	3.39E-01	1.00E+00	6.04E-01	1.00E+00	8.99E-02	1.00E+00	6.53E-02	1.00E+00	5.03E-01	1.00E+00	8.58E-01	1.00E+00	5.99E-01	1.00E+00	8.03E-01	1.00E+00	secretory pathway	P
GO:0045047	18	5.02E-01	1.00E+00	2.83E-01	1.00E+00	5.80E-01	1.00E+00	5.56E-02	1.00E+00	5.14E-01	1.00E+00	5.56E-01	1.00E+00	8.59E-01	1.00E+00	4.40E-01	1.00E+00	protein targeting to ER	P
GO:0045055	73	8.20E-01	1.00E+00	9.62E-01	1.00E+00	6.40E-01	1.00E+00	4.29E-01	1.00E+00	7.54E-01	1.00E+00	9.93E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	regulated secretory pathway	P
GO:0045058	16	9.38E-01	1.00E+00	9.66E-01	1.00E+00	5.35E-01	1.00E+00	8.35E-01	1.00E+00	9.82E-01	1.00E+00	9.29E-01	1.00E+00	9.00E-01	1.00E+00	1.00E+00	1.00E+00	T cell selection	P
GO:0045061	10	9.21E-01	1.00E+00	9.48E-01	1.00E+00	4.05E-01	1.00E+00	6.70E-01	1.00E+00	9.51E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	thymic T cell selection	P
GO:0045069	14	8.07E-01	1.00E+00	9.92E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	5.64E-01	1.00E+00	9.83E-01	1.00E+00	8.19E-01	1.00E+00	4.41E-01	1.00E+00	regulation of viral genome replication	P
GO:0045072	13	2.25E-01	1.00E+00	8.46E-01	1.00E+00	1.10E-01	1.00E+00	9.70E-01	1.00E+00	3.43E-01	1.00E+00	5.09E-01	1.00E+00	4.75E-01	1.00E+00	9.99E-01	1.00E+00	regulation of interferon-gamma biosynthesis	P
GO:0045073	13	6.15E-01	1.00E+00	4.42E-01	1.00E+00	6.21E-01	1.00E+00	4.69E-01	1.00E+00	5.26E-01	1.00E+00	4.89E-01	1.00E+00	1.00E+00	1.00E+00	2.66E-01	1.00E+00	regulation of chemokine biosynthesis	P
GO:0045076	16	4.02E-01	1.00E+00	9.84E-01	1.00E+00	2.06E-01	1.00E+00	9.39E-01	1.00E+00	3.05E-01	1.00E+00	9.68E-01	1.00E+00	9.60E-01	1.00E+00	9.81E-01	1.00E+00	regulation of interleukin-2 biosynthesis	P
GO:0045078	10	2.86E-01	1.00E+00	5.16E-01	1.00E+00	1.79E-01	1.00E+00	8.58E-01	1.00E+00	2.35E-01	1.00E+00	2.44E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	positive regulation of interferon-gamma bios	P
GO:0045080	10	5.69E-01	1.00E+00	3.63E-01	1.00E+00	4.00E-01	1.00E+00	6.66E-01	1.00E+00	5.68E-01	1.00E+00	2.70E-01	1.00E+00	9.93E-01	1.00E+00	4.59E-01	1.00E+00	positive regulation of chemokine biosynthes	P
GO:0045086	10	1.13E-01	1.00E+00	6.14E-01	1.00E+00	6.66E-02	1.00E+00	4.39E-01	1.00E+00	1.04E-01	1.00E+00	6.58E-01	1.00E+00	6.42E-01	1.00E+00	5.98E-01	1.00E+00	positive regulation of interleukin-2 biosynthe	P
GO:0045087	126	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	innate immune response	P
GO:0045088	14	4.62E-01	1.00E+00	8.01E-01	1.00E+00	2.55E-01	1.00E+00	6.51E-01	1.00E+00	5.04E-01	1.00E+00	7.72E-01	1.00E+00	7.44E-01	1.00E+00	8.05E-01	1.00E+00	regulation of innate immune response	P
GO:0045089	12	8.18E-01	1.00E+00	8.58E-01	1.00E+00	5.22E-01	1.00E+00	6.65E-01	1.00E+00	7.40E-01	1.00E+00	8.47E-01	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	positive regulation of innate immune respon	P
GO:0045095	18	9.54E-01	1.00E+00	1.00E+00	1.00E+00	4.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.06E-01	1.00E+00	1.00E+00	1.00E+00	keratin filament	C
GO:0045103	15	9.24E-01	1.00E+00	5.97E-01	1.00E+00	8.79E-01	1.00E+00	9.49E-01	1.00E+00	7.38E-01	1.00E+00	4.26E-01	1.00E+00	1.00E+00	1.00E+00	5.99E-01	1.00E+00	intermediate filament-based process	P
GO:0045104	13	9.47E-01	1.00E+00	9.31E-01	1.00E+00	7.46E-01	1.00E+00	9.82E-01	1.00E+00	8.16E-01	1.00E+00	8.18E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	intermediate filament cytoskeleton organiza	P
GO:0045111	107	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	intermediate filament cytoskeleton	C
GO:0045120	12	1.42E-01	1.00E+00	2.22E-02	9.24E-01	1.76E-01	1.00E+00	1.01E-01	1.00E+00	9.40E-02	1.00E+00	1.75E-01	1.00E+00	5.79E-01	1.00E+00	3.29E-02	3.71E-01	pronucleus	C
GO:0045121	53	5.72E-01	1.00E+00	9.34E-01	1.00E+00	6.17E-02	1.00E+00	3.63E-01	1.00E+00	8.00E-01	1.00E+00	9.33E-01	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	lipid raft	C
GO:0045123	11	7.38E-01	1.00E+00	9.33E-01	1.00E+00	3.62E-01	1.00E+00	5.33E-01	1.00E+00	7.95E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	8.38E-01	1.00E+00	cellular extravasation	P
GO:0045125	20	9.79E-01	1.00E+00	7.46E-01	1.00E+00	9.99E-01	1.00E+00	1.95E-01	1.00E+00	8.27E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	6.45E-01	1.00E+00	bioactive lipid receptor activity	F
GO:0045137	71	9.96E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.29E-01	1.00E+00	1.00E+00	1.00E+00	development of primary sexual characteristi	P
GO:0045165	120	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell fate commitment	P
GO:0045168	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	cell-cell signaling during cell fate commitme	P
GO:0045177	126	9.27E-01	1.00E+00	9.87E-01	1.00E+00	3.85E-01	1.00E+00	3.79E-01	1.00E+00	9.46E-01	1.00E+00	9.94E-01	1.00E+00	9.88E-01	1.00E+00	9.97E-01	1.00E+00	apical part of cell	C
GO:0045178	26	8.06E-01	1.00E+00	9.57E-01	1.00E+00	6.93E-01	1.00E+00	9.99E-01	1.00E+00	7.80E-01	1.00E+00	8.86E-01	1.00E+00	7.05E-01	1.00E+00	7.25E-01	1.00E+00	basal part of cell	C
GO:0045182	118	3.82E-02	1.00E+00	8.56E-04	2.00E-02	1.46E-02	1.92E-01	1.39E-03	1.80E-02	9.80E-02	1.00E+00	4.99E-03	7.40E-02	6.29E-01	1.00E+00	8.54E-02	1.00E+00	translation regulator activity	F
GO:0045184	897	9.60E-04	1.60E-02	2.42E-06	1.41E-03	1.79E-06	8.48E-04	8.99E-06	9.66E-04	5.43E-03	1.35E-01	3.78E-04	1.02E-02	9.10E-01	1.00E+00	2.19E-01	1.00E+00	establishment of protein localization	P
GO:0045185	32	3.74E-01	1.00E+00	8.42E-01	1.00E+00	2.67E-01	1.00E+00	9.39E-01	1.00E+00	3.94E-01	1.00E+00	6.41E-01	1.00E+00	4.83E-01	1.00E+00	9.93E-01	1.00E+00	maintenance of protein localization	P
GO:0045190	24	4.11E-01	1.00E+00	2.86E-01	1.00E+00	6.71E-01	1.00E+00	5.21E-01	1.00E+00	2.27E-01	1.00E+00	2.25E-01	1.00E+00	9.19E-01	1.00E+00	5.19E-01	1.00E+00	isotype switching	P
GO:0045191	14	3.87E-01	1.00E+00	7.09E-01	1.00E+00	6.32E-01	1.00E+00	9.01E-01	1.00E+00	2.04E-01	1.00E+00	6.66E-01	1.00E+00	9.89E-01	1.00E+00	3.69E-01	1.00E+00	regulation of isotype switching	P
GO:0045202	264	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.00E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synapse	C
GO:0045211	125	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.31E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	postsynaptic membrane	C
GO:0045216	22	7.85E-01	1.00E+00	5.74E-01	1.00E+00	6.60E-01	1.00E+00	4.05E-01	1.00E+00	7.80E-01	1.00E+00	7.19E-01	1.00E+00	8.84E-01	1.00E+00	4.07E-01	1.00E+00	intercellular junction assembly and mainten	P
GO:0045255	16	1.40E-02	2.72E-01	1.93E-01	1.00E+00	3.90E-02	5.87E-01	3.66E-01	1.00E+00	1.07E-01	1.00E+00	1.72E-01	1.00E+00	2.54E-01	1.00E+00	4.65E-01	1.00E+00	hydrogen-translocating F-type ATPase com	C
GO:0045259	18	9.46E-03	1.77E-01	1.76E-01	1.00E+00	2.06E-02	2.36E-01	3.88E-01	1.00E+00	1.03E-01	1.00E+00	1.71E-01	1.00E+00	2.86E-01	1.00E+00	3.21E-01	1.00E+00	proton-transporting ATP synthase complex	C
GO:0045263	11	4.75E-03	1.37E-01	2.55E-01	1.00E+00	7.23E-03	1.57E-01	3.71E-01	1.00E+00	1.16E-01	1.00E+00	2.82E-01	1.00E+00	6.28E-01	1.00E+00	2.17E-01	1.00E+00	proton-transporting ATP synthase complex,	C

GO:0045271	37	3.71E-03	1.37E-01	1.49E-03	3.90E-02	2.30E-01	1.00E+00	2.60E-02	4.10E-01	6.35E-04	4.90E-03	2.10E-03	5.10E-02	5.65E-01	1.00E+00	9.97E-02	1.00E+00	respiratory chain complex I	C
GO:0045296	12	7.12E-01	1.00E+00	8.22E-01	1.00E+00	3.81E-01	1.00E+00	6.74E-01	1.00E+00	7.52E-01	1.00E+00	7.24E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	cadherin binding	F
GO:0045321	252	6.80E-01	1.00E+00	9.99E-01	1.00E+00	3.00E-01	1.00E+00	9.93E-01	1.00E+00	6.64E-01	1.00E+00	9.90E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	leukocyte activation	P
GO:0045333	48	1.92E-01	1.00E+00	1.32E-01	1.00E+00	7.01E-02	1.00E+00	3.14E-01	1.00E+00	3.64E-01	1.00E+00	9.58E-02	1.00E+00	4.73E-01	1.00E+00	7.17E-01	1.00E+00	cellular respiration	P
GO:0045334	10	7.11E-02	1.00E+00	8.19E-02	1.00E+00	1.30E-01	1.00E+00	5.93E-02	1.00E+00	8.74E-02	1.00E+00	1.33E-01	1.00E+00	5.28E-01	1.00E+00	9.46E-02	1.00E+00	clathrin-coated endocytic vesicle	C
GO:0045351	11	3.56E-01	1.00E+00	4.32E-01	1.00E+00	8.94E-01	1.00E+00	4.30E-01	1.00E+00	1.87E-01	1.00E+00	2.82E-01	1.00E+00	7.87E-01	1.00E+00	1.00E+00	1.00E+00	interferon type I biosynthesis	P
GO:0045408	11	6.52E-01	1.00E+00	9.81E-01	1.00E+00	8.55E-01	1.00E+00	1.00E+00	1.00E+00	5.12E-01	1.00E+00	9.72E-01	1.00E+00	9.32E-01	1.00E+00	8.57E-01	1.00E+00	regulation of interleukin-6 biosynthesis	P
GO:0045428	16	1.13E-01	1.00E+00	3.66E-01	1.00E+00	2.29E-01	1.00E+00	4.12E-01	1.00E+00	5.93E-02	1.00E+00	4.44E-01	1.00E+00	9.63E-01	1.00E+00	1.50E-01	1.00E+00	regulation of nitric oxide biosynthesis	P
GO:0045429	13	1.59E-01	1.00E+00	4.26E-01	1.00E+00	2.85E-01	1.00E+00	3.67E-01	1.00E+00	9.41E-02	1.00E+00	4.65E-01	1.00E+00	8.99E-01	1.00E+00	2.86E-01	1.00E+00	positive regulation of nitric oxide biosynthes	P
GO:0045444	29	7.99E-01	1.00E+00	4.37E-01	1.00E+00	6.32E-01	1.00E+00	5.34E-01	1.00E+00	8.44E-01	1.00E+00	3.34E-01	1.00E+00	8.28E-01	1.00E+00	8.37E-01	1.00E+00	fat cell differentiation	P
GO:0045445	47	9.73E-01	1.00E+00	1.00E+00	1.00E+00	8.03E-01	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	myoblast differentiation	P
GO:0045446	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	7.63E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	endothelial cell differentiation	P
GO:0045449	2599	9.95E-01	1.00E+00	1.61E-04	5.53E-03	4.98E-02	8.68E-01	6.79E-08	0.00E+00	9.96E-01	1.00E+00	5.57E-03	7.40E-02	1.00E+00	1.00E+00	6.65E-01	1.00E+00	regulation of transcription	P
GO:0045453	19	9.94E-01	1.00E+00	8.32E-01	1.00E+00	1.00E+00	1.00E+00	8.52E-01	1.00E+00	9.66E-01	1.00E+00	7.28E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	bone resorption	P
GO:0045454	56	1.73E-01	1.00E+00	5.75E-01	1.00E+00	5.67E-01	1.00E+00	3.51E-01	1.00E+00	1.53E-01	1.00E+00	6.43E-01	1.00E+00	4.91E-01	1.00E+00	7.49E-01	1.00E+00	cell redox homeostasis	P
GO:0045471	18	9.28E-01	1.00E+00	6.89E-01	1.00E+00	3.00E-01	1.00E+00	8.68E-01	1.00E+00	9.84E-01	1.00E+00	5.86E-01	1.00E+00	8.51E-01	1.00E+00	9.92E-01	1.00E+00	response to ethanol	P
GO:0045494	20	1.00E+00	1.00E+00	9.50E-01	1.00E+00	9.81E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	7.85E-01	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	photoreceptor maintenance	P
GO:0045577	12	1.25E-01	1.00E+00	5.63E-01	1.00E+00	2.71E-02	4.97E-01	5.94E-01	1.00E+00	7.03E-01	1.00E+00	7.34E-01	1.00E+00	1.71E-01	1.00E+00	6.02E-01	1.00E+00	regulation of B cell differentiation	P
GO:0045580	18	7.80E-01	1.00E+00	6.58E-01	1.00E+00	5.53E-01	1.00E+00	2.71E-01	1.00E+00	8.91E-01	1.00E+00	7.67E-01	1.00E+00	7.21E-01	1.00E+00	9.00E-01	1.00E+00	regulation of T cell differentiation	P
GO:0045582	11	4.88E-01	1.00E+00	1.91E-01	1.00E+00	5.05E-01	1.00E+00	1.20E-01	1.00E+00	6.13E-01	1.00E+00	2.22E-01	1.00E+00	2.97E-01	1.00E+00	6.22E-01	1.00E+00	positive regulation of T cell differentiation	P
GO:0045595	200	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of cell differentiation	P
GO:0045596	97	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of cell differentiation	P
GO:0045597	81	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of cell differentiation	P
GO:0045619	26	4.18E-01	1.00E+00	7.53E-01	1.00E+00	8.01E-02	1.00E+00	4.67E-01	1.00E+00	9.03E-01	1.00E+00	8.19E-01	1.00E+00	2.81E-01	1.00E+00	9.74E-01	1.00E+00	regulation of lymphocyte differentiation	P
GO:0045621	15	2.36E-01	1.00E+00	8.99E-02	1.00E+00	1.54E-01	1.00E+00	1.15E-01	1.00E+00	4.05E-01	1.00E+00	1.35E-01	1.00E+00	2.46E-01	1.00E+00	6.57E-01	1.00E+00	positive regulation of lymphocyte differentia	P
GO:0045637	45	9.93E-01	1.00E+00	9.96E-01	1.00E+00	7.97E-01	1.00E+00	9.66E-01	1.00E+00	9.96E-01	1.00E+00	9.85E-01	1.00E+00	8.71E-01	1.00E+00	1.00E+00	1.00E+00	regulation of myeloid cell differentiation	P
GO:0045638	22	8.86E-01	1.00E+00	9.57E-01	1.00E+00	5.54E-01	1.00E+00	8.79E-01	1.00E+00	9.49E-01	1.00E+00	8.60E-01	1.00E+00	5.94E-01	1.00E+00	9.95E-01	1.00E+00	negative regulation of myeloid cell differenti	P
GO:0045639	20	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	9.36E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of myeloid cell differentia	P
GO:0045646	14	7.70E-01	1.00E+00	7.10E-01	1.00E+00	7.14E-01	1.00E+00	3.93E-01	1.00E+00	6.16E-01	1.00E+00	7.56E-01	1.00E+00	9.97E-01	1.00E+00	8.10E-01	1.00E+00	regulation of erythrocyte differentiation	P
GO:0045664	43	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	7.61E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	regulation of neuron differentiation	P
GO:0045665	26	1.00E+00	1.00E+00	9.53E-01	1.00E+00	1.00E+00	1.00E+00	7.11E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	negative regulation of neuron differentiation	P
GO:0045666	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of neuron differentiation	P
GO:0045667	23	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.99E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	regulation of osteoblast differentiation	P
GO:0045669	18	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.57E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.82E-01	1.00E+00	positive regulation of osteoblast differentiati	P
GO:0045670	16	9.96E-01	1.00E+00	8.64E-01	1.00E+00	9.98E-01	1.00E+00	9.37E-01	1.00E+00	9.48E-01	1.00E+00	7.21E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of osteoclast differentiation	P
GO:0045685	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	regulation of glial cell differentiation	P
GO:0045727	64	8.82E-01	1.00E+00	8.41E-01	1.00E+00	4.31E-01	1.00E+00	6.03E-01	1.00E+00	8.22E-01	1.00E+00	6.88E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	positive regulation of protein biosynthesis	P
GO:0045735	79	6.35E-01	1.00E+00	9.76E-01	1.00E+00	7.59E-01	1.00E+00	7.26E-01	1.00E+00	6.80E-01	1.00E+00	9.83E-01	1.00E+00	3.45E-01	1.00E+00	8.76E-01	1.00E+00	nutrient reservoir activity	F
GO:0045736	10	2.61E-01	1.00E+00	6.02E-02	1.00E+00	2.10E-01	1.00E+00	3.20E-03	5.60E-02	2.16E-01	1.00E+00	5.52E-01	1.00E+00	1.00E+00	1.00E+00	3.13E-02	3.18E-01	negative regulation of cyclin-dependent pro	P
GO:0045740	15	7.11E-01	1.00E+00	7.14E-01	1.00E+00	3.11E-01	1.00E+00	5.92E-01	1.00E+00	7.61E-01	1.00E+00	7.54E-01	1.00E+00	9.96E-01	1.00E+00	6.46E-01	1.00E+00	positive regulation of DNA replication	P
GO:0045761	42	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	5.71E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	regulation of adenylate cyclase activity	P
GO:0045762	25	9.64E-01	1.00E+00	8.96E-01	1.00E+00	9.29E-01	1.00E+00	3.09E-01	1.00E+00	9.61E-01	1.00E+00	9.91E-01	1.00E+00	6.28E-01	1.00E+00	9.68E-01	1.00E+00	positive regulation of adenylate cyclase acti	P
GO:0045763	12	3.68E-01	1.00E+00	4.06E-01	1.00E+00	1.43E-01	1.00E+00	3.37E-01	1.00E+00	3.94E-01	1.00E+00	5.03E-01	1.00E+00	8.50E-01	1.00E+00	3.68E-01	1.00E+00	negative regulation of amino acid metabolis	P
GO:0045764	44	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.35E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of amino acid metabolisr	P
GO:0045765	48	7.84E-01	1.00E+00	9.88E-01	1.00E+00	4.72E-01	1.00E+00	9.99E-01	1.00E+00	7.76E-01	1.00E+00	9.50E-01	1.00E+00	9.73E-01	1.00E+00	9.63E-01	1.00E+00	regulation of angiogenesis	P
GO:0045766	16	8.09E-01	1.00E+00	9.96E-01	1.00E+00	5.62E-01	1.00E+00	1.00E+00	1.00E+00	7.67E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	positive regulation of angiogenesis	P
GO:0045767	15	3.83E-01	1.00E+00	1.33E-01	1.00E+00	2.03E-01	1.00E+00	1.04E-01	1.00E+00	3.69E-01	1.00E+00	1.99E-01	1.00E+00	9.54E-01	1.00E+00	6.29E-01	1.00E+00	regulation of anti-apoptosis	P
GO:0045768	11	7.45E-01	1.00E+00	1.43E-01	1.00E+00	1.54E-01	1.00E+00	8.24E-02	1.00E+00	8.31E-01	1.00E+00	1.50E-01	1.00E+00	9.26E-01	1.00E+00	4.70E-01	1.00E+00	positive regulation of anti-apoptosis	P
GO:0045778	17	7.99E-01	1.00E+00	9.31E-01	1.00E+00	9.09E-01	1.00E+00	9.44E-01	1.00E+00	6.00E-01	1.00E+00	7.83E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of ossification	P
GO:0045785	13	4.09E-01	1.00E+00	6.52E-01	1.00E+00	2.30E-01	1.00E+00	8.29E-01	1.00E+00	3.29E-01	1.00E+00	5.55E-01	1.00E+00	1.00E+00	1.00E+00	5.14E-01	1.00E+00	positive regulation of cell adhesion	P
GO:0045786	224	5.11E-01	1.00E+00	9.78E-01	1.00E+00	1.25E-02	1.92E-01	1.58E-01	1.00E+00	6.60E-01	1.00E+00	9.99E-01	1.00E+00	9.62E-01	1.00E+00	8.10E-01	1.00E+00	negative regulation of progression through	P
GO:0045787	40	8.42E-01	1.00E+00	6.28E-01	1.00E+00	9.11E-01	1.00E+00	7.97E-01	1.00E+00	6.72E-01	1.00E+00	5.77E-01	1.00E+00	9.16E-01	1.00E+00	7.27E-01	1.00E+00	positive regulation of progression through c	P
GO:0045792	67	5.97E-01	1.00E+00	9.93E-01	1.00E+00	2.25E-01	1.00E+00	5.72E-01	1.00E+00	6.28E-01	1.00E+00	9.96E-01	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	negative regulation of cell size	P
GO:0045793	10	9.93E-01	1.00E+00	6.53E-01	1.00E+00	1.00E+00	1.00E+00	2.04E-01	1.00E+00	8.62E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	7.94E-01	1.00E+00	positive regulation of cell size	P
GO:0045807	19	6.25E-01	1.00E+00	8.46E-01	1.00E+00	6.94E-01	1.00E+00	8.54E-01	1.00E+00	3.72E-01	1.00E+00	8.84E-01	1.00E+00	9.84E-01	1.00E+00	3.59E-01	1.00E+00	positive regulation of endocytosis	P
GO:0045814	19	1.27E-01	1.00E+00	2.49E-01	1.00E+00	2.41E-01	1.00E+00	3.88E-01	1.00E+00	9.33E-02	1.00E+00	1.35E-01	1.00E+00	7.22E-01	1.00E+00	9.48E-01	1.00E+00	negative regulation of gene expression, epi	P
GO:0045830	10	5.58E-01	1.00E+00	7.13E-01	1.00E+00	5.88E-01	1.00E+00	9.75E-01	1.00E+00	3.39E-01	1.00E+00	7.10E-01	1.00E+00	1.00E+00	1.00E+00	1.86E-01	1.00E+00	positive regulation of isotype switching	P
GO:0045833	10	6.85E-01	1.00E+00	3.04E-01	1.00E+00	6.06E-01	1.00E+00	2.63E-01	1.00E+00	6.69E-01	1.00E+00	2.83E-01	1.00E+00	6.99E-01	1.00E+00	6.10E-01	1.00E+00	negative regulation of lipid metabolism	P
GO:0045834	14	5.95E-01	1.00E+00	7.74E-01	1.00E+00	4.50E-01	1.00E+00	3.95E-01	1.00E+00	5.22E-01	1.00E+00	7.18E-01	1.00E+00	9.68E-01	1.00E+00	9.97E-01	1.00E+00	positive regulation of lipid metabolism	P
GO:0045840	22	8.93E-01	1.00E+00	5.89E-01	1.00E+00	9.11E-01	1.00E+00	9.51E-01	1.00E+00	7.85E-01	1.00E+00	4.37E-01	1.00E+00	9.10E-01	1.00E+00	8.61E-01	1.00E+00	positive regulation of mitosis	P
GO:0045843	10	4.46E-01	1.00E+00	8.19E-01	1.00E+00	2.43E-01	1.00E+00	9.92E-01	1.00E+00	5.30E-01	1.00E+00	7.60E-01	1.00E+00	9.50E-01	1.00E+00	7.24E-01	1.00E+00	negative regulation of striated muscle devel	P
GO:0045859	244	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.60E-01	1.00E+00	4.79E-01	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	regulation of protein kinase activity	P
GO:0045860	149	9.86E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	7.25E-01	1.00E+00	9.24E-01	1.00E+00	9.96E-01	1.00E+00	9.04E-01	1.00E+00	9.94E-01	1.00E+00	positive regulation of protein kinase activity	P
GO:0045884	15	8.35E-01	1.00E+00	8.70E-01	1.00E+00	4.41E-01	1.00E+00	9.81E-01	1.00E+00	8.33E-01	1.00E+00	5.80E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	regulation of survival gene product activity	P
GO:0045892	262	9.44E-01	1.00E+00	7.44E-01	1.00E+00	6.76E-01	1.00E+00	1.62E-01	1.00E+00	8.84E-01	1.00E+00	8.77E-01	1.00E+00	1.00E+00	1.00E+00	8.72E-01	1.00E+00	negative regulation of transcription, DNA-de	P
GO:0045893	338	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.70E-01	1.00E+00	8.04E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	positive regulation of transcription, DNA-dep	P
GO:0045913	14	2.55E-01	1.00E+00	4.05E-01	1.00E+00	1.40E-01	1.00E+00	1.36E-01	1.00E+00	1.27E-01	1.00E+00	4.45E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	positive regulation of carbohydrate metabol	P
GO:0045926	78	4.86E-01	1.00E+00	8.95E-01	1.00E+00	1.31E-01	1.00E+00	4.56E-01	1.00E+00	4.81E-01	1.00E+00	9.14E-01	1.00E+00	9.96E-01	1.00E+00	9.43E-01	1.00E+00	negative regulation of growth	P
GO:0045927	33	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.88E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	positive regulation of growth	P
GO:0045930	14	4.72E-01	1.00E+00	5.81E-01	1.00E+00	4.80E-01	1.00E+00	5.09E-01	1.00E+00	4.45E-01	1.00E+00	5.00E-01	1.00E+00	5.70E-01	1.00E+00	9.65E-01	1.00E+00	negative regulation of progression through	P
GO:0045934	380	7.49E-01	1.00E+00	4.38E-01	1.00E+00	2.31E-01	1.00E+00	2.94E-02	5.42E-01	6.30E-01	1.00E+00	6.60E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	negative regulation of nucleobase, nucleosi	P
GO:0045935	423	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.72E-01	1.00E+00	8.92E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	positive regulation of nucleobase, nucleosid	P
GO:0045936	19	5.60E-01	1.00E+00	3.87E-01	1.00E+00	1.77E-01	1.00E+00	3.67E-01	1.00E+00	9.47E-01	1.00E+00	4.81E-01	1.00E+00	3.59E-01	1.00E+00	3.46E-01	1.00E+00	negative regulation of phosphate metabolisr	P
GO:0045937	40	9.73E-01	1.00E+00	1.00E+00	1.00E+00	4.37E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of phosphate metabolisn	P
GO:0045941	402	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.97E-01	1.00E+00	8.68E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	positive regulation of transcription	P

GO:0045944	240	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of transcription from RN/	P
GO:0046006	10	3.47E-01	1.00E+00	9.84E-01	1.00E+00	1.21E-01	1.00E+00	8.50E-01	1.00E+00	3.41E-01	1.00E+00	9.68E-01	1.00E+00	9.54E-01	1.00E+00	7.59E-01	1.00E+00	regulation of activated T cell proliferation	P
GO:0046034	39	5.46E-03	1.37E-01	1.11E-01	1.00E+00	1.37E-02	1.92E-01	1.47E-01	1.00E+00	2.47E-02	6.55E-01	1.44E-01	1.00E+00	5.50E-01	1.00E+00	5.77E-01	1.00E+00	ATP metabolism	P
GO:0046036	11	3.10E-01	1.00E+00	7.53E-01	1.00E+00	3.54E-01	1.00E+00	3.31E-01	1.00E+00	2.73E-01	1.00E+00	9.12E-01	1.00E+00	6.29E-01	1.00E+00	9.66E-01	1.00E+00	CTP metabolism	P
GO:0046039	10	2.95E-01	1.00E+00	7.77E-01	1.00E+00	3.60E-01	1.00E+00	4.40E-01	1.00E+00	2.24E-01	1.00E+00	9.09E-01	1.00E+00	6.27E-01	1.00E+00	9.34E-01	1.00E+00	GTP metabolism	P
GO:0046051	10	2.95E-01	1.00E+00	7.77E-01	1.00E+00	3.60E-01	1.00E+00	4.40E-01	1.00E+00	2.24E-01	1.00E+00	9.09E-01	1.00E+00	6.27E-01	1.00E+00	9.34E-01	1.00E+00	UTP metabolism	P
GO:0046058	25	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.40E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cAMP metabolism	P
GO:0046068	15	9.88E-01	1.00E+00	9.99E-01	1.00E+00	5.60E-01	1.00E+00	9.98E-01	1.00E+00	9.43E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cGMP metabolism	P
GO:0046112	10	4.56E-02	1.00E+00	5.22E-02	1.00E+00	7.03E-02	1.00E+00	3.10E-02	5.42E-01	3.71E-02	1.00E+00	1.35E-01	1.00E+00	1.99E-01	1.00E+00	9.00E-02	1.00E+00	nucleobase biosynthesis	P
GO:0046128	10	4.02E-01	1.00E+00	5.46E-02	1.00E+00	1.95E-02	2.36E-01	8.68E-03	1.12E-01	9.54E-01	1.00E+00	9.94E-02	1.00E+00	6.61E-01	1.00E+00	3.71E-01	1.00E+00	purine ribonucleoside metabolism	P
GO:0046148	38	1.92E-01	1.00E+00	9.09E-02	1.00E+00	7.56E-02	1.00E+00	2.65E-01	1.00E+00	1.67E-01	1.00E+00	1.15E-01	1.00E+00	8.53E-01	1.00E+00	1.82E-01	1.00E+00	pigment biosynthesis	P
GO:0046164	90	3.76E-02	1.00E+00	2.05E-02	9.24E-01	2.92E-02	5.65E-01	1.01E-01	1.00E+00	7.16E-02	1.00E+00	2.90E-02	1.00E+00	6.08E-01	1.00E+00	1.21E-01	1.00E+00	alcohol catabolism	P
GO:0046165	35	6.81E-01	1.00E+00	6.30E-01	1.00E+00	4.22E-01	1.00E+00	5.86E-01	1.00E+00	5.75E-01	1.00E+00	5.40E-01	1.00E+00	9.94E-01	1.00E+00	7.75E-01	1.00E+00	alcohol biosynthesis	P
GO:0046209	28	3.33E-01	1.00E+00	4.67E-01	1.00E+00	3.22E-01	1.00E+00	3.83E-01	1.00E+00	1.95E-01	1.00E+00	6.16E-01	1.00E+00	9.84E-01	1.00E+00	2.56E-01	1.00E+00	nitric oxide metabolism	P
GO:0046320	12	7.68E-02	1.00E+00	3.34E-01	1.00E+00	2.98E-02	5.65E-01	6.83E-02	1.00E+00	2.44E-01	1.00E+00	3.75E-01	1.00E+00	1.82E-01	1.00E+00	9.38E-01	1.00E+00	regulation of fatty acid oxidation	P
GO:0046323	19	9.82E-01	1.00E+00	4.91E-01	1.00E+00	7.36E-01	1.00E+00	9.40E-01	1.00E+00	9.66E-01	1.00E+00	2.82E-01	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	glucose import	P
GO:0046324	18	9.89E-01	1.00E+00	5.28E-01	1.00E+00	8.21E-01	1.00E+00	9.87E-01	1.00E+00	9.69E-01	1.00E+00	2.91E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	regulation of glucose import	P
GO:0046325	11	9.95E-01	1.00E+00	5.23E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	3.21E-01	1.00E+00	1.00E+00	1.00E+00	8.45E-01	1.00E+00	negative regulation of glucose import	P
GO:0046328	27	9.86E-01	1.00E+00	9.15E-01	1.00E+00	5.66E-01	1.00E+00	9.47E-01	1.00E+00	9.99E-01	1.00E+00	8.92E-01	1.00E+00	9.18E-01	1.00E+00	5.34E-01	1.00E+00	regulation of JNK cascade	P
GO:0046330	17	9.62E-01	1.00E+00	9.83E-01	1.00E+00	5.53E-01	1.00E+00	9.59E-01	1.00E+00	9.96E-01	1.00E+00	9.59E-01	1.00E+00	8.70E-01	1.00E+00	9.48E-01	1.00E+00	positive regulation of JNK cascade	P
GO:0046332	16	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.92E-01	1.00E+00	1.69E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.26E-01	1.00E+00	SMAD binding	F
GO:0046356	24	2.09E-01	1.00E+00	6.59E-02	1.00E+00	4.70E-02	8.68E-01	5.07E-01	1.00E+00	3.37E-01	1.00E+00	1.86E-02	5.65E-01	9.13E-01	1.00E+00	7.97E-01	1.00E+00	acetyl-CoA catabolism	P
GO:0046364	34	6.85E-01	1.00E+00	5.99E-01	1.00E+00	4.32E-01	1.00E+00	5.91E-01	1.00E+00	5.49E-01	1.00E+00	5.09E-01	1.00E+00	9.98E-01	1.00E+00	7.31E-01	1.00E+00	monosaccharide biosynthesis	P
GO:0046365	82	1.17E-02	2.72E-01	4.20E-03	6.30E-02	8.02E-03	1.57E-01	5.16E-02	1.00E+00	2.20E-02	4.78E-01	8.06E-03	1.05E-01	6.54E-01	1.00E+00	5.29E-02	8.10E-01	monosaccharide catabolism	P
GO:0046394	93	7.18E-01	1.00E+00	7.40E-01	1.00E+00	3.44E-01	1.00E+00	2.65E-01	1.00E+00	7.29E-01	1.00E+00	8.34E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	carboxylic acid biosynthesis	P
GO:0046395	10	6.67E-03	1.37E-01	1.32E-02	3.84E-01	1.42E-05	9.71E-04	3.31E-01	1.00E+00	3.21E-02	6.55E-01	1.39E-02	5.65E-01	3.15E-01	1.00E+00	1.13E-01	1.00E+00	carboxylic acid catabolism	P
GO:0046425	24	9.49E-01	1.00E+00	9.06E-01	1.00E+00	2.82E-01	1.00E+00	6.76E-01	1.00E+00	9.91E-01	1.00E+00	7.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of JAK-STAT cascade	P
GO:0046427	14	9.65E-01	1.00E+00	9.46E-01	1.00E+00	3.29E-01	1.00E+00	9.44E-01	1.00E+00	1.00E+00	1.00E+00	7.46E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of JAK-STAT cascade	P
GO:0046456	29	7.53E-01	1.00E+00	5.16E-01	1.00E+00	9.56E-01	1.00E+00	7.87E-01	1.00E+00	5.59E-01	1.00E+00	3.90E-01	1.00E+00	8.36E-01	1.00E+00	5.75E-01	1.00E+00	icosanoid biosynthesis	P
GO:0046466	26	5.38E-01	1.00E+00	4.10E-01	1.00E+00	1.58E-01	1.00E+00	4.82E-01	1.00E+00	4.77E-01	1.00E+00	4.60E-01	1.00E+00	9.58E-01	1.00E+00	6.17E-01	1.00E+00	membrane lipid catabolism	P
GO:0046467	108	8.08E-01	1.00E+00	1.42E-01	1.00E+00	3.30E-01	1.00E+00	3.68E-02	1.00E+00	7.61E-01	1.00E+00	2.81E-01	1.00E+00	9.95E-01	1.00E+00	7.55E-01	1.00E+00	membrane lipid biosynthesis	P
GO:0046470	15	3.72E-01	1.00E+00	1.83E-01	1.00E+00	8.36E-01	1.00E+00	1.58E-01	1.00E+00	1.90E-01	1.00E+00	2.27E-01	1.00E+00	9.94E-01	1.00E+00	5.77E-01	1.00E+00	phosphatidylcholine metabolism	P
GO:0046474	53	6.76E-01	1.00E+00	2.14E-01	1.00E+00	6.76E-01	1.00E+00	1.30E-01	1.00E+00	5.38E-01	1.00E+00	3.71E-01	1.00E+00	9.54E-01	1.00E+00	6.32E-01	1.00E+00	glycerophospholipid biosynthesis	P
GO:0046483	91	3.42E-02	1.00E+00	1.79E-03	3.90E-02	1.53E-03	1.60E-02	1.84E-02	4.10E-01	2.64E-01	1.00E+00	8.46E-03	1.05E-01	7.63E-01	1.00E+00	1.22E-01	1.00E+00	heterocycle metabolism	P
GO:0046486	38	7.88E-01	1.00E+00	9.44E-01	1.00E+00	4.89E-01	1.00E+00	8.95E-01	1.00E+00	6.91E-01	1.00E+00	9.41E-01	1.00E+00	9.91E-01	1.00E+00	8.41E-01	1.00E+00	glycerolipid metabolism	P
GO:0046488	15	1.88E-01	1.00E+00	1.88E-01	1.00E+00	1.01E-01	1.00E+00	3.81E-01	1.00E+00	2.44E-01	1.00E+00	1.65E-01	1.00E+00	2.77E-01	1.00E+00	4.68E-01	1.00E+00	phosphatidylinositol metabolism	P
GO:0046489	36	4.70E-01	1.00E+00	1.15E-01	1.00E+00	4.11E-01	1.00E+00	1.19E-01	1.00E+00	4.00E-01	1.00E+00	2.60E-01	1.00E+00	6.92E-01	1.00E+00	2.58E-01	1.00E+00	phosphoinositide biosynthesis	P
GO:0046519	36	4.76E-02	1.00E+00	1.94E-02	9.24E-01	1.11E-03	1.25E-02	2.42E-02	4.10E-01	1.06E-01	1.00E+00	2.49E-02	7.69E-01	7.29E-01	1.00E+00	1.76E-01	1.00E+00	sphingoid metabolism	P
GO:0046520	10	2.17E-01	1.00E+00	3.48E-02	1.00E+00	5.46E-02	1.00E+00	1.23E-02	1.57E-01	3.78E-01	1.00E+00	3.21E-02	1.00E+00	3.12E-01	1.00E+00	3.13E-01	1.00E+00	sphingoid biosynthesis	P
GO:0046530	14	9.96E-01	1.00E+00	7.47E-01	1.00E+00	8.94E-01	1.00E+00	8.46E-01	1.00E+00	9.96E-01	1.00E+00	7.75E-01	1.00E+00	1.00E+00	1.00E+00	3.93E-01	1.00E+00	photoreceptor cell differentiation	P
GO:0046545	41	7.31E-01	1.00E+00	9.77E-01	1.00E+00	4.88E-01	1.00E+00	9.48E-01	1.00E+00	9.37E-01	1.00E+00	9.60E-01	1.00E+00	2.50E-01	1.00E+00	9.41E-01	1.00E+00	development of primary female sexual char	P
GO:0046546	30	9.98E-01	1.00E+00	9.82E-01	1.00E+00	9.60E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	9.44E-01	1.00E+00	6.17E-01	1.00E+00	9.95E-01	1.00E+00	development of primary male sexual charac	P
GO:0046620	11	9.98E-01	1.00E+00	9.66E-01	1.00E+00	9.96E-01	1.00E+00	4.82E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	5.74E-01	1.00E+00	4.95E-01	1.00E+00	regulation of organ size	P
GO:0046631	33	5.32E-01	1.00E+00	9.65E-01	1.00E+00	3.84E-01	1.00E+00	9.88E-01	1.00E+00	3.64E-01	1.00E+00	8.92E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	alpha-beta T cell activation	P
GO:0046632	26	7.98E-01	1.00E+00	9.32E-01	1.00E+00	6.64E-01	1.00E+00	9.22E-01	1.00E+00	6.51E-01	1.00E+00	8.78E-01	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	alpha-beta T cell differentiation	P
GO:0046649	221	6.24E-01	1.00E+00	9.98E-01	1.00E+00	2.26E-01	1.00E+00	9.63E-01	1.00E+00	6.22E-01	1.00E+00	9.89E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	lymphocyte activation	P
GO:0046651	78	6.70E-01	1.00E+00	9.96E-01	1.00E+00	5.25E-01	1.00E+00	9.45E-01	1.00E+00	5.43E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	lymphocyte proliferation	P
GO:0046658	13	9.98E-01	1.00E+00	9.91E-01	1.00E+00	9.19E-01	1.00E+00	4.57E-01	1.00E+00	9.60E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	anchored to plasma membrane	C
GO:0046660	43	8.12E-01	1.00E+00	9.88E-01	1.00E+00	5.49E-01	1.00E+00	9.65E-01	1.00E+00	9.63E-01	1.00E+00	9.77E-01	1.00E+00	2.84E-01	1.00E+00	9.63E-01	1.00E+00	female sex differentiation	P
GO:0046661	46	9.99E-01	1.00E+00	9.93E-01	1.00E+00	8.80E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.70E-01	1.00E+00	9.30E-01	1.00E+00	9.97E-01	1.00E+00	male sex differentiation	P
GO:0046677	32	5.59E-01	1.00E+00	9.34E-01	1.00E+00	2.74E-01	1.00E+00	6.54E-01	1.00E+00	5.89E-01	1.00E+00	8.89E-01	1.00E+00	9.16E-01	1.00E+00	9.98E-01	1.00E+00	response to antibiotic	P
GO:0046716	10	7.08E-01	1.00E+00	9.99E-01	1.00E+00	5.22E-01	1.00E+00	9.79E-01	1.00E+00	9.49E-01	1.00E+00	1.00E+00	1.00E+00	1.58E-01	1.00E+00	4.87E-01	1.00E+00	muscle maintenance	P
GO:0046718	10	7.82E-01	1.00E+00	8.27E-01	1.00E+00	7.34E-01	1.00E+00	6.61E-01	1.00E+00	4.94E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	6.05E-01	1.00E+00	entry of virus into host cell	P
GO:0046777	59	2.56E-01	1.00E+00	2.15E-01	1.00E+00	1.83E-01	1.00E+00	1.97E-01	1.00E+00	1.81E-01	1.00E+00	1.78E-01	1.00E+00	9.91E-01	1.00E+00	7.63E-01	1.00E+00	protein amino acid autophosphorylation	P
GO:0046785	16	9.93E-01	1.00E+00	9.99E-01	1.00E+00	5.80E-01	1.00E+00	6.36E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	microtubule polymerization	P
GO:0046822	44	3.99E-01	1.00E+00	6.60E-02	1.00E+00	4.04E-01	1.00E+00	8.77E-02	1.00E+00	3.65E-01	1.00E+00	5.49E-02	1.00E+00	7.69E-01	1.00E+00	4.66E-01	1.00E+00	regulation of nucleocytoplasmic transport	P
GO:0046823	17	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.63E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	9.88E-01	1.00E+00	negative regulation of nucleocytoplasmic tra	P
GO:0046824	19	3.68E-01	1.00E+00	1.05E-01	1.00E+00	4.32E-01	1.00E+00	6.64E-02	1.00E+00	4.12E-01	1.00E+00	1.21E-01	1.00E+00	4.05E-01	1.00E+00	4.33E-01	1.00E+00	positive regulation of nucleocytoplasmic tra	P
GO:0046834	17	4.64E-02	1.00E+00	4.45E-02	1.00E+00	4.30E-02	7.24E-01	7.63E-02	1.00E+00	9.09E-02	1.00E+00	1.23E-01	1.00E+00	1.00E-01	1.00E+00	1.55E-02	1.38E-01	lipid phosphorylation	P
GO:0046839	16	9.97E-01	1.00E+00	8.67E-01	1.00E+00	5.65E-01	1.00E+00	3.31E-01	1.00E+00	9.99E-01	1.00E+00	8.92E-01	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	phospholipid dephosphorylation	P
GO:0046847	17	3.93E-01	1.00E+00	2.00E-01	1.00E+00	3.64E-01	1.00E+00	1.50E-01	1.00E+00	3.16E-01	1.00E+00	1.13E-01	1.00E+00	7.29E-01	1.00E+00	8.62E-01	1.00E+00	filopodium formation	P
GO:0046849	154	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	bone remodeling	P
GO:0046850	38	8.92E-01	1.00E+00	9.18E-01	1.00E+00	7.91E-01	1.00E+00	9.82E-01	1.00E+00	8.14E-01	1.00E+00	6.97E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	regulation of bone remodeling	P
GO:0046851	14	5.91E-01	1.00E+00	9.83E-01	1.00E+00	4.78E-01	1.00E+00	9.21E-01	1.00E+00	5.35E-01	1.00E+00	9.26E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of bone remodeling	P
GO:0046852	18	8.31E-01	1.00E+00	9.56E-01	1.00E+00	9.11E-01	1.00E+00	9.55E-01	1.00E+00	6.45E-01	1.00E+00	8.31E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of bone remodeling	P
GO:0046854	16	2.72E-02	1.00E+00	3.23E-02	1.00E+00	2.66E-02	4.97E-01	5.36E-02	1.00E+00	6.51E-02	1.00E+00	1.06E-01	1.00E+00	7.46E-02	1.00E+00	1.04E-02	1.38E-01	phosphoinositide phosphorylation	P
GO:0046872	4263	1.00E+00	1.00E+00	7.31E-01	1.00E+00	1.67E-03	1.60E-02	5.11E-03	6.84E-02	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	metal ion binding	F
GO:0046873	69	7.76E-01	1.00E+00	4.55E-01	1.00E+00	6.27E-01	1.00E+00	2.77E-01	1.00E+00	6.55E-01	1.00E+00	3.26E-01	1.00E+00	9.63E-01	1.00E+00	9.92E-01	1.00E+00	metal ion transporter activity	F
GO:0046879	59	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	7.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.61E-01	1.00E+00	1.00E+00	1.00E+00	hormone secretion	P
GO:0046883	32	9.37E-01	1.00E+00	9.92E-01	1.00E+00	5.59E-01	1.00E+00	5.41E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	6.00E-01	1.00E+00	9.96E-01	1.00E+00	regulation of hormone secretion	P
GO:0046888	15	7.27E-01	1.00E+00	9.65E-01	1.00E+00	4.53E-01	1.00E+00	7.45E-01	1.00E+00	9.77E-01	1.00E+00	9.85E-01	1.00E+00	3.91E-01	1.00E+00	9.90E-01	1.00E+00	negative regulation of hormone secretion	P
GO:0046890	18	5.60E-01	1.00E+00	3.87E-01	1.00E+00	2.58E-01	1.00E+00	1.32E-01	1.00E+00	5.88E-01	1.00E+00	3.56E-01	1.00E+00	8.43E-01	1.00E+00	9.22E-01	1.00E+00	regulation of lipid biosynthesis	P
GO:0046903	376	7.86E-01	1.00E+00	9.92E-01	1.00E+00	4.51E-01	1.00E+00	3.09E-01	1.00E+00	8.00E-01	1.00E+00	9.99E-01	1.00E+00	9.07E-01	1.00E+00	9.98E-01	1.00E+00	secretion	P
GO:0046906	166	9.72E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.30E-01	1.00E+00	1.00E+00	1.00E+00	tetrapyrrole binding	F
GO:0046907	838	3.05E-04	1.10E-02	5.86E-06	1.41E-03	1.86E-10	0.00E+00	2.97E-06	0.00E+00	1.46E-02	3.01E-01	2.33E-03	5.10E-02	8.83E-01	1.00E+00	2.67E-01	1.00E+00	intracellular transport	P

GO:0046914	2856	8.07E-01	1.00E+00	9.26E-04	2.00E-02	5.95E-03	9.30E-02	1.38E-05	2.00E-03	9.34E-01	1.00E+00	1.88E-02	5.65E-01	9.80E-01	1.00E+00	4.88E-01	1.00E+00	transition metal ion binding	F
GO:0046915	35	5.84E-01	1.00E+00	1.30E-01	1.00E+00	5.95E-01	1.00E+00	1.07E-01	1.00E+00	5.44E-01	1.00E+00	1.02E-01	1.00E+00	5.74E-01	1.00E+00	8.69E-01	1.00E+00	transition metal ion transporter activity	F
GO:0046916	45	3.50E-01	1.00E+00	6.81E-01	1.00E+00	5.83E-02	1.00E+00	9.43E-01	1.00E+00	6.46E-01	1.00E+00	5.67E-01	1.00E+00	4.39E-01	1.00E+00	7.29E-01	1.00E+00	transition metal ion homeostasis	P
GO:0046928	22	9.95E-01	1.00E+00	1.00E+00	1.00E+00	7.33E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of neurotransmitter secretion	P
GO:0046930	72	6.76E-05	5.00E-03	4.14E-10	1.00E-03	4.54E-06	9.71E-04	8.68E-07	0.00E+00	3.70E-04	4.00E-03	2.58E-08	1.05E-04	1.19E-01	1.00E+00	1.64E-04	5.00E-04	pore complex	C
GO:0046933	21	5.32E-02	1.00E+00	2.58E-01	1.00E+00	8.41E-02	1.00E+00	1.30E-01	1.00E+00	1.26E-01	1.00E+00	2.96E-01	1.00E+00	4.87E-01	1.00E+00	9.72E-01	1.00E+00	hydrogen-transporting ATP synthase activity	F
GO:0046942	143	9.16E-01	1.00E+00	8.54E-01	1.00E+00	4.24E-01	1.00E+00	4.59E-01	1.00E+00	9.12E-01	1.00E+00	6.80E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	carboxylic acid transport	P
GO:0046943	123	9.83E-01	1.00E+00	9.82E-01	1.00E+00	8.06E-01	1.00E+00	5.87E-01	1.00E+00	9.69E-01	1.00E+00	9.53E-01	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	carboxylic acid transporter activity	F
GO:0046961	35	7.94E-02	1.00E+00	2.10E-01	1.00E+00	5.57E-02	1.00E+00	5.36E-02	1.00E+00	2.17E-01	1.00E+00	3.27E-01	1.00E+00	3.90E-01	1.00E+00	8.48E-01	1.00E+00	hydrogen-transporting ATPase activity, rotat	F
GO:0046966	35	8.02E-01	1.00E+00	1.80E-01	1.00E+00	3.24E-01	1.00E+00	9.82E-02	1.00E+00	8.56E-01	1.00E+00	1.45E-01	1.00E+00	9.74E-01	1.00E+00	8.34E-01	1.00E+00	thyroid hormone receptor binding	F
GO:0046982	163	9.85E-01	1.00E+00	9.95E-01	1.00E+00	3.78E-01	1.00E+00	9.52E-01	1.00E+00	9.91E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	protein heterodimerization activity	F
GO:0046983	432	8.96E-01	1.00E+00	8.49E-01	1.00E+00	9.96E-02	1.00E+00	3.01E-01	1.00E+00	9.72E-01	1.00E+00	9.22E-01	1.00E+00	9.81E-01	1.00E+00	9.31E-01	1.00E+00	protein dimerization activity	F
GO:0047485	50	5.53E-01	1.00E+00	3.14E-01	1.00E+00	4.41E-01	1.00E+00	3.11E-01	1.00E+00	4.85E-01	1.00E+00	3.19E-01	1.00E+00	9.76E-01	1.00E+00	3.88E-01	1.00E+00	protein N-terminus binding	F
GO:0048002	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation of pep	P
GO:0048008	11	9.98E-01	1.00E+00	1.00E+00	1.00E+00	4.66E-01	1.00E+00	4.18E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	platelet-derived growth factor receptor signa	P
GO:0048009	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	insulin-like growth factor receptor signaling	P
GO:0048010	15	9.64E-01	1.00E+00	9.58E-01	1.00E+00	9.61E-01	1.00E+00	7.68E-01	1.00E+00	9.24E-01	1.00E+00	9.88E-01	1.00E+00	9.48E-01	1.00E+00	6.76E-01	1.00E+00	vascular endothelial growth factor receptor	P
GO:0048011	10	8.14E-01	1.00E+00	8.39E-02	1.00E+00	3.99E-01	1.00E+00	6.18E-03	8.10E-02	8.39E-01	1.00E+00	1.53E-01	1.00E+00	1.00E+00	1.00E+00	8.84E-01	1.00E+00	nerve growth factor receptor signaling pathv	P
GO:0048015	110	9.96E-01	1.00E+00	9.57E-01	1.00E+00	8.71E-01	1.00E+00	7.39E-01	1.00E+00	9.93E-01	1.00E+00	9.35E-01	1.00E+00	9.96E-01	1.00E+00	9.96E-01	1.00E+00	phosphoinositide-mediated signaling	P
GO:0048019	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.56E-01	1.00E+00	receptor antagonist activity	F
GO:0048029	20	9.30E-01	1.00E+00	6.36E-01	1.00E+00	9.31E-01	1.00E+00	4.75E-01	1.00E+00	9.06E-01	1.00E+00	7.67E-01	1.00E+00	4.90E-01	1.00E+00	2.81E-01	1.00E+00	monosaccharide binding	F
GO:0048037	262	4.39E-02	1.00E+00	1.29E-02	3.84E-01	9.42E-04	1.25E-02	6.19E-03	8.10E-02	1.66E-01	1.00E+00	1.98E-02	5.65E-01	7.45E-01	1.00E+00	6.89E-01	1.00E+00	cofactor binding	F
GO:0048041	15	9.87E-01	1.00E+00	5.81E-01	1.00E+00	8.37E-01	1.00E+00	2.49E-01	1.00E+00	9.54E-01	1.00E+00	6.20E-01	1.00E+00	1.00E+00	1.00E+00	7.12E-01	1.00E+00	focal adhesion formation	P
GO:0048066	19	9.48E-01	1.00E+00	7.04E-01	1.00E+00	8.37E-01	1.00E+00	6.59E-01	1.00E+00	9.28E-01	1.00E+00	5.82E-01	1.00E+00	7.88E-01	1.00E+00	9.96E-01	1.00E+00	pigmentation during development	P
GO:0048144	23	5.75E-01	1.00E+00	3.83E-01	1.00E+00	9.73E-01	1.00E+00	1.41E-01	1.00E+00	4.21E-01	1.00E+00	5.75E-01	1.00E+00	5.44E-01	1.00E+00	7.74E-01	1.00E+00	fibroblast proliferation	P
GO:0048145	23	5.75E-01	1.00E+00	3.83E-01	1.00E+00	9.73E-01	1.00E+00	1.41E-01	1.00E+00	4.21E-01	1.00E+00	5.75E-01	1.00E+00	5.44E-01	1.00E+00	7.74E-01	1.00E+00	regulation of fibroblast proliferation	P
GO:0048146	18	9.66E-01	1.00E+00	6.78E-01	1.00E+00	1.00E+00	1.00E+00	1.92E-01	1.00E+00	8.07E-01	1.00E+00	9.75E-01	1.00E+00	9.99E-01	1.00E+00	6.42E-01	1.00E+00	positive regulation of fibroblast proliferation	P
GO:0048167	38	9.40E-01	1.00E+00	7.22E-01	1.00E+00	4.86E-01	1.00E+00	9.03E-01	1.00E+00	9.57E-01	1.00E+00	4.25E-01	1.00E+00	7.84E-01	1.00E+00	1.00E+00	1.00E+00	regulation of synaptic plasticity	P
GO:0048168	19	1.00E+00	1.00E+00	8.53E-01	1.00E+00	4.40E-01	1.00E+00	5.75E-01	1.00E+00	1.00E+00	1.00E+00	8.22E-01	1.00E+00	9.94E-01	1.00E+00	9.96E-01	1.00E+00	regulation of neuronal synaptic plasticity	P
GO:0048169	11	1.00E+00	1.00E+00	9.05E-01	1.00E+00	9.51E-01	1.00E+00	5.38E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	regulation of long-term neuronal synaptic pl	P
GO:0048193	91	1.89E-01	1.00E+00	1.23E-02	3.84E-01	1.70E-02	2.36E-01	3.24E-03	5.60E-02	5.21E-01	1.00E+00	3.43E-02	1.00E+00	3.44E-01	1.00E+00	2.01E-01	1.00E+00	Golgi vesicle transport	P
GO:0048194	11	1.55E-02	3.10E-01	4.04E-02	1.00E+00	6.13E-02	1.00E+00	1.71E-01	1.00E+00	3.19E-02	6.55E-01	3.08E-02	1.00E+00	2.70E-02	2.56E-01	2.15E-01	1.00E+00	Golgi vesicle budding	P
GO:0048199	12	8.58E-03	1.56E-01	3.77E-02	1.00E+00	4.32E-02	7.24E-01	2.40E-01	1.00E+00	1.67E-02	3.81E-01	2.42E-02	7.69E-01	1.11E-01	1.00E+00	1.34E-01	1.00E+00	vesicle targeting, to, from or within Golgi	P
GO:0048200	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	Golgi transport vesicle coating	P
GO:0048204	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	vesicle targeting, inter-Golgi cisterna	P
GO:0048205	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	COPI coating of Golgi vesicle	P
GO:0048206	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	vesicle targeting, cis-Golgi to rough ER	P
GO:0048219	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	inter-Golgi cisterna vesicle-mediated transp	P
GO:0048220	10	3.90E-02	1.00E+00	8.28E-02	1.00E+00	1.17E-01	1.00E+00	2.57E-01	1.00E+00	7.01E-02	1.00E+00	6.68E-02	1.00E+00	5.08E-02	1.00E+00	2.14E-01	1.00E+00	cis-Golgi to rough ER vesicle-mediated tran	P
GO:0048232	251	8.11E-01	1.00E+00	3.30E-01	1.00E+00	7.72E-01	1.00E+00	1.75E-01	1.00E+00	6.30E-01	1.00E+00	3.35E-01	1.00E+00	9.73E-01	1.00E+00	8.13E-01	1.00E+00	male gamete generation	P
GO:0048265	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to pain	P
GO:0048278	22	2.69E-01	1.00E+00	5.35E-01	1.00E+00	1.32E-01	1.00E+00	3.69E-01	1.00E+00	2.38E-01	1.00E+00	4.48E-01	1.00E+00	9.27E-01	1.00E+00	8.26E-01	1.00E+00	vesicle docking	P
GO:0048286	11	9.14E-01	1.00E+00	9.30E-01	1.00E+00	9.22E-01	1.00E+00	9.04E-01	1.00E+00	8.99E-01	1.00E+00	8.16E-01	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	alveolus development	P
GO:0048305	11	9.28E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	6.84E-01	1.00E+00	9.49E-01	1.00E+00	9.98E-01	1.00E+00	8.06E-01	1.00E+00	immunoglobulin secretion	P
GO:0048306	21	9.71E-01	1.00E+00	8.85E-01	1.00E+00	6.27E-01	1.00E+00	4.32E-01	1.00E+00	9.94E-01	1.00E+00	8.14E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	calcium-dependent protein binding	F
GO:0048332	35	9.62E-01	1.00E+00	9.83E-01	1.00E+00	9.47E-01	1.00E+00	3.87E-01	1.00E+00	8.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mesoderm morphogenesis	P
GO:0048333	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	mesodermal cell differentiation	P
GO:0048468	580	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell development	P
GO:0048469	81	9.96E-01	1.00E+00	1.00E+00	1.00E+00	4.09E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cell maturation	P
GO:0048471	88	7.69E-01	1.00E+00	5.77E-01	1.00E+00	1.12E-01	1.00E+00	2.81E-01	1.00E+00	8.98E-01	1.00E+00	4.87E-01	1.00E+00	9.94E-01	1.00E+00	9.93E-01	1.00E+00	perinuclear region	C
GO:0048475	65	2.77E-04	1.10E-02	1.30E-04	4.00E-03	9.31E-05	4.57E-03	8.45E-04	1.03E-02	6.16E-04	4.90E-03	3.11E-04	1.02E-02	4.27E-01	1.00E+00	3.14E-01	1.00E+00	coated membrane	C
GO:0048477	24	2.41E-01	1.00E+00	5.79E-01	1.00E+00	5.31E-01	1.00E+00	8.88E-01	1.00E+00	1.81E-01	1.00E+00	4.35E-01	1.00E+00	7.84E-01	1.00E+00	7.25E-01	1.00E+00	oogenesis	P
GO:0048483	11	9.41E-01	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	8.27E-01	1.00E+00	9.95E-01	1.00E+00	8.97E-01	1.00E+00	9.98E-01	1.00E+00	autonomic nervous system development	P
GO:0048487	11	2.95E-01	1.00E+00	3.44E-02	1.00E+00	9.07E-01	1.00E+00	3.00E-01	1.00E+00	1.45E-01	1.00E+00	1.21E-02	3.46E-01	4.36E-01	1.00E+00	7.04E-01	1.00E+00	beta-tubulin binding	F
GO:0048488	10	1.35E-01	1.00E+00	3.78E-01	1.00E+00	3.36E-01	1.00E+00	1.27E-01	1.00E+00	1.07E-01	1.00E+00	6.94E-01	1.00E+00	8.70E-01	1.00E+00	8.99E-01	1.00E+00	synaptic vesicle endocytosis	P
GO:0048489	26	6.43E-01	1.00E+00	8.82E-01	1.00E+00	4.51E-01	1.00E+00	1.92E-01	1.00E+00	6.45E-01	1.00E+00	9.88E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	synaptic vesicle transport	P
GO:0048500	11	7.87E-01	1.00E+00	1.56E-01	1.00E+00	8.12E-01	1.00E+00	7.25E-02	1.00E+00	7.68E-01	1.00E+00	2.67E-01	1.00E+00	7.50E-01	1.00E+00	2.39E-01	1.00E+00	signal recognition particle	C
GO:0048511	79	9.27E-01	1.00E+00	9.45E-01	1.00E+00	7.80E-01	1.00E+00	7.30E-01	1.00E+00	9.19E-01	1.00E+00	9.13E-01	1.00E+00	7.41E-01	1.00E+00	9.98E-01	1.00E+00	rhythmic process	P
GO:0048513	1376	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organ development	P
GO:0048514	194	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.00E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	blood vessel morphogenesis	P
GO:0048515	39	2.83E-01	1.00E+00	3.81E-01	1.00E+00	6.30E-01	1.00E+00	7.13E-01	1.00E+00	2.47E-01	1.00E+00	1.98E-01	1.00E+00	3.71E-01	1.00E+00	9.68E-01	1.00E+00	spermatid differentiation	P
GO:0048518	1504	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	4.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of biological process	P
GO:0048519	1475	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.75E-01	1.00E+00	4.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of biological process	P
GO:0048522	1170	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.82E-01	1.00E+00	4.43E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of cellular process	P
GO:0048523	1273	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.47E-01	1.00E+00	4.01E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of cellular process	P
GO:0048534	251	8.74E-01	1.00E+00	9.95E-01	1.00E+00	3.65E-01	1.00E+00	9.50E-01	1.00E+00	9.42E-01	1.00E+00	9.80E-01	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	hemopoietic or lymphoid organ developmer	P
GO:0048536	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	spleen development	P
GO:0048538	12	3.23E-01	1.00E+00	7.22E-01	1.00E+00	6.80E-01	1.00E+00	5.59E-01	1.00E+00	3.16E-01	1.00E+00	8.64E-01	1.00E+00	3.09E-01	1.00E+00	4.69E-01	1.00E+00	thymus development	P
GO:0048545	59	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.11E-01	1.00E+00	3.49E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	response to steroid hormone stimulus	P
GO:0048546	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	digestive tract morphogenesis	P
GO:0048547	13	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.32E-01	1.00E+00	9.81E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	gut morphogenesis	P
GO:0048562	19	9.55E-01	1.00E+00	9.11E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	9.02E-01	1.00E+00	8.88E-01	1.00E+00	8.21E-01	1.00E+00	7.90E-01	1.00E+00	embryonic organ morphogenesis	P
GO:0048565	24	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	gut development	P
GO:0048566	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.24E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	embryonic gut development	P
GO:0048568	37	9.72E-01	1.00E+00	9.88E-01	1.00E+00	9.85E-01	1.00E+00	9.28E-01	1.00E+00	9.15E-01	1.00E+00	9.90E-01	1.00E+00	8.75E-01	1.00E+00	9.28E-01	1.00E+00	embryonic organ development	P

GO:0048583	11	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.44E-01	1.00E+00	9.31E-01	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of response to stimulus	P
GO:0048589	49	9.94E-01	1.00E+00	8.09E-01	1.00E+00	9.98E-01	1.00E+00	9.71E-01	1.00E+00	9.22E-01	1.00E+00	7.52E-01	1.00E+00	9.99E-01	1.00E+00	5.10E-01	1.00E+00	developmental growth	P
GO:0048592	34	9.61E-01	1.00E+00	8.92E-01	1.00E+00	6.27E-01	1.00E+00	9.51E-01	1.00E+00	9.95E-01	1.00E+00	8.70E-01	1.00E+00	4.04E-01	1.00E+00	8.62E-01	1.00E+00	eye morphogenesis	P
GO:0048593	18	7.67E-01	1.00E+00	7.31E-01	1.00E+00	3.79E-01	1.00E+00	7.50E-01	1.00E+00	9.33E-01	1.00E+00	7.95E-01	1.00E+00	2.25E-01	1.00E+00	5.08E-01	1.00E+00	eye morphogenesis (sensu Vertebrata)	P
GO:0048598	200	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic morphogenesis	P
GO:0048599	13	2.50E-01	1.00E+00	9.87E-01	1.00E+00	6.92E-01	1.00E+00	8.70E-01	1.00E+00	2.30E-01	1.00E+00	9.99E-01	1.00E+00	6.25E-01	1.00E+00	5.52E-01	1.00E+00	oocyte development	P
GO:0048609	124	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.26E-01	1.00E+00	1.00E+00	1.00E+00	reproductive organismal physiological proce	P
GO:0048627	25	5.64E-01	1.00E+00	1.00E+00	1.00E+00	2.73E-01	1.00E+00	9.99E-01	1.00E+00	5.62E-01	1.00E+00	1.00E+00	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	myoblast development	P
GO:0048628	24	5.03E-01	1.00E+00	1.00E+00	1.00E+00	2.46E-01	1.00E+00	9.99E-01	1.00E+00	4.94E-01	1.00E+00	1.00E+00	1.00E+00	8.88E-01	1.00E+00	1.00E+00	1.00E+00	myoblast maturation	P
GO:0048637	80	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	9.98E-01	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	skeletal muscle development	P
GO:0048644	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.99E-01	1.00E+00	8.83E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	muscle morphogenesis	P
GO:0048646	68	9.95E-01	1.00E+00	9.78E-01	1.00E+00	9.94E-01	1.00E+00	8.00E-01	1.00E+00	9.80E-01	1.00E+00	9.33E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	anatomical structure formation	P
GO:0048659	34	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.98E-01	1.00E+00	6.63E-01	1.00E+00	smooth muscle cell proliferation	P
GO:0048660	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	7.69E-01	1.00E+00	6.49E-01	1.00E+00	regulation of smooth muscle cell proliferatio	P
GO:0048661	22	1.00E+00	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.88E-01	1.00E+00	9.69E-01	1.00E+00	7.86E-01	1.00E+00	4.08E-01	1.00E+00	positive regulation of smooth muscle cell pr	P
GO:0048662	10	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	5.46E-01	1.00E+00	9.82E-01	1.00E+00	negative regulation of smooth muscle cell p	P
GO:0048663	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron fate commitment	P
GO:0048665	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron fate specification	P
GO:0048666	250	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron development	P
GO:0048667	180	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neuron morphogenesis during differentiatior	P
GO:0048675	23	8.63E-01	1.00E+00	9.31E-01	1.00E+00	2.21E-01	1.00E+00	9.76E-01	1.00E+00	9.68E-01	1.00E+00	9.47E-01	1.00E+00	9.85E-01	1.00E+00	6.80E-01	1.00E+00	axon extension	P
GO:0048699	375	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	generation of neurons	P
GO:0048704	43	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	embryonic skeletal morphogenesis	P
GO:0048705	53	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	skeletal morphogenesis	P
GO:0048706	57	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	embryonic skeletal development	P
GO:0048709	18	7.90E-01	1.00E+00	9.76E-01	1.00E+00	3.79E-01	1.00E+00	7.54E-01	1.00E+00	9.59E-01	1.00E+00	9.94E-01	1.00E+00	6.27E-01	1.00E+00	8.89E-01	1.00E+00	oligodendrocyte differentiation	P
GO:0048729	115	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tissue morphogenesis	P
GO:0048730	81	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	epidermis morphogenesis	P
GO:0048731	906	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	system development	P
GO:0048732	73	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gland development	P
GO:0048736	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	appendage development	P
GO:0048738	11	3.28E-01	1.00E+00	4.64E-01	1.00E+00	2.69E-01	1.00E+00	2.29E-01	1.00E+00	5.54E-01	1.00E+00	5.29E-01	1.00E+00	1.87E-01	1.00E+00	6.29E-01	1.00E+00	cardiac muscle development	P
GO:0048741	79	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.27E-01	1.00E+00	9.98E-01	1.00E+00	9.19E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	skeletal muscle fiber development	P
GO:0048747	80	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.18E-01	1.00E+00	9.94E-01	1.00E+00	8.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	muscle fiber development	P
GO:0048754	52	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	branching morphogenesis of a tube	P
GO:0048762	40	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.35E-01	1.00E+00	1.00E+00	1.00E+00	mesenchymal cell differentiation	P
GO:0048770	84	4.74E-02	1.00E+00	3.20E-04	8.26E-03	1.52E-01	1.00E+00	2.33E-02	4.10E-01	2.28E-02	4.78E-01	4.10E-04	1.02E-02	5.10E-01	1.00E+00	4.69E-02	8.10E-01	pigment granule	C
GO:0048771	169	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	tissue remodeling	P
GO:0048806	16	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.10E-01	1.00E+00	genitalia development	P
GO:0048812	180	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurite morphogenesis	P
GO:0048813	14	9.49E-01	1.00E+00	9.30E-01	1.00E+00	4.35E-01	1.00E+00	7.54E-01	1.00E+00	9.92E-01	1.00E+00	8.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	dendrite morphogenesis	P
GO:0048820	10	1.00E+00	1.00E+00	9.62E-01	1.00E+00	9.97E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	9.97E-01	1.00E+00	9.61E-01	1.00E+00	hair follicle maturation	P
GO:0048821	10	3.83E-01	1.00E+00	9.07E-01	1.00E+00	1.13E-01	1.00E+00	9.98E-01	1.00E+00	9.79E-01	1.00E+00	7.62E-01	1.00E+00	5.69E-01	1.00E+00	9.99E-01	1.00E+00	erythrocyte development	P
GO:0048839	50	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inner ear development	P
GO:0048856	2319	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	anatomical structure development	P
GO:0048858	180	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell projection morphogenesis	P
GO:0050136	44	2.98E-02	1.00E+00	1.03E-02	3.84E-01	3.70E-01	1.00E+00	4.42E-02	1.00E+00	5.60E-03	1.35E-01	1.91E-02	5.65E-01	8.71E-01	1.00E+00	1.62E-01	1.00E+00	NADH dehydrogenase (quinone) activity	F
GO:0050381	25	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.39E-01	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	unspecific monooxygenase activity	F
GO:0050435	14	1.48E-01	1.00E+00	5.75E-01	1.00E+00	4.88E-02	8.68E-01	3.48E-01	1.00E+00	1.97E-01	1.00E+00	5.87E-01	1.00E+00	9.99E-01	1.00E+00	7.22E-01	1.00E+00	beta-amyloid metabolism	P
GO:0050650	11	5.69E-01	1.00E+00	9.78E-01	1.00E+00	3.37E-01	1.00E+00	8.53E-01	1.00E+00	6.68E-01	1.00E+00	9.73E-01	1.00E+00	5.91E-01	1.00E+00	9.59E-01	1.00E+00	chondroitin sulfate proteoglycan biosynthes	P
GO:0050654	11	5.69E-01	1.00E+00	9.78E-01	1.00E+00	3.37E-01	1.00E+00	8.53E-01	1.00E+00	6.68E-01	1.00E+00	9.73E-01	1.00E+00	5.91E-01	1.00E+00	9.59E-01	1.00E+00	chondroitin sulfate proteoglycan metabolism	P
GO:0050657	90	2.38E-02	1.00E+00	2.25E-05	2.21E-03	1.60E-03	1.60E-02	8.18E-06	8.32E-04	8.21E-02	1.00E+00	1.44E-04	2.29E-03	4.31E-01	1.00E+00	7.43E-02	1.00E+00	nucleic acid transport	P
GO:0050658	90	2.38E-02	1.00E+00	2.25E-05	2.21E-03	1.60E-03	1.60E-02	8.18E-06	8.32E-04	8.21E-02	1.00E+00	1.44E-04	2.29E-03	4.31E-01	1.00E+00	7.43E-02	1.00E+00	RNA transport	P
GO:0050660	85	4.02E-01	1.00E+00	9.67E-02	1.00E+00	3.22E-01	1.00E+00	4.34E-02	1.00E+00	3.66E-01	1.00E+00	1.67E-01	1.00E+00	8.76E-01	1.00E+00	3.51E-01	1.00E+00	FAD binding	F
GO:0050661	34	1.58E-01	1.00E+00	4.43E-01	1.00E+00	1.89E-01	1.00E+00	1.27E-01	1.00E+00	2.04E-01	1.00E+00	7.56E-01	1.00E+00	1.42E-01	1.00E+00	3.74E-01	1.00E+00	NADP binding	F
GO:0050662	190	6.13E-02	1.00E+00	6.93E-02	1.00E+00	2.87E-02	5.65E-01	3.38E-02	5.42E-01	1.22E-01	1.00E+00	6.17E-02	1.00E+00	6.40E-01	1.00E+00	9.26E-01	1.00E+00	coenzyme binding	F
GO:0050663	32	7.41E-01	1.00E+00	9.16E-01	1.00E+00	9.47E-01	1.00E+00	8.51E-01	1.00E+00	4.50E-01	1.00E+00	9.16E-01	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	cytokine secretion	P
GO:0050670	58	6.88E-01	1.00E+00	1.00E+00	1.00E+00	3.42E-01	1.00E+00	9.92E-01	1.00E+00	6.09E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	regulation of lymphocyte proliferation	P
GO:0050671	40	5.30E-01	1.00E+00	9.79E-01	1.00E+00	3.88E-01	1.00E+00	8.39E-01	1.00E+00	4.12E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	8.70E-01	1.00E+00	positive regulation of lymphocyte proliferatic	P
GO:0050672	22	9.91E-01	1.00E+00	1.00E+00	1.00E+00	8.11E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of lymphocyte proliferati	P
GO:0050673	47	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	epithelial cell proliferation	P
GO:0050678	41	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of epithelial cell proliferation	P
GO:0050679	21	6.05E-01	1.00E+00	9.95E-01	1.00E+00	5.43E-01	1.00E+00	1.00E+00	1.00E+00	4.61E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	positive regulation of epithelial cell proliferat	P
GO:0050680	18	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.18E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of epithelial cell prolifera	P
GO:0050681	26	5.99E-01	1.00E+00	1.97E-01	1.00E+00	1.38E-01	1.00E+00	4.27E-02	1.00E+00	7.47E-01	1.00E+00	4.13E-01	1.00E+00	7.75E-01	1.00E+00	4.17E-01	1.00E+00	androgen receptor binding	F
GO:0050688	17	1.38E-01	1.00E+00	7.12E-01	1.00E+00	3.23E-01	1.00E+00	3.63E-01	1.00E+00	7.35E-02	1.00E+00	6.21E-01	1.00E+00	8.68E-01	1.00E+00	9.98E-01	1.00E+00	regulation of antiviral response	P
GO:0050701	16	3.27E-01	1.00E+00	5.24E-01	1.00E+00	9.00E-01	1.00E+00	8.21E-01	1.00E+00	1.48E-01	1.00E+00	4.24E-01	1.00E+00	9.75E-01	1.00E+00	6.41E-01	1.00E+00	interleukin-1 secretion	P
GO:0050702	15	4.23E-01	1.00E+00	4.45E-01	1.00E+00	8.57E-01	1.00E+00	7.56E-01	1.00E+00	2.47E-01	1.00E+00	3.51E-01	1.00E+00	9.56E-01	1.00E+00	5.80E-01	1.00E+00	interleukin-1 beta secretion	P
GO:0050704	14	3.31E-01	1.00E+00	5.91E-01	1.00E+00	8.92E-01	1.00E+00	7.81E-01	1.00E+00	1.61E-01	1.00E+00	5.29E-01	1.00E+00	9.54E-01	1.00E+00	6.48E-01	1.00E+00	regulation of interleukin-1 secretion	P
GO:0050706	13	4.28E-01	1.00E+00	5.13E-01	1.00E+00	8.45E-01	1.00E+00	7.07E-01	1.00E+00	2.66E-01	1.00E+00	4.54E-01	1.00E+00	9.25E-01	1.00E+00	5.87E-01	1.00E+00	regulation of interleukin-1 beta secretion	P
GO:0050707	28	6.86E-01	1.00E+00	9.19E-01	1.00E+00	9.12E-01	1.00E+00	8.02E-01	1.00E+00	4.13E-01	1.00E+00	9.34E-01	1.00E+00	1.00E+00	1.00E+00	9.44E-01	1.00E+00	regulation of cytokine secretion	P
GO:0050708	45	7.28E-01	1.00E+00	9.79E-01	1.00E+00	9.32E-01	1.00E+00	9.58E-01	1.00E+00	4.05E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	8.20E-01	1.00E+00	regulation of protein secretion	P
GO:0050709	16	7.70E-01	1.00E+00	9.95E-01	1.00E+00	7.35E-01	1.00E+00	9.65E-01	1.00E+00	6.76E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.43E-01	1.00E+00	negative regulation of protein secretion	P
GO:0050710	13	6.33E-01	1.00E+00	9.68E-01	1.00E+00	5.79E-01	1.00E+00	8.87E-01	1.00E+00	5.52E-01	1.00E+00	9.93E-01	1.00E+00	9.70E-01	1.00E+00	8.59E-01	1.00E+00	negative regulation of cytokine secretion	P
GO:0050714	26	5.16E-01	1.00E+00	7.87E-01	1.00E+00	9.10E-01	1.00E+00	8.13E-01	1.00E+00	3.04E-01	1.00E+00	8.29E-01	1.00E+00	8.71E-01	1.00E+00	6.22E-01	1.00E+00	positive regulation of protein secretion	P

GO:0050715	20	5.56E-01	1.00E+00	7.86E-01	1.00E+00	9.74E-01	1.00E+00	7.56E-01	1.00E+00	2.97E-01	1.00E+00	7.80E-01	1.00E+00	9.91E-01	1.00E+00	8.22E-01	1.00E+00	positive regulation of cytokine secretion	P
GO:0050716	12	2.07E-01	1.00E+00	4.30E-01	1.00E+00	7.85E-01	1.00E+00	6.19E-01	1.00E+00	9.65E-02	1.00E+00	3.77E-01	1.00E+00	8.82E-01	1.00E+00	5.22E-01	1.00E+00	positive regulation of interleukin-1 secretion	P
GO:0050718	11	2.90E-01	1.00E+00	3.47E-01	1.00E+00	7.12E-01	1.00E+00	5.21E-01	1.00E+00	1.76E-01	1.00E+00	3.01E-01	1.00E+00	8.22E-01	1.00E+00	4.54E-01	1.00E+00	positive regulation of interleukin-1 beta secr	P
GO:0050727	41	8.56E-01	1.00E+00	1.00E+00	1.00E+00	4.28E-01	1.00E+00	9.75E-01	1.00E+00	7.51E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.50E-01	1.00E+00	regulation of inflammatory response	P
GO:0050728	18	9.54E-01	1.00E+00	1.00E+00	1.00E+00	3.86E-01	1.00E+00	9.78E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.23E-01	1.00E+00	negative regulation of inflammatory respons	P
GO:0050729	14	2.63E-01	1.00E+00	6.73E-01	1.00E+00	1.14E-01	1.00E+00	3.49E-01	1.00E+00	2.49E-01	1.00E+00	8.12E-01	1.00E+00	8.54E-01	1.00E+00	5.47E-01	1.00E+00	positive regulation of inflammatory respons	P
GO:0050730	46	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.30E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of peptidyl-tyrosine phosphorylati	P
GO:0050731	29	9.96E-01	1.00E+00	1.00E+00	1.00E+00	6.36E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of peptidyl-tyrosine phos	P
GO:0050750	11	9.94E-01	1.00E+00	8.68E-01	1.00E+00	2.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.51E-01	1.00E+00	1.00E+00	1.00E+00	8.32E-01	1.00E+00	low-density lipoprotein receptor binding	F
GO:0050755	14	5.44E-01	1.00E+00	4.54E-01	1.00E+00	4.71E-01	1.00E+00	5.35E-01	1.00E+00	4.82E-01	1.00E+00	4.85E-01	1.00E+00	1.00E+00	1.00E+00	2.54E-01	1.00E+00	chemokine metabolism	P
GO:0050764	11	1.86E-01	1.00E+00	4.62E-01	1.00E+00	3.27E-01	1.00E+00	7.47E-01	1.00E+00	8.59E-02	1.00E+00	5.39E-01	1.00E+00	8.14E-01	1.00E+00	1.30E-01	1.00E+00	regulation of phagocytosis	P
GO:0050767	57	9.25E-01	1.00E+00	9.70E-01	1.00E+00	4.87E-01	1.00E+00	9.46E-01	1.00E+00	9.58E-01	1.00E+00	8.88E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	regulation of neurogenesis	P
GO:0050768	19	5.69E-01	1.00E+00	8.11E-01	1.00E+00	6.31E-01	1.00E+00	7.23E-01	1.00E+00	5.06E-01	1.00E+00	6.40E-01	1.00E+00	7.83E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of neurogenesis	P
GO:0050769	24	8.79E-01	1.00E+00	8.12E-01	1.00E+00	6.11E-01	1.00E+00	6.31E-01	1.00E+00	9.46E-01	1.00E+00	7.66E-01	1.00E+00	8.36E-01	1.00E+00	9.07E-01	1.00E+00	positive regulation of neurogenesis	P
GO:0050770	34	9.85E-01	1.00E+00	1.00E+00	1.00E+00	5.19E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of axonogenesis	P
GO:0050772	16	9.05E-01	1.00E+00	1.00E+00	1.00E+00	7.52E-01	1.00E+00	9.89E-01	1.00E+00	9.35E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.99E-01	1.00E+00	positive regulation of axonogenesis	P
GO:0050776	121	9.43E-01	1.00E+00	9.98E-01	1.00E+00	4.65E-01	1.00E+00	9.98E-01	1.00E+00	9.28E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of immune response	P
GO:0050777	14	2.58E-01	1.00E+00	9.49E-01	1.00E+00	8.58E-02	1.00E+00	9.76E-01	1.00E+00	3.74E-01	1.00E+00	8.90E-01	1.00E+00	9.52E-01	1.00E+00	9.76E-01	1.00E+00	negative regulation of immune response	P
GO:0050778	103	9.83E-01	1.00E+00	9.89E-01	1.00E+00	8.52E-01	1.00E+00	9.89E-01	1.00E+00	9.51E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of immune response	P
GO:0050785	14	8.94E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.91E-01	1.00E+00	7.32E-01	1.00E+00	6.77E-01	1.00E+00	7.80E-01	1.00E+00	advanced glycation end-product receptor ac	F
GO:0050789	4955	1.00E+00	1.00E+00	3.78E-01	1.00E+00	9.20E-02	1.00E+00	5.02E-06	8.32E-04	1.00E+00	1.00E+00	7.22E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	regulation of biological process	P
GO:0050790	596	6.23E-01	1.00E+00	5.01E-01	1.00E+00	4.35E-01	1.00E+00	3.41E-03	5.60E-02	5.60E-01	1.00E+00	7.52E-01	1.00E+00	9.65E-01	1.00E+00	9.89E-01	1.00E+00	regulation of catalytic activity	P
GO:0050791	4307	1.00E+00	1.00E+00	8.52E-02	1.00E+00	3.29E-02	5.87E-01	2.63E-06	0.00E+00	1.00E+00	1.00E+00	3.20E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	regulation of physiological process	P
GO:0050792	17	8.49E-01	1.00E+00	9.91E-01	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	5.58E-01	1.00E+00	9.84E-01	1.00E+00	9.21E-01	1.00E+00	5.64E-01	1.00E+00	regulation of viral life cycle	P
GO:0050793	271	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of development	P
GO:0050794	4370	1.00E+00	1.00E+00	6.98E-02	1.00E+00	4.92E-02	8.68E-01	3.29E-07	0.00E+00	1.00E+00	1.00E+00	3.58E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	regulation of cellular process	P
GO:0050796	17	8.97E-01	1.00E+00	7.12E-01	1.00E+00	5.22E-01	1.00E+00	1.23E-01	1.00E+00	9.56E-01	1.00E+00	9.05E-01	1.00E+00	9.80E-01	1.00E+00	9.36E-01	1.00E+00	regulation of insulin secretion	P
GO:0050798	13	2.61E-01	1.00E+00	8.91E-01	1.00E+00	1.12E-01	1.00E+00	5.61E-01	1.00E+00	2.81E-01	1.00E+00	9.30E-01	1.00E+00	7.25E-01	1.00E+00	7.02E-01	1.00E+00	activated T cell proliferation	P
GO:0050801	226	7.90E-01	1.00E+00	9.99E-01	1.00E+00	6.86E-02	1.00E+00	9.83E-01	1.00E+00	9.09E-01	1.00E+00	9.87E-01	1.00E+00	9.82E-01	1.00E+00	9.96E-01	1.00E+00	ion homeostasis	P
GO:0050803	68	9.97E-01	1.00E+00	8.59E-01	1.00E+00	7.59E-01	1.00E+00	9.95E-01	1.00E+00	9.96E-01	1.00E+00	4.76E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	regulation of synapse structure and functior	P
GO:0050804	65	9.99E-01	1.00E+00	9.24E-01	1.00E+00	7.80E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	6.05E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	regulation of synaptic transmission	P
GO:0050806	21	9.98E-01	1.00E+00	7.65E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	4.40E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	positive regulation of synaptic transmission	P
GO:0050808	34	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	9.38E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	synapse organization and biogenesis	P
GO:0050810	11	5.88E-01	1.00E+00	4.64E-01	1.00E+00	1.69E-01	1.00E+00	7.66E-02	1.00E+00	7.99E-01	1.00E+00	5.14E-01	1.00E+00	5.95E-01	1.00E+00	9.06E-01	1.00E+00	regulation of steroid biosynthesis	P
GO:0050817	156	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	coagulation	P
GO:0050818	33	5.03E-01	1.00E+00	7.01E-01	1.00E+00	4.72E-01	1.00E+00	8.32E-01	1.00E+00	3.10E-01	1.00E+00	4.78E-01	1.00E+00	9.76E-01	1.00E+00	9.79E-01	1.00E+00	regulation of coagulation	P
GO:0050819	28	5.30E-01	1.00E+00	9.73E-01	1.00E+00	4.80E-01	1.00E+00	9.99E-01	1.00E+00	3.22E-01	1.00E+00	8.41E-01	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	negative regulation of coagulation	P
GO:0050821	20	4.54E-01	1.00E+00	3.16E-01	1.00E+00	4.14E-01	1.00E+00	1.76E-01	1.00E+00	5.09E-01	1.00E+00	3.83E-01	1.00E+00	3.09E-01	1.00E+00	4.08E-01	1.00E+00	protein stabilization	P
GO:0050824	193	9.96E-01	1.00E+00	9.95E-01	1.00E+00	4.86E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	water binding	F
GO:0050825	193	9.96E-01	1.00E+00	9.95E-01	1.00E+00	4.86E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	ice binding	F
GO:0050826	193	9.96E-01	1.00E+00	9.95E-01	1.00E+00	4.86E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	response to freezing	P
GO:0050830	12	1.14E-02	2.72E-01	6.95E-01	1.00E+00	2.52E-01	1.00E+00	9.43E-01	1.00E+00	8.02E-03	2.02E-01	5.65E-01	1.00E+00	2.81E-01	1.00E+00	8.45E-01	1.00E+00	defense response to Gram-positive bacteriu	P
GO:0050832	14	5.76E-01	1.00E+00	8.14E-01	1.00E+00	2.33E-01	1.00E+00	9.56E-01	1.00E+00	8.75E-01	1.00E+00	6.17E-01	1.00E+00	3.43E-01	1.00E+00	1.00E+00	1.00E+00	defense response to fungus	P
GO:0050839	17	7.68E-01	1.00E+00	5.60E-01	1.00E+00	3.74E-01	1.00E+00	1.94E-01	1.00E+00	8.25E-01	1.00E+00	5.31E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	cell adhesion molecule binding	F
GO:0050848	16	2.07E-01	1.00E+00	5.01E-01	1.00E+00	2.72E-01	1.00E+00	3.00E-01	1.00E+00	1.80E-01	1.00E+00	6.80E-01	1.00E+00	5.36E-01	1.00E+00	2.53E-01	1.00E+00	regulation of calcium-mediated signaling	P
GO:0050850	14	3.64E-01	1.00E+00	7.76E-01	1.00E+00	4.69E-01	1.00E+00	7.68E-01	1.00E+00	3.27E-01	1.00E+00	8.34E-01	1.00E+00	5.92E-01	1.00E+00	3.13E-01	1.00E+00	positive regulation of calcium-mediated sigr	P
GO:0050851	33	1.66E-01	1.00E+00	4.74E-01	1.00E+00	8.72E-03	1.57E-01	7.54E-01	1.00E+00	3.44E-01	1.00E+00	3.04E-01	1.00E+00	1.00E+00	1.00E+00	9.38E-01	1.00E+00	antigen receptor-mediated signaling pathwa	P
GO:0050852	21	4.30E-01	1.00E+00	9.60E-01	1.00E+00	2.73E-02	4.97E-01	9.40E-01	1.00E+00	7.61E-01	1.00E+00	9.32E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	T cell receptor signaling pathway	P
GO:0050853	13	3.38E-01	1.00E+00	2.93E-01	1.00E+00	5.48E-02	1.00E+00	8.62E-01	1.00E+00	5.72E-01	1.00E+00	1.98E-01	1.00E+00	8.01E-01	1.00E+00	9.10E-01	1.00E+00	B cell receptor signaling pathway	P
GO:0050854	10	3.74E-01	1.00E+00	9.01E-01	1.00E+00	1.04E-01	1.00E+00	9.38E-01	1.00E+00	5.63E-01	1.00E+00	7.90E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	regulation of antigen receptor-mediated sigr	P
GO:0050863	71	4.72E-01	1.00E+00	9.78E-01	1.00E+00	5.74E-02	1.00E+00	7.40E-01	1.00E+00	6.38E-01	1.00E+00	9.69E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	regulation of T cell activation	P
GO:0050864	39	2.55E-01	1.00E+00	7.14E-01	1.00E+00	1.26E-01	1.00E+00	6.80E-01	1.00E+00	3.33E-01	1.00E+00	8.07E-01	1.00E+00	5.64E-01	1.00E+00	3.03E-01	1.00E+00	regulation of B cell activation	P
GO:0050868	19	8.69E-01	1.00E+00	1.00E+00	1.00E+00	4.24E-01	1.00E+00	1.00E+00	1.00E+00	8.00E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of T cell activation	P
GO:0050869	10	5.24E-01	1.00E+00	9.50E-01	1.00E+00	2.75E-01	1.00E+00	9.08E-01	1.00E+00	9.02E-01	1.00E+00	9.61E-01	1.00E+00	3.38E-01	1.00E+00	6.39E-01	1.00E+00	negative regulation of B cell activation	P
GO:0050870	50	3.67E-01	1.00E+00	7.59E-01	1.00E+00	1.78E-01	1.00E+00	4.77E-01	1.00E+00	4.80E-01	1.00E+00	7.46E-01	1.00E+00	8.77E-01	1.00E+00	9.78E-01	1.00E+00	positive regulation of T cell activation	P
GO:0050871	27	4.15E-01	1.00E+00	5.65E-01	1.00E+00	3.21E-01	1.00E+00	5.68E-01	1.00E+00	3.44E-01	1.00E+00	7.36E-01	1.00E+00	9.11E-01	1.00E+00	2.07E-01	1.00E+00	positive regulation of B cell activation	P
GO:0050874	2736	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organismal physiological process	P
GO:0050875	11263	5.55E-01	1.00E+00	3.49E-03	6.30E-02	4.06E-14	0.00E+00	2.98E-15	0.00E+00	9.26E-01	1.00E+00	1.53E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	cellular physiological process	P
GO:0050876	125	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.17E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.61E-01	1.00E+00	1.00E+00	1.00E+00	reproductive physiological process	P
GO:0050877	782	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurophysiological process	P
GO:0050878	170	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of body fluids	P
GO:0050879	52	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.33E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organismal movement	P
GO:0050880	55	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.78E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of blood vessel size	P
GO:0050881	36	9.65E-01	1.00E+00	9.96E-01	1.00E+00	4.38E-01	1.00E+00	9.05E-01	1.00E+00	9.82E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	musculoskeletal movement	P
GO:0050885	31	9.73E-01	1.00E+00	9.98E-01	1.00E+00	3.61E-01	1.00E+00	9.47E-01	1.00E+00	9.89E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of balance	P
GO:0050886	16	9.78E-01	1.00E+00	1.00E+00	1.00E+00	5.03E-01	1.00E+00	9.60E-01	1.00E+00	9.70E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endocrine physiological process	P
GO:0050892	13	2.15E-01	1.00E+00	2.52E-01	1.00E+00	7.16E-02	1.00E+00	1.61E-01	1.00E+00	3.75E-01	1.00E+00	3.19E-01	1.00E+00	4.84E-01	1.00E+00	3.83E-01	1.00E+00	intestinal absorption	P
GO:0050896	2545	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to stimulus	P
GO:0050897	15	4.11E-01	1.00E+00	3.89E-01	1.00E+00	5.73E-01	1.00E+00	9.38E-02	1.00E+00	2.68E-01	1.00E+00	3.86E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	cobalt ion binding	F
GO:0050900	50	9.63E-01	1.00E+00	6.64E-01	1.00E+00	9.16E-01	1.00E+00	6.24E-01	1.00E+00	8.30E-01	1.00E+00	7.36E-01	1.00E+00	1.00E+00	1.00E+00	3.28E-01	1.00E+00	leukocyte migration	P
GO:0050905	16	9.40E-01	1.00E+00	9.78E-01	1.00E+00	8.53E-01	1.00E+00	6.44E-01	1.00E+00	8.99E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	8.74E-01	1.00E+00	neuromuscular physiological process	P
GO:0050906	17	9.97E-01	1.00E+00	7.84E-01	1.00E+00	9.98E-01	1.00E+00	2.61E-01	1.00E+00	9.88E-01	1.00E+00	8.59E-01	1.00E+00	9.96E-01	1.00E+00	9.93E-01	1.00E+00	detection of stimulus during sensory percep	P
GO:0050909	17	8.30E-01	1.00E+00	9.45E-01	1.00E+00	6.02E-01	1.00E+00	7.35E-01	1.00E+00	9.16E-01	1.00E+00	9.99E-01	1.00E+00	4.90E-01	1.00E+00	2.60E-01	1.00E+00	sensory perception of taste	P
GO:0050918	14	9.96E-01	1.00E+00	9.81E-01	1.00E+00	9.29E-01	1.00E+00	4.50E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	positive chemotaxis	P
GO:0050920	15	9.95E-01	1.00E+00	9.56E-01	1.00E+00	9.33E-01	1.00E+00	3.04E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.37E-01	1.00E+00	regulation of chemotaxis	P

GO:0050921	14	9.98E-01	1.00E+00	9.90E-01	1.00E+00	9.03E-01	1.00E+00	4.38E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	positive regulation of chemotaxis	P
GO:0050926	12	9.94E-01	1.00E+00	9.72E-01	1.00E+00	8.55E-01	1.00E+00	4.13E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	regulation of positive chemotaxis	P
GO:0050927	12	9.94E-01	1.00E+00	9.72E-01	1.00E+00	8.55E-01	1.00E+00	4.13E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	positive regulation of positive chemotaxis	P
GO:0050930	10	9.80E-01	1.00E+00	9.17E-01	1.00E+00	7.63E-01	1.00E+00	3.51E-01	1.00E+00	9.98E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	induction of positive chemotaxis	P
GO:0050931	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	pigment cell differentiation	P
GO:0050953	214	9.79E-01	1.00E+00	9.98E-01	1.00E+00	4.70E-01	1.00E+00	8.93E-01	1.00E+00	9.57E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	sensory perception of light stimulus	P
GO:0050954	146	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of mechanical stimulus	P
GO:0050999	10	4.45E-01	1.00E+00	5.50E-01	1.00E+00	3.48E-01	1.00E+00	6.11E-01	1.00E+00	4.04E-01	1.00E+00	6.42E-01	1.00E+00	7.34E-01	1.00E+00	5.34E-01	1.00E+00	regulation of nitric-oxide synthase activity	P
GO:0051015	39	8.64E-01	1.00E+00	7.25E-01	1.00E+00	4.07E-01	1.00E+00	1.82E-01	1.00E+00	9.14E-01	1.00E+00	9.03E-01	1.00E+00	9.06E-01	1.00E+00	5.77E-01	1.00E+00	actin filament binding	F
GO:0051016	20	2.92E-02	1.00E+00	2.27E-01	1.00E+00	1.53E-02	1.92E-01	1.50E-01	1.00E+00	2.96E-02	6.55E-01	3.39E-01	1.00E+00	8.30E-01	1.00E+00	2.40E-01	1.00E+00	barbed-end actin filament capping	P
GO:0051017	23	7.33E-01	1.00E+00	3.98E-01	1.00E+00	9.80E-02	1.00E+00	1.61E-01	1.00E+00	9.09E-01	1.00E+00	5.86E-01	1.00E+00	9.91E-01	1.00E+00	2.78E-01	1.00E+00	actin filament bundle formation	P
GO:0051020	79	4.56E-01	1.00E+00	3.06E-01	1.00E+00	3.80E-01	1.00E+00	1.16E-01	1.00E+00	4.13E-01	1.00E+00	4.28E-01	1.00E+00	6.48E-01	1.00E+00	4.63E-01	1.00E+00	GTPase binding	F
GO:0051028	80	4.33E-02	1.00E+00	2.28E-04	8.26E-03	1.66E-03	1.60E-02	4.05E-05	3.91E-03	1.88E-01	1.00E+00	5.81E-04	1.02E-02	3.24E-01	1.00E+00	9.68E-02	1.00E+00	mRNA transport	P
GO:0051046	102	9.32E-01	1.00E+00	1.00E+00	1.00E+00	8.54E-01	1.00E+00	9.83E-01	1.00E+00	8.67E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	9.99E-01	1.00E+00	regulation of secretion	P
GO:0051047	38	5.15E-01	1.00E+00	9.03E-01	1.00E+00	6.05E-01	1.00E+00	8.14E-01	1.00E+00	4.66E-01	1.00E+00	9.26E-01	1.00E+00	4.45E-01	1.00E+00	8.65E-01	1.00E+00	positive regulation of secretion	P
GO:0051048	34	7.78E-01	1.00E+00	9.99E-01	1.00E+00	5.38E-01	1.00E+00	9.33E-01	1.00E+00	8.63E-01	1.00E+00	1.00E+00	1.00E+00	6.30E-01	1.00E+00	9.98E-01	1.00E+00	negative regulation of secretion	P
GO:0051049	156	7.14E-01	1.00E+00	8.66E-02	1.00E+00	6.78E-01	1.00E+00	5.13E-02	1.00E+00	4.52E-01	1.00E+00	1.24E-01	1.00E+00	1.00E+00	1.00E+00	7.14E-01	1.00E+00	regulation of transport	P
GO:0051050	63	8.40E-01	1.00E+00	2.84E-01	1.00E+00	7.69E-01	1.00E+00	1.44E-01	1.00E+00	7.47E-01	1.00E+00	3.08E-01	1.00E+00	9.89E-01	1.00E+00	7.39E-01	1.00E+00	positive regulation of transport	P
GO:0051051	44	9.99E-01	1.00E+00	8.08E-01	1.00E+00	9.73E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	5.78E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	negative regulation of transport	P
GO:0051052	73	8.92E-02	1.00E+00	3.36E-02	1.00E+00	5.33E-02	1.00E+00	1.52E-02	2.81E-01	1.14E-01	1.00E+00	9.59E-02	1.00E+00	5.92E-01	1.00E+00	2.02E-01	1.00E+00	regulation of DNA metabolism	P
GO:0051053	23	3.71E-02	1.00E+00	5.95E-02	1.00E+00	2.37E-02	4.97E-01	5.34E-02	1.00E+00	5.38E-02	1.00E+00	1.31E-01	1.00E+00	2.23E-01	1.00E+00	1.44E-01	1.00E+00	negative regulation of DNA metabolism	P
GO:0051054	22	4.98E-01	1.00E+00	4.52E-01	1.00E+00	2.84E-01	1.00E+00	5.45E-01	1.00E+00	5.82E-01	1.00E+00	5.02E-01	1.00E+00	8.40E-01	1.00E+00	3.49E-01	1.00E+00	positive regulation of DNA metabolism	P
GO:0051056	158	9.55E-01	1.00E+00	9.88E-01	1.00E+00	1.71E-01	1.00E+00	3.82E-01	1.00E+00	9.90E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	regulation of small GTPase mediated signa	P
GO:0051057	11	4.27E-01	1.00E+00	4.62E-01	1.00E+00	1.90E-01	1.00E+00	5.46E-01	1.00E+00	5.79E-01	1.00E+00	2.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of small GTPase mediat	P
GO:0051059	39	1.00E+00	1.00E+00	4.00E-01	1.00E+00	5.99E-01	1.00E+00	7.08E-01	1.00E+00	1.00E+00	1.00E+00	3.34E-01	1.00E+00	9.99E-01	1.00E+00	3.95E-01	1.00E+00	NF-kappaB binding	F
GO:0051082	128	1.04E-02	1.77E-01	1.03E-03	2.00E-02	5.94E-03	9.30E-02	3.93E-01	1.00E+00	4.69E-02	1.00E+00	9.74E-05	2.29E-03	4.55E-01	1.00E+00	2.65E-01	1.00E+00	unfolded protein binding	F
GO:0051084	12	4.46E-01	1.00E+00	3.27E-01	1.00E+00	3.16E-01	1.00E+00	3.42E-01	1.00E+00	6.01E-01	1.00E+00	2.23E-01	1.00E+00	2.98E-01	1.00E+00	9.65E-01	1.00E+00	posttranslational protein folding	P
GO:0051087	17	1.19E-01	1.00E+00	3.19E-01	1.00E+00	4.52E-01	1.00E+00	1.73E-01	1.00E+00	1.83E-01	1.00E+00	3.95E-01	1.00E+00	7.03E-02	1.00E+00	4.25E-01	1.00E+00	chaperone binding	F
GO:0051090	61	6.87E-01	1.00E+00	8.80E-02	1.00E+00	2.64E-01	1.00E+00	2.68E-01	1.00E+00	7.28E-01	1.00E+00	7.58E-02	1.00E+00	9.49E-01	1.00E+00	1.56E-01	1.00E+00	regulation of transcription factor activity	P
GO:0051091	38	5.92E-01	1.00E+00	4.15E-01	1.00E+00	2.15E-01	1.00E+00	4.44E-01	1.00E+00	6.98E-01	1.00E+00	3.03E-01	1.00E+00	8.77E-01	1.00E+00	8.64E-01	1.00E+00	positive regulation of transcription factor act	P
GO:0051092	30	3.63E-01	1.00E+00	4.23E-01	1.00E+00	1.04E-01	1.00E+00	3.53E-01	1.00E+00	5.31E-01	1.00E+00	3.45E-01	1.00E+00	7.72E-01	1.00E+00	8.11E-01	1.00E+00	activation of NF-kappaB transcription factor	P
GO:0051093	116	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of development	P
GO:0051094	115	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of development	P
GO:0051098	34	3.58E-01	1.00E+00	4.01E-01	1.00E+00	4.50E-01	1.00E+00	4.97E-01	1.00E+00	4.24E-01	1.00E+00	3.48E-01	1.00E+00	4.44E-01	1.00E+00	7.97E-01	1.00E+00	regulation of binding	P
GO:0051099	10	4.48E-01	1.00E+00	1.00E+00	1.00E+00	6.10E-01	1.00E+00	1.00E+00	1.00E+00	3.36E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	8.99E-01	1.00E+00	positive regulation of binding	P
GO:0051101	16	4.10E-01	1.00E+00	5.81E-01	1.00E+00	4.10E-01	1.00E+00	8.57E-01	1.00E+00	4.44E-01	1.00E+00	5.47E-01	1.00E+00	7.59E-01	1.00E+00	6.14E-01	1.00E+00	regulation of DNA binding	P
GO:0051119	46	3.81E-01	1.00E+00	5.50E-01	1.00E+00	3.91E-01	1.00E+00	1.21E-01	1.00E+00	3.38E-01	1.00E+00	7.06E-01	1.00E+00	8.85E-01	1.00E+00	8.52E-01	1.00E+00	sugar transporter activity	F
GO:0051128	118	7.92E-02	1.00E+00	2.45E-01	1.00E+00	1.65E-02	1.92E-01	2.43E-02	4.10E-01	5.88E-02	1.00E+00	3.55E-01	1.00E+00	9.68E-01	1.00E+00	8.08E-01	1.00E+00	regulation of cell organization and biogenes	P
GO:0051129	51	4.73E-02	1.00E+00	1.42E-01	1.00E+00	2.23E-02	2.63E-01	1.98E-02	4.10E-01	3.88E-02	1.00E+00	3.22E-01	1.00E+00	9.02E-01	1.00E+00	4.67E-01	1.00E+00	negative regulation of cell organization and	P
GO:0051130	27	8.10E-01	1.00E+00	9.92E-01	1.00E+00	2.70E-01	1.00E+00	3.83E-01	1.00E+00	8.99E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.86E-01	1.00E+00	positive regulation of cell organization and b	P
GO:0051145	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	smooth muscle cell differentiation	P
GO:0051146	29	4.08E-01	1.00E+00	9.94E-01	1.00E+00	1.39E-01	1.00E+00	8.10E-01	1.00E+00	4.79E-01	1.00E+00	9.92E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	striated muscle cell differentiation	P
GO:0051168	55	4.18E-02	1.00E+00	1.24E-02	3.84E-01	4.29E-03	3.50E-02	8.32E-03	1.12E-01	1.11E-01	1.00E+00	2.77E-02	1.00E+00	5.97E-01	1.00E+00	2.96E-01	1.00E+00	nuclear export	P
GO:0051169	157	2.24E-02	1.00E+00	4.54E-03	7.00E-02	2.98E-03	3.50E-02	1.09E-03	1.30E-02	4.52E-02	1.00E+00	1.09E-02	2.12E-01	5.41E-01	1.00E+00	3.55E-01	1.00E+00	nuclear transport	P
GO:0051170	106	1.04E-01	1.00E+00	1.83E-02	9.24E-01	7.63E-02	1.00E+00	5.96E-03	8.10E-02	1.06E-01	1.00E+00	3.45E-02	1.00E+00	5.39E-01	1.00E+00	4.72E-01	1.00E+00	nuclear import	P
GO:0051174	125	9.43E-01	1.00E+00	9.98E-01	1.00E+00	2.34E-01	1.00E+00	9.97E-01	1.00E+00	9.87E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	9.73E-01	1.00E+00	regulation of phosphorus metabolism	P
GO:0051179	3508	9.88E-01	1.00E+00	9.96E-01	1.00E+00	3.11E-03	3.50E-02	1.40E-02	2.81E-01	9.97E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	localization	P
GO:0051180	18	4.70E-01	1.00E+00	4.39E-01	1.00E+00	1.15E-01	1.00E+00	7.59E-01	1.00E+00	5.48E-01	1.00E+00	2.34E-01	1.00E+00	9.76E-01	1.00E+00	9.89E-01	1.00E+00	vitamin transport	P
GO:0051181	23	2.96E-01	1.00E+00	2.49E-01	1.00E+00	5.77E-02	1.00E+00	1.95E-01	1.00E+00	6.61E-01	1.00E+00	1.91E-01	1.00E+00	3.98E-01	1.00E+00	9.16E-01	1.00E+00	cofactor transport	P
GO:0051183	10	5.07E-01	1.00E+00	6.57E-01	1.00E+00	2.46E-01	1.00E+00	4.72E-01	1.00E+00	5.87E-01	1.00E+00	5.43E-01	1.00E+00	5.42E-01	1.00E+00	1.00E+00	1.00E+00	vitamin transporter activity	F
GO:0051184	23	6.21E-01	1.00E+00	5.52E-01	1.00E+00	1.32E-01	1.00E+00	1.71E-01	1.00E+00	8.26E-01	1.00E+00	5.74E-01	1.00E+00	6.13E-01	1.00E+00	9.64E-01	1.00E+00	cofactor transporter activity	F
GO:0051186	263	7.30E-03	1.37E-01	1.55E-04	5.53E-03	1.75E-04	4.57E-03	4.18E-03	6.84E-02	7.59E-02	1.00E+00	3.69E-04	1.02E-02	6.89E-01	1.00E+00	3.52E-01	1.00E+00	cofactor metabolism	P
GO:0051187	32	2.89E-01	1.00E+00	8.92E-02	1.00E+00	4.16E-02	5.87E-01	4.79E-01	1.00E+00	4.76E-01	1.00E+00	2.43E-02	7.69E-01	9.07E-01	1.00E+00	8.10E-01	1.00E+00	cofactor catabolism	P
GO:0051188	152	8.68E-02	1.00E+00	1.53E-02	3.84E-01	4.27E-03	3.50E-02	1.34E-01	1.00E+00	3.08E-01	1.00E+00	2.38E-02	7.69E-01	7.81E-01	1.00E+00	1.82E-01	1.00E+00	cofactor biosynthesis	P
GO:0051213	60	1.45E-01	1.00E+00	4.22E-01	1.00E+00	8.97E-02	1.00E+00	4.74E-01	1.00E+00	1.44E-01	1.00E+00	4.16E-01	1.00E+00	9.96E-01	1.00E+00	5.87E-01	1.00E+00	dioxygenase activity	F
GO:0051216	63	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cartilage development	P
GO:0051219	14	3.14E-01	1.00E+00	1.28E-01	1.00E+00	8.82E-02	1.00E+00	8.03E-02	1.00E+00	4.75E-01	1.00E+00	1.52E-01	1.00E+00	6.74E-01	1.00E+00	4.27E-01	1.00E+00	phosphoprotein binding	F
GO:0051220	11	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	9.82E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.68E-01	1.00E+00	cytoplasmic sequestering of protein	P
GO:0051222	23	4.60E-01	1.00E+00	6.44E-02	1.00E+00	4.10E-01	1.00E+00	1.99E-01	1.00E+00	4.82E-01	1.00E+00	4.94E-02	1.00E+00	6.12E-01	1.00E+00	3.99E-01	1.00E+00	positive regulation of protein transport	P
GO:0051223	47	6.47E-01	1.00E+00	7.18E-02	1.00E+00	4.80E-01	1.00E+00	1.89E-01	1.00E+00	6.13E-01	1.00E+00	4.74E-02	1.00E+00	9.33E-01	1.00E+00	5.64E-01	1.00E+00	regulation of protein transport	P
GO:0051224	18	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	negative regulation of protein transport	P
GO:0051234	3451	9.87E-01	1.00E+00	9.95E-01	1.00E+00	3.67E-03	3.50E-02	1.54E-02	2.81E-01	9.97E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	establishment of localization	P
GO:0051235	50	4.08E-01	1.00E+00	8.22E-01	1.00E+00	6.06E-02	1.00E+00	9.56E-01	1.00E+00	5.29E-01	1.00E+00	5.62E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	maintenance of localization	P
GO:0051236	90	2.38E-02	1.00E+00	2.25E-05	2.21E-03	1.60E-03	1.60E-02	8.18E-06	8.32E-04	8.21E-02	1.00E+00	1.44E-04	2.29E-03	4.31E-01	1.00E+00	7.43E-02	1.00E+00	establishment of RNA localization	P
GO:0051238	12	4.05E-01	1.00E+00	3.85E-01	1.00E+00	2.02E-01	1.00E+00	5.31E-01	1.00E+00	4.03E-01	1.00E+00	2.37E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	sequestering of metal ion	P
GO:0051239	335	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of organismal physiological proce	P
GO:0051240	147	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.24E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	positive regulation of organismal physiologi	P
GO:0051241	42	3.55E-01	1.00E+00	9.88E-01	1.00E+00	7.81E-02	1.00E+00	9.66E-01	1.00E+00	4.66E-01	1.00E+00	9.74E-01	1.00E+00	9.70E-01	1.00E+00	9.99E-01	1.00E+00	negative regulation of organismal physiolog	P
GO:0051242	1033	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.24E-01	1.00E+00	4.05E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	positive regulation of cellular physiological p	P
GO:0051243	1135	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.32E-01	1.00E+00	1.70E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of cellular physiological	P
GO:0051244	4026	9.99E-01	1.00E+00	8.90E-03	3.84E-01	2.08E-02	2.36E-01	5.62E-08	0.00E+00	9.99E-01	1.00E+00	1.13E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	regulation of cellular physiological process	P
GO:0051246	388	2.10E-01	1.00E+00	1.90E-01	1.00E+00	5.33E-03	9.30E-02	3.19E-02	5.42E-01	3.09E-01	1.00E+00	1.83E-01	1.00E+00	9.98E-01	1.00E+00	9.44E-01	1.00E+00	regulation of protein metabolism	P
GO:0051247	119	9.86E-01	1.00E+00	9.97E-01	1.00E+00	4.11E-01	1.00E+00	9.71E-01	1.00E+00	9.72E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	positive regulation of protein metabolism	P
GO:0051248	112	2.33E-01	1.00E+00	4.64E-01	1.00E+00	6.71E-02	1.00E+00	1.21E-01	1.00E+00	2.63E-01	1.00E+00	5.97E-01	1.00E+00	8.74E-01	1.00E+00	6.24E-01	1.00E+00	negative regulation of protein metabolism	P
GO:0051249	95	3.71E-01	1.00E+00	9.55E-01	1.00E+00	5.35E-02	1.00E+00	7.49E-01	1.00E+00	5.65E-01	1.00E+00	9.44E-01	1.00E+00	9.31E-01	1.00E+00	9.91E-01	1.00E+00	regulation of lymphocyte activation	P

GO:0051250	31	8.93E-01	1.00E+00	1.00E+00	1.00E+00	4.55E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of lymphocyte activatior	P
GO:0051251	65	3.19E-01	1.00E+00	6.36E-01	1.00E+00	1.32E-01	1.00E+00	4.75E-01	1.00E+00	3.75E-01	1.00E+00	6.65E-01	1.00E+00	9.44E-01	1.00E+00	8.32E-01	1.00E+00	positive regulation of lymphocyte activation	P
GO:0051252	27	6.23E-01	1.00E+00	5.66E-01	1.00E+00	5.27E-01	1.00E+00	2.74E-01	1.00E+00	5.22E-01	1.00E+00	6.66E-01	1.00E+00	9.99E-01	1.00E+00	6.42E-01	1.00E+00	regulation of RNA metabolism	P
GO:0051258	87	4.20E-01	1.00E+00	9.27E-01	1.00E+00	2.63E-02	4.97E-01	3.64E-01	1.00E+00	5.63E-01	1.00E+00	9.77E-01	1.00E+00	8.51E-01	1.00E+00	7.53E-01	1.00E+00	protein polymerization	P
GO:0051259	103	8.12E-01	1.00E+00	5.56E-01	1.00E+00	7.38E-02	1.00E+00	3.20E-01	1.00E+00	9.76E-01	1.00E+00	6.30E-01	1.00E+00	6.64E-01	1.00E+00	8.02E-01	1.00E+00	protein oligomerization	P
GO:0051260	70	9.95E-01	1.00E+00	9.11E-01	1.00E+00	3.91E-01	1.00E+00	8.44E-01	1.00E+00	1.00E+00	1.00E+00	9.05E-01	1.00E+00	8.76E-01	1.00E+00	9.44E-01	1.00E+00	protein homooligomerization	P
GO:0051261	41	5.47E-02	1.00E+00	1.18E-01	1.00E+00	7.76E-03	1.57E-01	3.84E-02	1.00E+00	7.46E-02	1.00E+00	1.90E-01	1.00E+00	9.15E-01	1.00E+00	5.09E-01	1.00E+00	protein depolymerization	P
GO:0051262	24	1.30E-01	1.00E+00	4.45E-01	1.00E+00	3.41E-02	5.87E-01	2.05E-01	1.00E+00	4.00E-01	1.00E+00	5.23E-01	1.00E+00	1.11E-01	1.00E+00	8.48E-01	1.00E+00	protein tetramerization	P
GO:0051270	96	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.62E-01	1.00E+00	6.34E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of cell motility	P
GO:0051271	30	9.64E-01	1.00E+00	9.32E-01	1.00E+00	2.56E-01	1.00E+00	9.47E-01	1.00E+00	9.81E-01	1.00E+00	9.11E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	negative regulation of cell motility	P
GO:0051272	40	9.89E-01	1.00E+00	9.59E-01	1.00E+00	9.81E-01	1.00E+00	3.46E-01	1.00E+00	9.79E-01	1.00E+00	9.46E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of cell motility	P
GO:0051276	392	8.37E-03	1.56E-01	6.66E-06	1.41E-03	5.62E-05	4.57E-03	8.82E-05	3.91E-03	4.12E-02	1.00E+00	8.82E-05	2.29E-03	9.27E-01	1.00E+00	7.12E-02	1.00E+00	chromosome organization and biogenesis	P
GO:0051287	40	1.30E-01	1.00E+00	9.13E-01	1.00E+00	1.65E-01	1.00E+00	7.10E-01	1.00E+00	1.40E-01	1.00E+00	7.96E-01	1.00E+00	4.83E-01	1.00E+00	1.00E+00	1.00E+00	NAD binding	F
GO:0051289	10	7.86E-01	1.00E+00	8.60E-01	1.00E+00	6.24E-01	1.00E+00	5.05E-01	1.00E+00	9.91E-01	1.00E+00	8.43E-01	1.00E+00	1.95E-01	1.00E+00	9.99E-01	1.00E+00	protein homotetramerization	P
GO:0051297	18	1.02E-01	1.00E+00	9.99E-03	3.84E-01	4.95E-02	8.68E-01	3.14E-02	5.42E-01	1.78E-01	1.00E+00	3.24E-02	1.00E+00	4.89E-01	1.00E+00	4.19E-02	8.10E-01	centrosome organization and biogenesis	P
GO:0051301	242	6.42E-03	1.37E-01	8.33E-07	1.00E-03	7.34E-05	4.57E-03	6.29E-06	8.32E-04	1.46E-01	1.00E+00	7.89E-05	2.29E-03	2.53E-01	1.00E+00	5.28E-03	6.60E-02	cell division	P
GO:0051318	18	1.74E-01	1.00E+00	2.24E-01	1.00E+00	1.99E-02	2.36E-01	1.03E-01	1.00E+00	2.85E-01	1.00E+00	3.47E-01	1.00E+00	5.12E-01	1.00E+00	3.86E-01	1.00E+00	G1 phase	P
GO:0051320	15	3.73E-01	1.00E+00	3.20E-01	1.00E+00	5.03E-01	1.00E+00	5.80E-01	1.00E+00	5.11E-01	1.00E+00	3.07E-01	1.00E+00	1.58E-01	1.00E+00	2.13E-01	1.00E+00	S phase	P
GO:0051321	88	3.44E-01	1.00E+00	2.13E-03	5.10E-02	3.21E-01	1.00E+00	3.80E-02	1.00E+00	4.21E-01	1.00E+00	7.55E-03	1.05E-01	4.86E-01	1.00E+00	4.51E-02	8.10E-01	meiotic cell cycle	P
GO:0051324	11	2.22E-01	1.00E+00	1.53E-01	1.00E+00	8.23E-01	1.00E+00	2.79E-01	1.00E+00	1.03E-01	1.00E+00	1.98E-01	1.00E+00	5.05E-01	1.00E+00	1.75E-01	1.00E+00	prophase	P
GO:0051325	100	4.31E-02	1.00E+00	4.63E-02	1.00E+00	5.86E-03	9.30E-02	8.94E-03	1.12E-01	7.56E-02	1.00E+00	1.80E-01	1.00E+00	4.52E-01	1.00E+00	2.18E-01	1.00E+00	interphase	P
GO:0051327	86	3.83E-01	1.00E+00	2.72E-03	5.10E-02	4.87E-01	1.00E+00	5.03E-02	1.00E+00	4.30E-01	1.00E+00	9.42E-03	1.43E-01	4.33E-01	1.00E+00	3.99E-02	8.10E-01	M phase of meiotic cell cycle	P
GO:0051329	98	3.66E-02	1.00E+00	3.40E-02	1.00E+00	5.36E-03	9.30E-02	6.67E-03	8.10E-02	6.88E-02	1.00E+00	1.52E-01	1.00E+00	4.09E-01	1.00E+00	1.79E-01	1.00E+00	interphase of mitotic cell cycle	P
GO:0051336	212	2.00E-01	1.00E+00	3.95E-01	1.00E+00	3.80E-01	1.00E+00	5.55E-02	1.00E+00	2.13E-01	1.00E+00	6.10E-01	1.00E+00	3.71E-01	1.00E+00	5.87E-01	1.00E+00	regulation of hydrolase activity	P
GO:0051338	256	9.92E-01	1.00E+00	9.86E-01	1.00E+00	9.05E-01	1.00E+00	4.06E-01	1.00E+00	9.76E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	regulation of transferase activity	P
GO:0051339	44	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.98E-01	1.00E+00	5.75E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	regulation of lyase activity	P
GO:0051340	82	6.82E-02	1.00E+00	2.51E-02	1.00E+00	1.22E-01	1.00E+00	1.76E-03	2.70E-02	9.14E-02	1.00E+00	1.07E-01	1.00E+00	3.60E-01	1.00E+00	2.80E-01	1.00E+00	regulation of ligase activity	P
GO:0051341	15	7.06E-02	1.00E+00	1.02E-01	1.00E+00	1.02E-01	1.00E+00	1.37E-01	1.00E+00	7.09E-02	1.00E+00	1.72E-01	1.00E+00	3.31E-01	1.00E+00	3.64E-01	1.00E+00	regulation of oxidoreductase activity	P
GO:0051345	64	8.23E-02	1.00E+00	4.45E-02	1.00E+00	7.10E-01	1.00E+00	1.47E-02	2.81E-01	4.15E-02	1.00E+00	1.11E-01	1.00E+00	3.20E-01	1.00E+00	9.27E-02	1.00E+00	positive regulation of hydrolase activity	P
GO:0051346	10	5.17E-01	1.00E+00	8.40E-01	1.00E+00	3.61E-01	1.00E+00	5.10E-01	1.00E+00	4.27E-01	1.00E+00	7.89E-01	1.00E+00	1.00E+00	1.00E+00	9.44E-01	1.00E+00	negative regulation of hydrolase activity	P
GO:0051347	157	9.87E-01	1.00E+00	9.91E-01	1.00E+00	9.99E-01	1.00E+00	6.78E-01	1.00E+00	9.28E-01	1.00E+00	9.91E-01	1.00E+00	9.32E-01	1.00E+00	9.93E-01	1.00E+00	positive regulation of transferase activity	P
GO:0051348	64	9.84E-01	1.00E+00	9.63E-01	1.00E+00	4.19E-01	1.00E+00	7.07E-01	1.00E+00	9.72E-01	1.00E+00	9.53E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	negative regulation of transferase activity	P
GO:0051349	25	9.64E-01	1.00E+00	8.96E-01	1.00E+00	9.29E-01	1.00E+00	3.09E-01	1.00E+00	9.61E-01	1.00E+00	9.91E-01	1.00E+00	6.28E-01	1.00E+00	9.68E-01	1.00E+00	positive regulation of lyase activity	P
GO:0051350	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of lyase activity	P
GO:0051351	76	5.63E-02	1.00E+00	2.50E-02	1.00E+00	1.50E-01	1.00E+00	1.11E-03	1.30E-02	7.64E-02	1.00E+00	1.01E-01	1.00E+00	3.34E-01	1.00E+00	3.65E-01	1.00E+00	positive regulation of ligase activity	P
GO:0051352	70	7.12E-02	1.00E+00	7.52E-02	1.00E+00	1.96E-01	1.00E+00	7.95E-03	8.10E-02	6.90E-02	1.00E+00	1.61E-01	1.00E+00	4.55E-01	1.00E+00	4.70E-01	1.00E+00	negative regulation of ligase activity	P
GO:0051384	23	9.12E-01	1.00E+00	8.27E-01	1.00E+00	3.55E-01	1.00E+00	2.70E-01	1.00E+00	9.36E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	response to glucocorticoid stimulus	P
GO:0051402	59	7.78E-01	1.00E+00	4.99E-01	1.00E+00	6.94E-01	1.00E+00	6.89E-01	1.00E+00	8.17E-01	1.00E+00	4.12E-01	1.00E+00	6.70E-01	1.00E+00	7.00E-01	1.00E+00	neuron apoptosis	P
GO:0051427	77	8.50E-01	1.00E+00	1.96E-01	1.00E+00	2.48E-01	1.00E+00	1.68E-02	4.10E-01	8.89E-01	1.00E+00	2.74E-01	1.00E+00	9.98E-01	1.00E+00	9.71E-01	1.00E+00	hormone receptor binding	F
GO:0051436	69	6.03E-02	1.00E+00	6.76E-02	1.00E+00	1.70E-01	1.00E+00	7.24E-03	8.10E-02	6.33E-02	1.00E+00	1.46E-01	1.00E+00	4.31E-01	1.00E+00	4.69E-01	1.00E+00	negative regulation of ubiquitin ligase activit	P
GO:0051437	72	5.66E-02	1.00E+00	2.04E-02	9.24E-01	1.76E-01	1.00E+00	1.25E-03	1.30E-02	6.65E-02	1.00E+00	8.50E-02	1.00E+00	3.46E-01	1.00E+00	3.08E-01	1.00E+00	positive regulation of ubiquitin ligase activity	P
GO:0051438	79	6.82E-02	1.00E+00	1.79E-02	9.24E-01	1.29E-01	1.00E+00	1.54E-03	1.80E-02	9.03E-02	1.00E+00	8.15E-02	1.00E+00	3.56E-01	1.00E+00	2.50E-01	1.00E+00	regulation of ubiquitin ligase activity	P
GO:0051439	75	8.61E-02	1.00E+00	2.37E-02	1.00E+00	1.98E-01	1.00E+00	1.52E-03	1.80E-02	9.74E-02	1.00E+00	9.23E-02	1.00E+00	3.90E-01	1.00E+00	3.24E-01	1.00E+00	regulation of ubiquitin ligase activity during	P
GO:0051443	73	5.61E-02	1.00E+00	1.77E-02	9.24E-01	1.58E-01	1.00E+00	9.55E-04	1.11E-02	7.52E-02	1.00E+00	7.65E-02	1.00E+00	3.30E-01	1.00E+00	3.30E-01	1.00E+00	positive regulation of ubiquitin ligase activity	P
GO:0051444	70	7.12E-02	1.00E+00	7.52E-02	1.00E+00	1.96E-01	1.00E+00	7.95E-03	8.10E-02	6.90E-02	1.00E+00	1.61E-01	1.00E+00	4.55E-01	1.00E+00	4.70E-01	1.00E+00	negative regulation of ubiquitin ligase activit	P
GO:0051480	73	5.51E-01	1.00E+00	9.49E-01	1.00E+00	4.14E-01	1.00E+00	6.07E-01	1.00E+00	4.97E-01	1.00E+00	8.87E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	cytosolic calcium ion homeostasis	P
GO:0051493	13	4.00E-01	1.00E+00	9.32E-01	1.00E+00	1.23E-01	1.00E+00	5.57E-01	1.00E+00	4.87E-01	1.00E+00	9.05E-01	1.00E+00	6.88E-01	1.00E+00	1.00E+00	1.00E+00	regulation of cytoskeleton organization and	P
GO:0051536	51	9.51E-02	1.00E+00	4.33E-01	1.00E+00	6.71E-02	1.00E+00	1.36E-01	1.00E+00	1.65E-01	1.00E+00	3.91E-01	1.00E+00	3.26E-01	1.00E+00	9.99E-01	1.00E+00	iron-sulfur cluster binding	F
GO:0051537	14	1.43E-01	1.00E+00	4.21E-01	1.00E+00	2.33E-01	1.00E+00	2.35E-01	1.00E+00	1.36E-01	1.00E+00	4.49E-01	1.00E+00	2.45E-01	1.00E+00	9.14E-01	1.00E+00	2 iron, 2 sulfur cluster binding	F
GO:0051539	21	1.25E-02	2.72E-01	1.22E-01	1.00E+00	1.78E-02	2.36E-01	8.14E-02	1.00E+00	3.79E-02	1.00E+00	1.30E-01	1.00E+00	6.18E-01	1.00E+00	7.41E-01	1.00E+00	4 iron, 4 sulfur cluster binding	F
GO:0051540	51	9.51E-02	1.00E+00	4.33E-01	1.00E+00	6.71E-02	1.00E+00	1.36E-01	1.00E+00	1.65E-01	1.00E+00	3.91E-01	1.00E+00	3.26E-01	1.00E+00	9.99E-01	1.00E+00	metal cluster binding	F
GO:0051591	13	5.93E-01	1.00E+00	9.23E-01	1.00E+00	3.76E-01	1.00E+00	8.90E-01	1.00E+00	5.29E-01	1.00E+00	9.54E-01	1.00E+00	9.56E-01	1.00E+00	5.31E-01	1.00E+00	response to cAMP	P
GO:0051592	15	9.98E-01	1.00E+00	9.21E-01	1.00E+00	9.89E-01	1.00E+00	9.64E-01	1.00E+00	9.93E-01	1.00E+00	6.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to calcium ion	P
GO:0051603	243	2.32E-02	1.00E+00	2.67E-04	8.26E-03	2.98E-02	5.65E-01	4.59E-07	0.00E+00	1.45E-01	1.00E+00	6.38E-03	1.05E-01	8.21E-01	1.00E+00	1.18E-01	1.00E+00	proteolysis during cellular protein catabolisr	P
GO:0051604	12	9.04E-01	1.00E+00	1.00E+00	1.00E+00	8.06E-01	1.00E+00	9.22E-01	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	protein maturation	P
GO:0051605	11	8.45E-01	1.00E+00	1.00E+00	1.00E+00	7.44E-01	1.00E+00	8.71E-01	1.00E+00	8.16E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.96E-01	1.00E+00	proteolysis during protein maturation	P
GO:0051606	87	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.89E-01	1.00E+00	7.18E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	detection of stimulus	P
GO:0051607	23	6.89E-01	1.00E+00	8.90E-01	1.00E+00	7.09E-01	1.00E+00	9.93E-01	1.00E+00	5.07E-01	1.00E+00	6.57E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	defense response to virus	P
GO:0051640	35	2.21E-02	1.00E+00	2.26E-02	9.24E-01	4.11E-02	5.87E-01	1.80E-02	4.10E-01	5.86E-02	1.00E+00	3.27E-02	1.00E+00	2.83E-02	2.56E-01	4.19E-01	1.00E+00	organelle localization	P
GO:0051641	876	1.53E-04	1.10E-02	2.41E-06	1.41E-03	4.56E-11	0.00E+00	1.27E-06	0.00E+00	1.38E-02	3.01E-01	1.19E-03	1.02E-02	7.87E-01	1.00E+00	3.14E-01	1.00E+00	cellular localization	P
GO:0051649	855	6.40E-05	5.00E-03	1.46E-06	1.00E-03	4.60E-11	0.00E+00	1.15E-06	0.00E+00	6.30E-03	1.48E-01	8.83E-04	1.02E-02	7.65E-01	1.00E+00	2.71E-01	1.00E+00	establishment of cellular localization	P
GO:0051656	24	6.30E-03	1.37E-01	3.18E-03	6.30E-02	5.26E-02	1.00E+00	4.15E-03	6.84E-02	9.83E-03	2.02E-01	3.11E-03	6.40E-02	1.14E-02	2.07E-01	4.21E-01	1.00E+00	establishment of organelle localization	P
GO:0051668	14	7.93E-01	1.00E+00	3.86E-01	1.00E+00	3.84E-01	1.00E+00	6.38E-01	1.00E+00	9.44E-01	1.00E+00	2.81E-01	1.00E+00	4.78E-01	1.00E+00	9.76E-01	1.00E+00	localization within membrane	P
GO:0051674	497	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	localization of cell	P
GO:0051693	20	2.92E-02	1.00E+00	2.27E-01	1.00E+00	1.53E-02	1.92E-01	1.50E-01	1.00E+00	2.96E-02	6.55E-01	3.39E-01	1.00E+00	8.30E-01	1.00E+00	2.40E-01	1.00E+00	actin filament capping	P
GO:0051701	23	7.88E-01	1.00E+00	7.92E-01	1.00E+00	5.53E-01	1.00E+00	8.23E-01	1.00E+00	6.33E-01	1.00E+00	7.11E-01	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	interaction with host	P
GO:0051704	370	9.25E-01	1.00E+00	7.13E-01	1.00E+00	1.04E-01	1.00E+00	3.45E-01	1.00E+00	9.90E-01	1.00E+00	7.86E-01	1.00E+00	9.12E-01	1.00E+00	8.52E-01	1.00E+00	interaction between organisms	P
GO:0051705	28	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	behavioral interaction between organisms	P
GO:0051706	80	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.97E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.93E-01	1.00E+00	1.00E+00	1.00E+00	physiological interaction between organisms	P
GO:0051707	223	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.77E-01	1.00E+00	7.91E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	response to other organism	P
GO:0051716	20	2.11E-01	1.00E+00	3.81E-01	1.00E+00	1.11E-01	1.00E+00	2.23E-01	1.00E+00	4.03E-01	1.00E+00	6.73E-01	1.00E+00	3.09E-01	1.00E+00	1.27E-01	1.00E+00	cellular response to stimulus	P
GO:0051726	378	2.54E-01	1.00E+00	3.12E-01	1.00E+00	2.60E-03	1.80E-02	1.18E-02	1.27E-01	4.70E-01	1.00E+00	7.28E-01	1.00E+00	9.72E-01	1.00E+00	5.29E-01	1.00E+00	regulation of cell cycle	P
GO:0051789	86	8.99E-01	1.00E+00	5.55E-01	1.00E+00	4.38E-01	1.00E+00	7.30E-01	1.00E+00	9.62E-01	1.00E+00	4.05E-01	1.00E+00	9.16E-01	1.00E+00	7.32E-01	1.00E+00	response to protein stimulus	P
GO:0051806	10	7.82E-01	1.00E+00	8.27E-01	1.00E+00	7.34E-01	1.00E+00	6.61E-01	1.00E+00	4.94E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	6.05E-01	1.00E+00	entry into cell of other organism during sym	P
GO:0051828	10	7.82E-01	1.00E+00	8.27E-01	1.00E+00	7.34E-01	1.00E+00	6.61E-01	1.00E+00	4.94E-01	1.00E+00	8.85E-01	1.00E+00	1.00E+00	1.00E+00	6.05E-01	1.00E+00	entry into other organism during symbiotic i	P

GO:0051869	1674	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	physiological response to stimulus	P
GO:0051881	11	1.15E-01	1.00E+00	9.44E-02	1.00E+00	2.37E-01	1.00E+00	6.79E-02	1.00E+00	2.49E-01	1.00E+00	3.25E-01	1.00E+00	1.36E-01	1.00E+00	9.08E-02	1.00E+00	regulation of mitochondrial membrane potei	P
GO:0051899	14	8.43E-02	1.00E+00	5.80E-01	1.00E+00	1.62E-02	1.92E-01	3.72E-01	1.00E+00	2.05E-01	1.00E+00	5.06E-01	1.00E+00	5.29E-01	1.00E+00	9.73E-01	1.00E+00	membrane depolarization	P
GO:0051924	20	9.52E-01	1.00E+00	6.55E-01	1.00E+00	7.92E-01	1.00E+00	2.28E-01	1.00E+00	8.83E-01	1.00E+00	8.95E-01	1.00E+00	9.44E-01	1.00E+00	8.31E-01	1.00E+00	regulation of calcium ion transport	P
GO:0051969	67	9.99E-01	1.00E+00	9.48E-01	1.00E+00	8.09E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.56E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	regulation of transmission of nerve impulse	P
GO:0051970	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of transmission of nerve	P
GO:0051971	22	9.99E-01	1.00E+00	8.13E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	4.88E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	positive regulation of transmission of nerve	P
GO:0055001	17	3.12E-01	1.00E+00	1.00E+00	1.00E+00	1.57E-01	1.00E+00	9.98E-01	1.00E+00	3.38E-01	1.00E+00	1.00E+00	1.00E+00	7.17E-01	1.00E+00	1.00E+00	1.00E+00	muscle cell development	P
GO:0055002	16	2.87E-01	1.00E+00	1.00E+00	1.00E+00	1.46E-01	1.00E+00	9.96E-01	1.00E+00	3.19E-01	1.00E+00	9.99E-01	1.00E+00	6.78E-01	1.00E+00	1.00E+00	1.00E+00	striated muscle cell development	P
GO:0055008	16	9.97E-01	1.00E+00	1.00E+00	1.00E+00	6.79E-01	1.00E+00	8.10E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cardiac muscle morphogensis	P
GO:0055010	14	9.84E-01	1.00E+00	1.00E+00	1.00E+00	5.29E-01	1.00E+00	7.82E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ventricular cardiac muscle morphogenesis	P

		B+		B-		B1+		B1-		B2+		B2-		B4+		B4-			
GO term id	genes	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	GO term description	GO term catecory
GO:0000003	462	2.75E-03	2.12E-01	9.80E-03	4.69E-01	7.54E-03	6.41E-01	9.90E-02	1.00E+00	3.49E-02	1.00E+00	2.20E-02	1.00E+00	1.24E-02	4.24E-01	1.87E-02	7.36E-01	reproduction	P
GO:0000030	13	1.79E-01	1.00E+00	1.10E-01	1.00E+00	1.27E-01	1.00E+00	4.66E-02	1.00E+00	5.66E-01	1.00E+00	1.70E-01	1.00E+00	2.56E-01	1.00E+00	3.67E-01	1.00E+00	mannosyltransferase activity	F
GO:0000041	75	2.59E-01	1.00E+00	1.03E-01	1.00E+00	2.44E-01	1.00E+00	1.41E-01	1.00E+00	3.88E-01	1.00E+00	1.01E-01	1.00E+00	5.36E-01	1.00E+00	6.47E-01	1.00E+00	transition metal ion transport	P
GO:0000045	14	5.34E-02	1.00E+00	3.89E-02	1.00E+00	6.95E-02	1.00E+00	1.05E-01	1.00E+00	3.41E-02	1.00E+00	1.11E-01	1.00E+00	5.69E-01	1.00E+00	4.12E-02	1.00E+00	autophagic vacuole formation	P
GO:0000049	21	2.84E-02	1.00E+00	4.94E-02	1.00E+00	2.56E-02	1.00E+00	7.36E-02	1.00E+00	2.81E-02	1.00E+00	1.14E-01	1.00E+00	1.03E-01	1.00E+00	1.92E-01	1.00E+00	tRNA binding	F
GO:0000051	16	4.30E-03	2.14E-01	2.75E-01	1.00E+00	1.43E-01	1.00E+00	7.30E-01	1.00E+00	5.65E-02	1.00E+00	4.03E-01	1.00E+00	4.14E-04	2.40E-02	5.86E-02	1.00E+00	urea cycle intermediate metabolism	P
GO:0000059	15	5.71E-04	8.86E-02	2.68E-04	4.40E-02	7.28E-04	4.90E-02	1.06E-04	1.30E-02	3.27E-02	1.00E+00	2.34E-02	1.00E+00	1.10E-01	1.00E+00	4.04E-03	2.01E-01	protein import into nucleus, docking	P
GO:0000060	22	8.42E-02	1.00E+00	6.75E-02	1.00E+00	6.21E-02	1.00E+00	2.00E-01	1.00E+00	1.94E-01	1.00E+00	3.48E-01	1.00E+00	1.98E-01	1.00E+00	6.00E-02	1.00E+00	protein import into nucleus, translocation	P
GO:0000062	12	1.05E-01	1.00E+00	2.55E-02	1.00E+00	2.88E-01	1.00E+00	3.14E-01	1.00E+00	1.26E-01	1.00E+00	3.28E-01	1.00E+00	2.14E-01	1.00E+00	1.43E-02	4.76E-01	acyl-CoA binding	F
GO:0000070	23	3.81E-02	1.00E+00	4.06E-06	4.51E-03	1.09E-02	6.53E-01	1.17E-09	0.00E+00	1.73E-01	1.00E+00	8.15E-03	4.21E-01	1.74E-01	1.00E+00	3.06E-02	9.99E-01	mitotic sister chromatid segregation	P
GO:0000074	255	1.72E-07	2.57E-03	3.20E-10	0.00E+00	8.18E-07	2.00E-03	2.54E-08	8.93E-04	6.84E-04	1.20E-01	1.30E-07	1.65E-03	5.03E-05	8.00E-03	6.47E-05	7.00E-03	regulation of progression through cell cycle	P
GO:0000075	44	7.96E-06	3.62E-03	1.22E-07	3.92E-03	9.30E-05	1.16E-02	9.01E-06	2.89E-03	3.73E-04	4.90E-02	1.30E-03	9.00E-02	2.03E-03	8.40E-02	3.81E-04	3.00E-02	cell cycle checkpoint	P
GO:0000077	24	3.90E-03	2.12E-01	3.59E-05	7.00E-03	2.21E-02	1.00E+00	1.30E-03	9.40E-02	1.97E-02	7.90E-01	2.21E-02	1.00E+00	3.98E-02	1.00E+00	5.64E-04	3.00E-02	DNA damage checkpoint	P
GO:0000079	22	9.41E-04	8.86E-02	9.73E-05	1.50E-02	1.63E-04	1.16E-02	6.51E-05	1.30E-02	1.94E-02	7.90E-01	4.48E-04	2.33E-02	8.44E-02	1.00E+00	6.07E-03	4.28E-01	regulation of cyclin-dependent protein kinas	P
GO:0000082	36	5.46E-01	1.00E+00	3.47E-01	1.00E+00	5.38E-01	1.00E+00	3.70E-01	1.00E+00	6.19E-01	1.00E+00	1.38E-01	1.00E+00	4.56E-01	1.00E+00	7.48E-01	1.00E+00	G1/S transition of mitotic cell cycle	P
GO:0000084	14	6.20E-02	1.00E+00	6.90E-03	3.12E-01	6.39E-02	1.00E+00	2.73E-02	1.00E+00	1.59E-01	1.00E+00	8.15E-03	4.21E-01	5.57E-01	1.00E+00	3.09E-01	1.00E+00	S phase of mitotic cell cycle	P
GO:0000086	10	2.37E-02	1.00E+00	6.14E-03	3.08E-01	9.37E-02	1.00E+00	1.69E-02	6.47E-01	1.84E-02	7.90E-01	1.81E-02	6.68E-01	5.73E-02	1.00E+00	1.55E-02	6.56E-01	G2/M transition of mitotic cell cycle	P
GO:0000087	198	6.56E-16	0.00E+00	3.94E-17	0.00E+00	3.47E-16	0.00E+00	4.32E-18	0.00E+00	1.33E-09	0.00E+00	1.57E-09	8.78E-04	2.95E-05	4.00E-03	6.38E-05	7.00E-03	M phase of mitotic cell cycle	P
GO:0000096	21	3.71E-02	1.00E+00	1.23E-02	6.07E-01	3.94E-02	1.00E+00	1.63E-02	6.47E-01	4.20E-01	1.00E+00	9.39E-03	5.03E-01	5.53E-02	1.00E+00	4.01E-01	1.00E+00	sulfur amino acid metabolism	P
GO:0000097	12	6.01E-03	3.09E-01	1.35E-02	6.07E-01	1.07E-02	6.53E-01	5.32E-03	2.88E-01	1.07E-01	1.00E+00	1.78E-02	6.68E-01	5.57E-02	1.00E+00	8.51E-01	1.00E+00	sulfur amino acid biosynthesis	P
GO:0000118	28	1.32E-02	6.08E-01	2.05E-04	2.40E-02	9.63E-03	6.53E-01	4.01E-04	4.20E-02	7.59E-02	1.00E+00	6.25E-03	4.21E-01	1.32E-01	1.00E+00	4.20E-03	2.01E-01	histone deacetylase complex	C
GO:0000119	23	2.40E-03	2.12E-01	4.81E-04	4.74E-02	2.17E-06	2.00E-03	2.39E-03	1.39E-01	1.39E-01	1.00E+00	5.41E-03	3.43E-01	3.44E-01	1.00E+00	1.04E-01	1.00E+00	mediator complex	C
GO:0000122	192	1.88E-04	1.72E-02	1.20E-03	9.65E-02	2.38E-05	3.00E-03	3.65E-03	2.57E-01	4.80E-02	1.00E+00	5.09E-02	1.00E+00	2.22E-03	8.40E-02	2.25E-03	7.90E-02	negative regulation of transcription from RN	P
GO:0000123	11	2.69E-02	1.00E+00	8.24E-05	1.50E-02	3.35E-02	1.00E+00	2.15E-04	1.30E-02	5.61E-02	1.00E+00	6.90E-04	4.48E-02	1.35E-01	1.00E+00	1.36E-02	4.76E-01	histone acetyltransferase complex	C
GO:0000139	315	9.45E-05	1.43E-02	1.99E-06	3.92E-03	8.79E-04	4.90E-02	1.77E-04	1.30E-02	4.47E-04	4.90E-02	5.45E-04	3.20E-02	3.60E-02	8.38E-01	1.80E-04	1.60E-02	Golgi membrane	C
GO:0000149	30	1.32E-01	1.00E+00	5.52E-01	1.00E+00	7.68E-01	1.00E+00	6.04E-01	1.00E+00	1.85E-01	1.00E+00	7.28E-01	1.00E+00	2.61E-02	8.38E-01	2.61E-01	1.00E+00	SNARE binding	F
GO:0000151	86	2.28E-05	7.00E-03	2.21E-07	3.92E-03	6.10E-07	2.00E-03	2.18E-06	2.89E-03	2.50E-02	1.00E+00	7.98E-06	5.87E-03	8.61E-03	2.75E-01	1.29E-02	4.76E-01	ubiquitin ligase complex	C
GO:0000152	11	2.00E-02	1.00E+00	3.41E-03	1.88E-01	4.60E-03	3.08E-01	1.07E-02	5.72E-01	3.80E-01	1.00E+00	1.38E-02	6.68E-01	1.49E-02	4.78E-01	7.14E-02	1.00E+00	nuclear ubiquitin ligase complex	C
GO:0000155	30	6.50E-01	1.00E+00	5.25E-01	1.00E+00	8.19E-01	1.00E+00	5.37E-01	1.00E+00	4.53E-01	1.00E+00	6.59E-01	1.00E+00	6.76E-01	1.00E+00	1.93E-01	1.00E+00	two-component sensor activity	F
GO:0000159	22	1.48E-01	1.00E+00	1.24E-01	1.00E+00	1.46E-01	1.00E+00	5.93E-01	1.00E+00	2.33E-01	1.00E+00	1.32E-01	1.00E+00	1.83E-01	1.00E+00	6.55E-02	1.00E+00	protein phosphatase type 2A complex	C
GO:0000160	32	5.97E-01	1.00E+00	6.04E-01	1.00E+00	8.93E-01	1.00E+00	8.49E-01	1.00E+00	4.69E-01	1.00E+00	6.89E-01	1.00E+00	3.45E-01	1.00E+00	2.13E-01	1.00E+00	two-component signal transduction system	P
GO:0000165	151	3.49E-02	1.00E+00	6.01E-04	5.90E-02	2.35E-01	1.00E+00	5.48E-02	1.00E+00	4.63E-02	1.00E+00	6.15E-03	4.21E-01	9.18E-02	1.00E+00	1.33E-04	1.60E-02	MAPKKK cascade	P
GO:0000166	2281	3.55E-39	0.00E+00	0.00E+00	0.00E+00	7.58E-39	0.00E+00	5.61E-45	0.00E+00	2.14E-23	0.00E+00	4.70E-37	0.00E+00	2.96E-10	0.00E+00	7.91E-23	0.00E+00	nucleotide binding	F
GO:0000175	10	1.22E-01	1.00E+00	1.00E-01	1.00E+00	6.60E-02	1.00E+00	1.73E-01	1.00E+00	2.45E-01	1.00E+00	1.15E-01	1.00E+00	6.83E-01	1.00E+00	1.14E-01	1.00E+00	3'-5'-exoribonuclease activity	F
GO:0000178	12	1.09E-03	8.86E-02	2.96E-01	1.00E+00	4.89E-04	4.90E-02	1.96E-01	1.00E+00	3.35E-03	2.13E-01	3.37E-01	1.00E+00	8.74E-02	1.00E+00	5.94E-01	1.00E+00	exosome (RNase complex)	C
GO:0000184	16	4.27E-05	9.52E-03	3.05E-03	1.88E-01	4.16E-05	9.82E-03	5.44E-03	2.88E-01	1.54E-03	1.20E-01	2.24E-04	2.33E-02	9.72E-03	2.75E-01	1.28E-01	1.00E+00	mRNA catabolism, nonsense-mediated dec	P
GO:0000186	16	8.18E-01	1.00E+00	1.76E-01	1.00E+00	4.54E-01	1.00E+00	4.83E-01	1.00E+00	8.52E-01	1.00E+00	3.70E-01	1.00E+00	9.09E-01	1.00E+00	2.53E-02	9.99E-01	activation of MAPKK activity	P
GO:0000187	52	1.68E-02	1.00E+00	1.19E-01	1.00E+00	1.05E-01	1.00E+00	3.88E-01	1.00E+00	2.89E-02	1.00E+00	5.57E-02	1.00E+00	5.17E-02	1.00E+00	1.15E-01	1.00E+00	activation of MAPK activity	P
GO:0000209	17	9.50E-03	6.08E-01	1.26E-02	6.07E-01	2.50E-02	1.00E+00	2.87E-02	1.00E+00	1.25E-01	1.00E+00	3.13E-02	1.00E+00	4.85E-02	1.00E+00	5.93E-02	1.00E+00	protein polyubiquitination	P
GO:0000226	90	5.30E-05	9.52E-03	1.50E-05	4.51E-03	2.28E-05	3.00E-03	1.27E-03	9.40E-02	1.55E-03	1.20E-01	2.32E-04	2.33E-02	4.29E-03	2.23E-01	1.52E-03	6.00E-02	microtubule cytoskeleton organization and b	P
GO:0000228	109	5.69E-09	2.57E-03	6.60E-09	8.90E-04	1.57E-09	9.80E-04	6.62E-09	8.93E-04	1.15E-05	3.00E-03	1.93E-05	5.87E-03	2.47E-03	8.40E-02	1.14E-02	4.76E-01	nuclear chromosome	C
GO:0000245	20	1.10E-02	6.08E-01	3.94E-02	1.00E+00	4.19E-02	1.00E+00	3.77E-02	1.00E+00	4.73E-02	1.00E+00	3.36E-01	1.00E+00	5.20E-03	2.23E-01	4.56E-02	1.00E+00	spliceosome assembly	P
GO:0000267	600	6.34E-03	3.09E-01	2.11E-06	3.92E-03	1.32E-02	6.53E-01	9.79E-05	1.30E-02	1.89E-02	7.90E-01	1.61E-04	2.33E-02	7.20E-02	1.00E+00	6.96E-05	7.00E-03	cell fraction	C
GO:0000271	42	6.00E-01	1.00E+00	2.30E-02	1.00E+00	8.34E-01	1.00E+00	1.69E-01	1.00E+00	2.75E-01	1.00E+00	2.39E-02	1.00E+00	6.75E-01	1.00E+00	1.88E-02	7.36E-01	polysaccharide biosynthesis	P
GO:0000272	15	3.76E-01	1.00E+00	9.12E-01	1.00E+00	6.16E-01	1.00E+00	7.56E-01	1.00E+00	9.50E-02	1.00E+00	9.65E-01	1.00E+00	6.39E-01	1.00E+00	8.45E-01	1.00E+00	polysaccharide catabolism	P
GO:0000278	281	1.01E-12	0.00E+00	5.03E-13	0.00E+00	7.03E-13	7.08E-04	1.50E-13	0.00E+00	6.72E-07	1.69E-03	9.65E-09	8.78E-04	2.41E-05	4.00E-03	2.17E-03	7.90E-02	mitotic cell cycle	P
GO:0000279	268	8.86E-18	0.00E+00	6.68E-22	0.00E+00	1.58E-18	0.00E+00	2.50E-21	0.00E+00	7.51E-10	0.00E+00	4.87E-12	6.20E-04	6.32E-06	1.00E-03	4.97E-06	2.91E-03	M phase	P
GO:0000287	389	5.03E-06	3.62E-03	2.79E-10	0.00E+00	8.05E-06	2.91E-03	1.05E-06	2.89E-03	3.05E-03	2.13E-01	4.40E-08	9.03E-04	4.63E-03	2.23E-01	8.99E-06	7.00E-03	magnesium ion binding	F
GO:0000299	15	1.63E-02	1.00E+00	1.10E-02	4.69E-01	9.78E-03	6.53E-01	2.66E-02	1.00E+00	4.73E-02	1.00E+00	9.57E-03	5.03E-01	4.71E-01	1.00E+00	1.43E-01	1.00E+00	integral to membrane of membrane fraction	C
GO:0000302	31	8.69E-04	8.86E-02	7.63E-04	8.10E-02	5.12E-03	3.08E-01	4.01E-03	2.88E-01	1.84E-02	7.90E-01	1.62E-04	2.33E-02	2.71E-03	8.40E-02	5.29E-02	1.00E+00	response to reactive oxygen species	P
GO:0000313	46	1.34E-04	1.43E-02	9.54E-03	4.69E-01	5.17E-05	9.82E-03	8.81E-02	1.00E+00	3.53E-03	2.13E-01	1.96E-03	1.27E-01	1.53E-01	1.00E+00	1.96E-01	1.00E+00	organellar ribosome	C
GO:0000314	14	1.63E-05	7.00E-03	2.75E-02	1.00E+00	1.44E-03	7.90E-02	1.12E-01	1.00E+00	1.07E-02	6.92E-01	1.04E-02	5.03E-01	1.46E-01	1.00E+00	9.73E-02	1.00E+00	organellar small ribosomal subunit	C
GO:0000315	24	3.30E-02	1.00E+00	1.42E-01	1.00E+00	1.47E-02	6.53E-01	1.40E-01	1.00E+00	2.92E-02	1.00E+00	1.41E-01	1.00E+00	5.22E-01	1.00E+00	4.59E-01	1.00E+00	organellar large ribosomal subunit	C
GO:0000323	201	1.66E-06	2.76E-03	3.09E-07	3.92E-03	1.98E-03	9.50E-02	1.48E-04	1.30E-02	3.25E-04	4.90E-02	2.95E-05	9.52E-03	1.41E-04	8.00E-03	5.56E-04	3.00E-02	lytic vacuole	C
GO:0000375	51	2.10E-04	1.72E-02	1.54E-03	9.65E-02	5.12E-03	3.08E-01	4.04E-03	2.88E-01	1.35E-03	1.20E-01	5.48E-03	3.43E-01	1.88E-03	8.40E-02	1.14E-01	1.00E+00	RNA splicing, via transesterification reactior	P
GO:0000377	51	2.10E-04	1.72E-02	1.54E-03	9.65E-02	5.12E-03	3.08E-01	4.04E-03	2.88E-01	1.35E-03	1.20E-01	5.48E-03	3.43E-01	1.88E-03	8.40E-02	1.14E-01	1.00E+00	RNA splicing, via transesterification reactior	P
GO:0000398	51	2.10E-04	1.72E-02	1.54E-03	9.65E-02	5.12E-03	3.08E-01	4.04E-03	2.88E-01	1.35E-03	1.20E-01	5.48E-03	3.43E-01	1.88E-03	8.40E-02	1.14E-01	1.00E+00	nuclear mRNA splicing, via spliceosome	P
GO:0000502	39	3.06E-02	1.00E+00	6.43E-02	1.00E+00	3.73E-02	1.00E+00	5.57E-02	1.00E+00	1.08E-01	1.00E+00	1.98E-02	7.56E-01	2.83E-01	1.00E+00	7.08E-01	1.00E+00	proteasome complex (sensu Eukaryota)	C
GO:0000723	26	8.15E-02	1.00E+00	5.33E-03	3.08E-01	6.01E-02	1.00E+00	2.31E-02	9.37E-01	1.46E-01	1.00E+00	1.09E-02	5.03E-01	1.74E-01	1.00E+00	5.99E-02	1.00E+00	telomere maintenance	P
GO:0000724	13	1.59E-02	1.00E+00	2.27E-05	7.00E-03	2.07E-03	9.50E-02	2.01E-04	1.30E-02	2.20E-01	1.00E+00	3.30E-03	1.51E-01	3.02E-01	1.00E+00	1.14E-03	6.00E-02	double-strand break repair via homologous	P
GO:0000725	13	1.59E-02	1.00E+00	2.27E-05	7.00E-03	2.07E-03	9.50E-02	2.01E-04	1.30E-02	2.20E-01	1.00E+00	3.30E-03	1.51E-01	3.02E-01	1.00E+00	1.14E-03	6.00E-02	recombinational repair	P
GO:0000775	81	1.29E-05	7.00E-03	2.31E-06	3.92E-03	1.06E-06	2.00E-03	6.25E-08	2.89E-03	6.50E-04	1.20E-01	5.76E-04	3.20E-02	1.56E-01	1.00E+00	2.85E-02	9.99E-01	chromosome, pericentric region	C
GO:0000776	41	1.79E-04	1.72E-02	1.09E-04	1.50E-02	3.11E-04	4.00E-02	1.65E-06	2.89E-03	9.04E-03	6.92E-01	8.00E-03	4.21E-01	5.39E-02	1.00E+00	3.66E-02	1.00E+00	kinetochore	C
GO:0000777	27	1.38E-02	6.08E-01	2.28E-03	1.71E-01	3.59E-02	1.00E+00	2.06E-05	9.57E-03	6.71E-03	6.92E-01	4.82E-02	1.00E+00	3.54E-01	1.00E+00	4.40E-02	1.00E+00	condensed chromosome kinetochore	C
GO:0000779	36	1.39E-02	6.08E-01	2.02E-03	1.30E-01	1.77E-02	1.00E+00	7.12E-05	1.30E-02	1.18E-02	6.92E-01	3.35E-02	1.00E+00	3.66E-01	1.00E+00	4.21E-02	1.00E+00	condensed chromosome, pericentric region	C
GO:0000781	22	1.68E-02	1.00E+00	1.40E-02	6.07E-01	1.91E-02	1.00E+00	1.36E-02	6.47E-01	4.74E-02	1.00E+00	5.37E-02	1.00E+00	7.27E-02	1.00E+00	1.03E-01	1.00E+00	chromosome, telomeric region	C
GO:0000784	10	1.19E-01	1.00E+00	2.56E-01	1.00E+00	7.34E-02	1.00E+00	8.31E-02	1.00E+00	2.45E-01	1.00E+00	4.25E-01	1.00E+00	2.46E-01	1.00E+00	8.76E-01	1.00E+00	nuclear chromosome, telomeric region	C
GO:0000785	314	5.15E-03	2.72E-01	2.16E-03	1.71E-01	1.59E-04	1.16E-02	2.83E-06	2.89E-03	1.99E-01	1.00E+00	1.14E-01	1.00E+00	7.88E-02	1.00E+00	1.22E-01	1.00E+00	chromatin	C
GO:0000786	163	9.35E-01	1.00E+00	9.48E-01	1.00E+00	6.40E-01	1.00E+00	1.63E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	5.88E-01	1.00E+00	9.93E-01	1.00E+00	nucleosome	C
GO:0000790	40	1.98E-05	7.00E-03	1.71E-05	4.51E-03	4.12E-05	9.82E-03	4.09E-05	9.57E-03	3.31E-03	2.13E-01	4.07E-04	2.33E-02	1.91E-02	6.36E-01	1.02E-02	4.76E-01	nuclear chromatin	C
GO:0000792	43	5.23E-04	4.40E-02	1.32E-04	1.50E-02	7.06E-04	4.90E-02	2.08E-04	1.30E-02	1.12E-02	6.92E-01	3.46E-03	1.51E-01	1.93E-02	6.36E-01	1.37E-02	4.76E-01	heterochromatin	C
GO:0000793	84	1.52E-05	7.00E-03	7.13E-07	3.92E-03	4.56E-06	2.91E-03	4.72E-07	2.89E-03	3.31E-05	6.33E-03	3.02E-04	2.33E-02	1.30E-01	1.00E+00	6.12E-03	4.28E-01	condensed chromosome	C
GO:0000794	39	1.67E-04	1.72E-02	3.17E-04	4.40E-02	1.51E-04	1.16E-02	4.37E-03	2.88E-01	8.63E-04	1.20E-01	3.10E-03	1.44E-01	4.13E-02	1.00E+00	7.63E-02	1.00E+00	condensed nuclear chromosome	C

GO:0000795	19	8.08E-03	6.08E-01	3.11E-02	1.00E+00	3.42E-02	1.00E+00	1.40E-01	1.00E+00	1.77E-02	7.90E-01	5.91E-03	4.21E-01	5.08E-02	1.00E+00	2.22E-01	1.00E+00	synaptonemal complex	C
GO:0000803	15	1.38E-03	8.86E-02	1.71E-02	7.63E-01	5.87E-03	4.69E-01	6.12E-03	2.88E-01	2.79E-02	1.00E+00	8.39E-02	1.00E+00	8.04E-03	2.75E-01	2.05E-01	1.00E+00	sex chromosome	C
GO:0000819	24	2.31E-02	1.00E+00	1.04E-06	3.92E-03	8.07E-03	6.41E-01	1.41E-10	0.00E+00	1.24E-01	1.00E+00	3.72E-03	1.80E-01	1.55E-01	1.00E+00	1.39E-02	4.76E-01	sister chromatid segregation	P
GO:0000902	584	2.57E-04	1.90E-02	6.19E-06	4.51E-03	2.43E-02	1.00E+00	5.81E-03	2.88E-01	1.67E-03	1.20E-01	2.33E-04	2.33E-02	3.73E-03	2.23E-01	1.28E-06	2.00E-03	cell morphogenesis	P
GO:0000904	219	3.90E-01	1.00E+00	2.77E-01	1.00E+00	7.56E-01	1.00E+00	6.38E-01	1.00E+00	2.31E-01	1.00E+00	5.11E-01	1.00E+00	2.94E-01	1.00E+00	2.93E-02	9.99E-01	cellular morphogenesis during differentiatio	P
GO:0000910	29	2.50E-04	1.90E-02	1.95E-04	2.40E-02	5.79E-04	4.90E-02	6.54E-05	1.30E-02	1.50E-02	6.92E-01	4.02E-02	1.00E+00	7.80E-02	1.00E+00	6.09E-02	1.00E+00	cytokinesis	P
GO:0000922	22	7.35E-03	3.15E-01	6.91E-04	5.90E-02	6.43E-04	4.90E-02	9.59E-04	9.40E-02	1.49E-02	6.92E-01	1.21E-02	5.03E-01	6.29E-02	1.00E+00	1.13E-02	4.76E-01	spindle pole	C
GO:0001501	288	5.08E-01	1.00E+00	9.76E-01	1.00E+00	8.92E-01	1.00E+00	9.51E-01	1.00E+00	3.54E-01	1.00E+00	9.45E-01	1.00E+00	3.31E-01	1.00E+00	8.97E-01	1.00E+00	skeletal development	P
GO:0001502	16	2.71E-01	1.00E+00	4.26E-01	1.00E+00	2.60E-01	1.00E+00	5.06E-01	1.00E+00	2.52E-01	1.00E+00	9.15E-01	1.00E+00	3.88E-01	1.00E+00	4.23E-03	2.01E-01	cartilage condensation	P
GO:0001503	150	3.33E-02	1.00E+00	2.47E-01	1.00E+00	4.27E-01	1.00E+00	2.77E-01	1.00E+00	2.27E-02	1.00E+00	3.44E-01	1.00E+00	5.15E-02	1.00E+00	3.17E-01	1.00E+00	ossification	P
GO:0001504	12	9.26E-01	1.00E+00	9.98E-01	1.00E+00	8.78E-01	1.00E+00	9.97E-01	1.00E+00	8.20E-01	1.00E+00	9.63E-01	1.00E+00	8.97E-01	1.00E+00	9.91E-01	1.00E+00	neurotransmitter uptake	P
GO:0001505	115	9.92E-01	1.00E+00	9.04E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.02E-01	1.00E+00	5.43E-01	1.00E+00	9.31E-01	1.00E+00	4.01E-01	1.00E+00	regulation of neurotransmitter levels	P
GO:0001508	51	4.90E-01	1.00E+00	1.55E-01	1.00E+00	3.38E-01	1.00E+00	2.50E-01	1.00E+00	5.47E-01	1.00E+00	3.39E-01	1.00E+00	6.72E-01	1.00E+00	7.23E-02	1.00E+00	regulation of action potential	P
GO:0001518	11	8.84E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.45E-01	1.00E+00	9.99E-01	1.00E+00	1.29E-01	1.00E+00	7.04E-02	1.00E+00	voltage-gated sodium channel complex	C
GO:0001522	13	8.69E-02	1.00E+00	8.86E-02	1.00E+00	7.95E-02	1.00E+00	8.96E-02	1.00E+00	2.14E-01	1.00E+00	4.63E-01	1.00E+00	1.41E-01	1.00E+00	1.18E-01	1.00E+00	pseudouridine synthesis	P
GO:0001523	16	9.98E-01	1.00E+00	7.18E-01	1.00E+00	9.84E-01	1.00E+00	9.29E-01	1.00E+00	9.88E-01	1.00E+00	4.80E-01	1.00E+00	9.92E-01	1.00E+00	5.28E-01	1.00E+00	retinoid metabolism	P
GO:0001525	160	2.28E-01	1.00E+00	4.88E-02	1.00E+00	6.04E-01	1.00E+00	3.46E-01	1.00E+00	3.85E-01	1.00E+00	4.69E-01	1.00E+00	4.86E-02	1.00E+00	5.34E-04	3.00E-02	angiogenesis	P
GO:0001533	20	9.80E-01	1.00E+00	9.96E-01	1.00E+00	9.77E-01	1.00E+00	9.80E-01	1.00E+00	9.97E-01	1.00E+00	9.97E-01	1.00E+00	7.30E-01	1.00E+00	9.89E-01	1.00E+00	cornified envelope	C
GO:0001539	40	5.32E-01	1.00E+00	1.87E-01	1.00E+00	5.64E-01	1.00E+00	3.64E-01	1.00E+00	3.55E-01	1.00E+00	4.54E-01	1.00E+00	6.52E-01	1.00E+00	8.63E-02	1.00E+00	ciliary or flagellar motility	P
GO:0001541	27	9.08E-03	6.08E-01	4.48E-02	1.00E+00	3.06E-02	1.00E+00	9.98E-02	1.00E+00	1.92E-02	7.90E-01	3.88E-02	1.00E+00	9.27E-02	1.00E+00	2.72E-01	1.00E+00	ovarian follicle development	P
GO:0001542	10	7.70E-01	1.00E+00	9.79E-01	1.00E+00	7.68E-01	1.00E+00	9.05E-01	1.00E+00	5.74E-01	1.00E+00	9.99E-01	1.00E+00	6.82E-01	1.00E+00	9.75E-01	1.00E+00	ovulation (sensu Mammalia)	P
GO:0001558	127	1.49E-02	1.00E+00	2.88E-03	1.88E-01	8.62E-02	1.00E+00	1.84E-02	9.37E-01	5.03E-02	1.00E+00	1.59E-02	6.68E-01	9.51E-02	1.00E+00	5.83E-03	4.28E-01	regulation of cell growth	P
GO:0001565	17	6.15E-01	1.00E+00	2.74E-01	1.00E+00	3.74E-01	1.00E+00	3.18E-01	1.00E+00	6.99E-01	1.00E+00	1.91E-01	1.00E+00	5.73E-01	1.00E+00	5.71E-01	1.00E+00	phorbol ester receptor activity	F
GO:0001568	244	2.04E-01	1.00E+00	1.53E-01	1.00E+00	6.34E-01	1.00E+00	6.54E-01	1.00E+00	4.47E-01	1.00E+00	3.60E-01	1.00E+00	6.09E-02	1.00E+00	5.71E-03	4.28E-01	blood vessel development	P
GO:0001569	22	6.26E-01	1.00E+00	8.38E-01	1.00E+00	9.49E-01	1.00E+00	9.78E-01	1.00E+00	7.04E-01	1.00E+00	9.95E-01	1.00E+00	1.24E-01	1.00E+00	5.04E-02	1.00E+00	patterning of blood vessels	P
GO:0001570	36	6.43E-01	1.00E+00	8.19E-01	1.00E+00	3.62E-01	1.00E+00	9.33E-01	1.00E+00	7.45E-01	1.00E+00	6.82E-01	1.00E+00	8.27E-01	1.00E+00	7.40E-01	1.00E+00	vasculogenesis	P
GO:0001580	19	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.89E-01	1.00E+00	detection of chemical stimulus during sensc	P
GO:0001584	1771	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	rhodopsin-like receptor activity	F
GO:0001595	63	5.37E-01	1.00E+00	4.36E-01	1.00E+00	9.90E-01	1.00E+00	9.40E-01	1.00E+00	3.06E-01	1.00E+00	9.76E-02	1.00E+00	1.68E-01	1.00E+00	5.17E-01	1.00E+00	angiotensin receptor activity	F
GO:0001603	23	9.53E-01	1.00E+00	8.40E-01	1.00E+00	7.69E-01	1.00E+00	6.29E-01	1.00E+00	8.32E-01	1.00E+00	8.70E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	vasopressin-like receptor activity	F
GO:0001608	138	9.70E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.09E-01	1.00E+00	9.66E-01	1.00E+00	4.18E-01	1.00E+00	4.72E-01	1.00E+00	nucleotide receptor activity, G-protein coupl	F
GO:0001614	139	9.67E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.05E-01	1.00E+00	9.64E-01	1.00E+00	4.11E-01	1.00E+00	4.38E-01	1.00E+00	purinergic nucleotide receptor activity	F
GO:0001619	27	2.63E-01	1.00E+00	2.68E-01	1.00E+00	2.08E-01	1.00E+00	2.13E-01	1.00E+00	5.70E-01	1.00E+00	8.50E-01	1.00E+00	1.32E-01	1.00E+00	7.23E-02	1.00E+00	lysosphingolipid and lysophosphatidic acid r	F
GO:0001633	29	8.04E-01	1.00E+00	4.97E-01	1.00E+00	9.30E-01	1.00E+00	8.99E-01	1.00E+00	9.50E-01	1.00E+00	3.32E-01	1.00E+00	1.73E-01	1.00E+00	1.47E-01	1.00E+00	secretin-like receptor activity	F
GO:0001637	48	7.77E-01	1.00E+00	8.62E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	6.86E-01	1.00E+00	5.59E-01	1.00E+00	1.44E-01	1.00E+00	3.22E-01	1.00E+00	G-protein chemoattractant receptor activity	F
GO:0001649	55	2.81E-01	1.00E+00	2.27E-01	1.00E+00	4.31E-01	1.00E+00	3.21E-01	1.00E+00	4.49E-01	1.00E+00	3.49E-01	1.00E+00	1.58E-01	1.00E+00	2.62E-01	1.00E+00	osteoblast differentiation	P
GO:0001653	719	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity	F
GO:0001654	102	1.15E-01	1.00E+00	5.95E-01	1.00E+00	1.09E-01	1.00E+00	5.04E-01	1.00E+00	2.64E-01	1.00E+00	5.83E-01	1.00E+00	1.37E-01	1.00E+00	6.69E-01	1.00E+00	eye development	P
GO:0001655	97	9.99E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	8.49E-01	1.00E+00	8.38E-01	1.00E+00	7.21E-01	1.00E+00	urogenital system development	P
GO:0001656	52	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	9.93E-01	1.00E+00	9.74E-01	1.00E+00	9.04E-01	1.00E+00	metanephros development	P
GO:0001657	41	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	8.86E-01	1.00E+00	9.57E-01	1.00E+00	ureteric bud development	P
GO:0001658	25	9.99E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	5.60E-01	1.00E+00	9.00E-01	1.00E+00	ureteric bud branching	P
GO:0001659	207	1.78E-01	1.00E+00	2.58E-01	1.00E+00	1.08E-01	1.00E+00	1.69E-01	1.00E+00	5.43E-01	1.00E+00	4.32E-01	1.00E+00	1.07E-01	1.00E+00	2.88E-01	1.00E+00	thermoregulation	P
GO:0001662	12	5.58E-01	1.00E+00	3.50E-01	1.00E+00	7.90E-01	1.00E+00	8.43E-01	1.00E+00	2.78E-01	1.00E+00	1.45E-01	1.00E+00	5.50E-01	1.00E+00	4.66E-01	1.00E+00	behavioral fear response	P
GO:0001664	81	2.59E-01	1.00E+00	6.95E-01	1.00E+00	3.30E-01	1.00E+00	9.92E-01	1.00E+00	5.35E-01	1.00E+00	3.12E-01	1.00E+00	7.25E-02	1.00E+00	2.70E-01	1.00E+00	G-protein-coupled receptor binding	F
GO:0001666	77	1.13E-02	6.08E-01	4.49E-03	2.61E-01	1.97E-01	1.00E+00	7.67E-03	4.92E-01	4.53E-01	1.00E+00	1.43E-02	6.68E-01	1.98E-05	4.00E-03	3.82E-02	1.00E+00	response to hypoxia	P
GO:0001669	36	4.53E-01	1.00E+00	3.77E-01	1.00E+00	7.78E-01	1.00E+00	3.80E-01	1.00E+00	7.11E-01	1.00E+00	8.34E-02	1.00E+00	1.50E-01	1.00E+00	9.53E-01	1.00E+00	acrosome	C
GO:0001676	16	2.31E-01	1.00E+00	7.16E-02	1.00E+00	1.28E-01	1.00E+00	5.29E-02	1.00E+00	6.47E-01	1.00E+00	1.05E-01	1.00E+00	8.90E-02	1.00E+00	2.48E-01	1.00E+00	long-chain fatty acid metabolism	P
GO:0001701	151	2.52E-08	2.57E-03	1.07E-06	3.92E-03	9.32E-07	2.00E-03	6.79E-06	2.89E-03	1.73E-05	5.37E-03	7.50E-04	4.48E-02	5.02E-04	3.44E-02	1.08E-03	6.00E-02	embryonic development (sensu Mammalia)	P
GO:0001702	27	2.29E-01	1.00E+00	7.89E-02	1.00E+00	1.83E-01	1.00E+00	4.22E-02	1.00E+00	1.06E-01	1.00E+00	1.87E-01	1.00E+00	8.87E-01	1.00E+00	3.58E-01	1.00E+00	gastrulation (sensu Deuterostomia)	P
GO:0001704	39	1.79E-02	1.00E+00	2.98E-03	1.88E-01	2.49E-03	1.07E-01	3.68E-02	1.00E+00	3.27E-01	1.00E+00	1.65E-02	6.68E-01	1.40E-01	1.00E+00	1.32E-02	4.76E-01	formation of primary germ layer	P
GO:0001707	35	1.26E-02	6.08E-01	8.15E-04	8.10E-02	2.56E-03	1.07E-01	2.07E-02	9.37E-01	2.06E-01	1.00E+00	6.61E-03	4.21E-01	1.66E-01	1.00E+00	8.62E-03	4.28E-01	mesoderm formation	P
GO:0001708	35	6.81E-01	1.00E+00	9.71E-01	1.00E+00	4.15E-01	1.00E+00	9.96E-01	1.00E+00	9.58E-01	1.00E+00	8.21E-01	1.00E+00	2.58E-01	1.00E+00	7.94E-01	1.00E+00	cell fate specification	P
GO:0001709	26	7.79E-01	1.00E+00	9.93E-01	1.00E+00	5.30E-01	1.00E+00	9.73E-01	1.00E+00	9.12E-01	1.00E+00	9.57E-01	1.00E+00	7.15E-01	1.00E+00	9.99E-01	1.00E+00	cell fate determination	P
GO:0001725	24	1.13E-04	1.43E-02	6.57E-05	7.00E-03	1.93E-03	9.50E-02	1.36E-02	6.47E-01	5.04E-04	4.90E-02	3.14E-05	9.52E-03	2.84E-03	8.40E-02	2.98E-03	1.27E-01	stress fiber	C
GO:0001726	46	3.28E-05	7.00E-03	1.12E-03	9.65E-02	3.92E-03	2.20E-01	1.64E-03	9.60E-02	2.34E-03	1.20E-01	8.88E-03	5.03E-01	3.60E-03	2.23E-01	3.06E-01	1.00E+00	ruffle	C
GO:0001727	24	9.16E-02	1.00E+00	5.85E-02	1.00E+00	8.16E-02	1.00E+00	3.94E-02	1.00E+00	2.20E-01	1.00E+00	1.53E-01	1.00E+00	2.41E-01	1.00E+00	1.06E-01	1.00E+00	lipid kinase activity	F
GO:0001738	12	8.51E-01	1.00E+00	1.61E-01	1.00E+00	9.08E-01	1.00E+00	2.32E-01	1.00E+00	5.95E-01	1.00E+00	2.43E-01	1.00E+00	8.57E-01	1.00E+00	2.86E-01	1.00E+00	morphogenesis of a polarized epithelium	P
GO:0001739	14	3.67E-03	2.12E-01	3.70E-02	1.00E+00	1.30E-02	6.53E-01	1.57E-02	6.47E-01	5.60E-02	1.00E+00	1.10E-01	1.00E+00	7.10E-03	2.75E-01	2.86E-01	1.00E+00	sex chromatin	C
GO:0001750	17	2.88E-01	1.00E+00	2.24E-01	1.00E+00	6.87E-01	1.00E+00	3.39E-01	1.00E+00	2.16E-01	1.00E+00	1.29E-01	1.00E+00	1.32E-01	1.00E+00	3.00E-01	1.00E+00	photoreceptor outer segment	C
GO:0001754	15	3.51E-01	1.00E+00	1.30E-01	1.00E+00	2.93E-01	1.00E+00	2.41E-01	1.00E+00	3.73E-01	1.00E+00	1.47E-01	1.00E+00	5.20E-01	1.00E+00	9.98E-02	1.00E+00	eye photoreceptor cell differentiation	P
GO:0001755	23	9.29E-01	1.00E+00	9.94E-01	1.00E+00	8.67E-01	1.00E+00	9.12E-01	1.00E+00	8.06E-01	1.00E+00	9.80E-01	1.00E+00	9.39E-01	1.00E+00	9.99E-01	1.00E+00	neural crest cell migration	P
GO:0001756	35	9.28E-01	1.00E+00	5.56E-01	1.00E+00	5.70E-01	1.00E+00	4.42E-01	1.00E+00	9.08E-01	1.00E+00	5.34E-01	1.00E+00	9.74E-01	1.00E+00	9.08E-01	1.00E+00	somitogenesis	P
GO:0001759	14	7.19E-01	1.00E+00	8.45E-01	1.00E+00	8.85E-01	1.00E+00	5.04E-01	1.00E+00	5.26E-01	1.00E+00	9.71E-01	1.00E+00	6.36E-01	1.00E+00	8.13E-01	1.00E+00	induction of an organ	P
GO:0001763	76	5.44E-01	1.00E+00	9.76E-01	1.00E+00	9.04E-01	1.00E+00	9.99E-01	1.00E+00	9.49E-01	1.00E+00	9.92E-01	1.00E+00	2.86E-02	8.38E-01	2.89E-01	1.00E+00	morphogenesis of a branching structure	P
GO:0001764	67	7.81E-01	1.00E+00	9.78E-01	1.00E+00	9.79E-01	1.00E+00	9.74E-01	1.00E+00	7.30E-01	1.00E+00	9.03E-01	1.00E+00	2.21E-01	1.00E+00	9.71E-01	1.00E+00	neuron migration	P
GO:0001772	24	5.00E-01	1.00E+00	2.15E-01	1.00E+00	4.13E-01	1.00E+00	3.80E-01	1.00E+00	6.41E-01	1.00E+00	3.22E-01	1.00E+00	3.90E-01	1.00E+00	1.28E-01	1.00E+00	immunological synapse	C
GO:0001775	293	1.65E-02	1.00E+00	8.31E-05	1.50E-02	1.56E-01	1.00E+00	1.94E-03	1.39E-01	4.54E-01	1.00E+00	3.98E-02	1.00E+00	8.23E-05	8.00E-03	2.49E-05	7.00E-03	cell activation	P
GO:0001776	37	6.50E-02	1.00E+00	1.79E-02	1.00E+00	7.24E-02	1.00E+00	1.19E-01	1.00E+00	2.92E-01	1.00E+00	5.89E-03	4.21E-01	7.11E-02	1.00E+00	1.10E-01	1.00E+00	leukocyte homeostasis	P
GO:0001782	13	2.76E-01	1.00E+00	4.46E-01	1.00E+00	2.92E-01	1.00E+00	5.52E-01	1.00E+00	3.44E-01	1.00E+00	1.74E-01	1.00E+00	4.21E-01	1.00E+00	6.55E-01	1.00E+00	B cell homeostasis	P
GO:0001816	119	8.64E-02	1.00E+00	5.40E-02	1.00E+00	6.73E-01	1.00E+00	5.02E-01	1.00E+00	3.82E-01	1.00E+00	4.85E-01	1.00E+00	2.42E-03	8.40E-02	2.60E-03	8.32E-02	cytokine production	P
GO:0001817	13	6.14E-01	1.00E+00	5.49E-01	1.00E+00	8.54E-01	1.00E+00	7.55E-01	1.00E+00	6.22E-01	1.00E+00	7.91E-01	1.00E+00	3.27E-01	1.00E+00	2.73E-01	1.00E+00	regulation of cytokine production	P
GO:0001822	87	9.95E-01	1.00E+00	8.98E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	9.91E-01	1.00E+00	7.71E-01	1.00E+00	6.97E-01	1.00E+00	6.25E-01	1.00E+00	kidney development	P
GO:0001824	41	5.68E-05	1.20E-02	3.16E-05	7.00E-03	7.54E-05	1.16E-02	7.00E-05	1.30E-02	3.26E-04	4.90E-02	1.47E-02	6.68E-01	5.19E-02	1.00E+00	1.57E-03	6.00E-02	blastocyst development	P
GO:0001825	14	3.16E-02	1.00E+00	7.35E-03	3.12E-01	1.24E-02	6.53E-01	3.58E-03	2.57E-01	1.79E-01	1.00E+00	2.96E-01	1.00E+00	4.07E-01	1.00E+00	1.61E-03	6.00E-02	blastocyst formation	P

GO:0001829	11	2.02E-02	1.00E+00	2.25E-02	1.00E+00	3.06E-03	1.35E-01	1.14E-02	6.47E-01	1.86E-01	1.00E+00	3.60E-01	1.00E+00	3.71E-01	1.00E+00	6.96E-03	4.28E-01	trophectodermal cell differentiation	P
GO:0001832	15	1.19E-02	6.08E-01	5.47E-03	3.08E-01	1.22E-02	6.53E-01	1.65E-03	9.60E-02	2.40E-02	1.00E+00	5.23E-02	1.00E+00	1.79E-01	1.00E+00	4.79E-02	1.00E+00	blastocyst growth	P
GO:0001836	17	8.34E-06	3.62E-03	7.88E-05	1.50E-02	2.13E-05	3.00E-03	2.70E-04	4.20E-02	3.63E-03	2.13E-01	2.53E-04	2.33E-02	2.90E-04	2.29E-02	2.28E-02	9.99E-01	release of cytochrome c from mitochondria	P
GO:0001837	11	2.59E-01	1.00E+00	2.63E-01	1.00E+00	1.49E-01	1.00E+00	2.72E-01	1.00E+00	9.37E-01	1.00E+00	2.53E-01	1.00E+00	5.35E-03	2.23E-01	1.73E-01	1.00E+00	epithelial to mesenchymal transition	P
GO:0001838	49	1.87E-01	1.00E+00	1.65E-01	1.00E+00	2.41E-01	1.00E+00	2.06E-01	1.00E+00	9.76E-02	1.00E+00	3.42E-01	1.00E+00	3.17E-01	1.00E+00	9.79E-02	1.00E+00	embryonic epithelial tube formation	P
GO:0001839	49	1.66E-01	1.00E+00	2.19E-02	1.00E+00	2.60E-01	1.00E+00	6.53E-02	1.00E+00	9.23E-02	1.00E+00	2.20E-01	1.00E+00	2.51E-01	1.00E+00	7.16E-03	4.28E-01	neural plate morphogenesis	P
GO:0001841	45	1.99E-01	1.00E+00	6.18E-02	1.00E+00	2.88E-01	1.00E+00	1.30E-01	1.00E+00	6.90E-02	1.00E+00	1.80E-01	1.00E+00	3.83E-01	1.00E+00	4.16E-02	1.00E+00	neural tube formation	P
GO:0001843	33	3.55E-01	1.00E+00	7.31E-02	1.00E+00	4.06E-01	1.00E+00	1.14E-01	1.00E+00	1.86E-01	1.00E+00	8.76E-02	1.00E+00	5.41E-01	1.00E+00	1.18E-01	1.00E+00	neural tube closure	P
GO:0001871	103	7.93E-01	1.00E+00	7.59E-01	1.00E+00	7.26E-01	1.00E+00	9.58E-01	1.00E+00	7.69E-01	1.00E+00	6.90E-01	1.00E+00	7.90E-01	1.00E+00	2.91E-01	1.00E+00	pattern binding	F
GO:0001889	34	5.20E-02	1.00E+00	1.20E-03	9.65E-02	1.56E-01	1.00E+00	5.54E-03	2.88E-01	6.61E-02	1.00E+00	3.34E-02	1.00E+00	1.25E-01	1.00E+00	2.41E-02	9.99E-01	liver development	P
GO:0001890	42	1.70E-03	2.12E-01	6.79E-04	5.90E-02	2.81E-03	1.35E-01	1.02E-03	9.40E-02	5.84E-02	1.00E+00	5.81E-02	1.00E+00	2.13E-02	6.36E-01	1.91E-02	7.36E-01	placenta development	P
GO:0001892	20	4.31E-03	2.14E-01	3.99E-03	1.88E-01	2.88E-04	4.00E-02	2.62E-03	1.61E-01	2.39E-01	1.00E+00	3.03E-01	1.00E+00	8.42E-02	1.00E+00	1.27E-03	6.00E-02	embryonic placenta development	P
GO:0001894	47	3.04E-01	1.00E+00	3.14E-02	1.00E+00	2.72E-01	1.00E+00	2.84E-01	1.00E+00	6.75E-01	1.00E+00	9.36E-03	5.03E-01	1.71E-01	1.00E+00	5.74E-02	1.00E+00	tissue homeostasis	P
GO:0001906	32	9.20E-01	1.00E+00	8.07E-01	1.00E+00	7.78E-01	1.00E+00	6.76E-01	1.00E+00	7.50E-01	1.00E+00	5.98E-01	1.00E+00	9.82E-01	1.00E+00	9.80E-01	1.00E+00	cell killing	P
GO:0001909	31	8.84E-01	1.00E+00	7.86E-01	1.00E+00	7.18E-01	1.00E+00	6.71E-01	1.00E+00	6.96E-01	1.00E+00	5.37E-01	1.00E+00	9.71E-01	1.00E+00	9.71E-01	1.00E+00	leukocyte mediated cytotoxicity	P
GO:0001910	23	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	9.92E-01	1.00E+00	9.80E-01	1.00E+00	9.93E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	regulation of leukocyte mediated cytotoxicity	P
GO:0001912	17	9.98E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	9.68E-01	1.00E+00	9.79E-01	1.00E+00	9.50E-01	1.00E+00	9.86E-01	1.00E+00	positive regulation of leukocyte mediated cy	P
GO:0001932	97	8.85E-01	1.00E+00	5.11E-01	1.00E+00	9.32E-01	1.00E+00	7.98E-01	1.00E+00	9.86E-01	1.00E+00	5.13E-01	1.00E+00	1.60E-01	1.00E+00	1.32E-01	1.00E+00	regulation of protein amino acid phosphoryl	P
GO:0001933	15	9.36E-01	1.00E+00	5.20E-01	1.00E+00	8.63E-01	1.00E+00	5.21E-01	1.00E+00	8.63E-01	1.00E+00	3.97E-01	1.00E+00	9.52E-01	1.00E+00	6.15E-01	1.00E+00	negative regulation of protein amino acid ph	P
GO:0001934	47	6.26E-01	1.00E+00	3.08E-01	1.00E+00	8.70E-01	1.00E+00	4.82E-01	1.00E+00	9.10E-01	1.00E+00	2.77E-01	1.00E+00	6.92E-02	1.00E+00	1.66E-01	1.00E+00	positive regulation of protein amino acid ph	P
GO:0001935	28	3.18E-01	1.00E+00	1.87E-01	1.00E+00	7.25E-01	1.00E+00	5.72E-01	1.00E+00	4.26E-01	1.00E+00	1.99E-01	1.00E+00	1.30E-01	1.00E+00	1.33E-01	1.00E+00	endothelial cell proliferation	P
GO:0001936	22	5.28E-01	1.00E+00	3.99E-01	1.00E+00	8.80E-01	1.00E+00	5.92E-01	1.00E+00	6.22E-01	1.00E+00	5.02E-01	1.00E+00	2.24E-01	1.00E+00	2.55E-01	1.00E+00	regulation of endothelial cell proliferation	P
GO:0001937	14	2.11E-01	1.00E+00	3.39E-01	1.00E+00	5.00E-01	1.00E+00	2.72E-01	1.00E+00	3.21E-01	1.00E+00	5.16E-01	1.00E+00	1.01E-01	1.00E+00	3.71E-01	1.00E+00	negative regulation of endothelial cell prolife	P
GO:0001942	43	3.41E-01	1.00E+00	2.90E-01	1.00E+00	8.86E-01	1.00E+00	4.74E-01	1.00E+00	4.36E-01	1.00E+00	3.24E-01	1.00E+00	1.92E-02	6.36E-01	8.68E-02	1.00E+00	hair follicle development	P
GO:0001944	247	1.93E-01	1.00E+00	1.67E-01	1.00E+00	6.40E-01	1.00E+00	6.74E-01	1.00E+00	4.48E-01	1.00E+00	3.47E-01	1.00E+00	4.62E-02	1.00E+00	7.30E-03	4.28E-01	vasculature development	P
GO:0001947	16	1.65E-01	1.00E+00	1.38E-01	1.00E+00	2.86E-01	1.00E+00	1.39E-01	1.00E+00	1.05E-01	1.00E+00	3.24E-01	1.00E+00	6.57E-01	1.00E+00	1.10E-01	1.00E+00	heart looping	P
GO:0001948	14	1.78E-01	1.00E+00	9.94E-02	1.00E+00	3.97E-01	1.00E+00	2.99E-01	1.00E+00	4.09E-01	1.00E+00	2.40E-01	1.00E+00	5.22E-02	1.00E+00	2.01E-02	7.36E-01	glycoprotein binding	F
GO:0001952	18	3.59E-01	1.00E+00	4.31E-01	1.00E+00	5.39E-01	1.00E+00	6.78E-01	1.00E+00	3.70E-01	1.00E+00	2.54E-01	1.00E+00	2.86E-01	1.00E+00	3.28E-01	1.00E+00	regulation of cell-matrix adhesion	P
GO:0001958	10	4.69E-01	1.00E+00	8.42E-01	1.00E+00	5.74E-01	1.00E+00	2.41E-01	1.00E+00	4.45E-01	1.00E+00	9.08E-01	1.00E+00	4.10E-01	1.00E+00	1.00E+00	1.00E+00	endochondral ossification	P
GO:0001963	13	9.76E-01	1.00E+00	9.99E-01	1.00E+00	7.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.49E-01	1.00E+00	6.44E-01	1.00E+00	9.86E-01	1.00E+00	synaptic transmission, dopaminergic	P
GO:0001964	11	9.77E-01	1.00E+00	9.61E-01	1.00E+00	8.29E-01	1.00E+00	9.57E-01	1.00E+00	9.91E-01	1.00E+00	7.95E-01	1.00E+00	9.69E-01	1.00E+00	9.05E-01	1.00E+00	startle response	P
GO:0001974	18	9.53E-01	1.00E+00	8.09E-01	1.00E+00	9.96E-01	1.00E+00	9.72E-01	1.00E+00	9.91E-01	1.00E+00	8.55E-01	1.00E+00	4.29E-01	1.00E+00	2.30E-01	1.00E+00	blood vessel remodeling	P
GO:0001975	11	2.80E-01	1.00E+00	4.92E-01	1.00E+00	4.07E-01	1.00E+00	7.27E-01	1.00E+00	6.54E-01	1.00E+00	4.22E-01	1.00E+00	6.95E-05	8.00E-03	3.09E-01	1.00E+00	response to amphetamine	P
GO:0001976	22	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	1.00E+00	1.00E+00	5.61E-01	1.00E+00	8.64E-01	1.00E+00	fast regulation of arterial pressure	P
GO:0001990	18	9.00E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	6.63E-01	1.00E+00	1.00E+00	1.00E+00	6.72E-01	1.00E+00	9.24E-01	1.00E+00	regulation of blood pressure by hormones	P
GO:0002009	141	4.85E-01	1.00E+00	3.17E-01	1.00E+00	5.15E-01	1.00E+00	7.94E-01	1.00E+00	5.76E-01	1.00E+00	4.51E-01	1.00E+00	2.71E-01	1.00E+00	8.71E-03	4.28E-01	morphogenesis of an epithelium	P
GO:0002026	12	2.65E-01	1.00E+00	4.90E-01	1.00E+00	4.22E-01	1.00E+00	6.05E-01	1.00E+00	7.78E-01	1.00E+00	6.91E-01	1.00E+00	7.14E-02	1.00E+00	2.12E-01	1.00E+00	cardiac inotropy	P
GO:0002053	15	9.82E-01	1.00E+00	7.04E-01	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	2.31E-01	1.00E+00	6.84E-01	1.00E+00	4.19E-01	1.00E+00	positive regulation of mesenchymal cell pro	P
GO:0002062	21	3.91E-01	1.00E+00	8.98E-01	1.00E+00	5.22E-01	1.00E+00	7.45E-01	1.00E+00	5.96E-01	1.00E+00	8.54E-01	1.00E+00	1.92E-01	1.00E+00	7.99E-01	1.00E+00	chondrocyte differentiation	P
GO:0002064	14	3.49E-01	1.00E+00	7.61E-01	1.00E+00	9.99E-01	1.00E+00	9.79E-01	1.00E+00	1.44E-01	1.00E+00	8.26E-01	1.00E+00	1.72E-01	1.00E+00	1.35E-01	1.00E+00	epithelial cell development	P
GO:0002076	10	2.63E-01	1.00E+00	3.59E-01	1.00E+00	4.02E-01	1.00E+00	4.24E-01	1.00E+00	4.73E-01	1.00E+00	5.70E-01	1.00E+00	1.64E-01	1.00E+00	1.83E-01	1.00E+00	osteoblast development	P
GO:0002088	13	3.14E-01	1.00E+00	4.46E-01	1.00E+00	2.06E-01	1.00E+00	6.96E-01	1.00E+00	8.24E-01	1.00E+00	1.81E-01	1.00E+00	2.82E-01	1.00E+00	5.63E-01	1.00E+00	lens development (sensu Vertebrata)	P
GO:0002200	30	2.47E-01	1.00E+00	8.52E-03	4.69E-01	4.44E-01	1.00E+00	7.11E-03	4.92E-01	3.27E-01	1.00E+00	3.02E-01	1.00E+00	2.10E-01	1.00E+00	3.76E-02	1.00E+00	somatic diversification of immune receptors	P
GO:0002204	25	2.54E-01	1.00E+00	6.07E-03	3.08E-01	4.19E-01	1.00E+00	2.87E-03	1.61E-01	2.75E-01	1.00E+00	4.16E-01	1.00E+00	2.69E-01	1.00E+00	4.13E-02	1.00E+00	somatic recombination of immunoglobulin g	P
GO:0002208	25	2.54E-01	1.00E+00	6.07E-03	3.08E-01	4.19E-01	1.00E+00	2.87E-03	1.61E-01	2.75E-01	1.00E+00	4.16E-01	1.00E+00	2.69E-01	1.00E+00	4.13E-02	1.00E+00	somatic diversification of immunoglobulins	P
GO:0002209	12	5.58E-01	1.00E+00	3.50E-01	1.00E+00	7.90E-01	1.00E+00	8.43E-01	1.00E+00	2.78E-01	1.00E+00	1.45E-01	1.00E+00	5.50E-01	1.00E+00	4.66E-01	1.00E+00	behavioral defense response	P
GO:0002217	434	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.99E-01	1.00E+00	5.54E-01	1.00E+00	physiological defense response	P
GO:0002228	20	8.25E-01	1.00E+00	5.35E-01	1.00E+00	6.33E-01	1.00E+00	4.52E-01	1.00E+00	6.64E-01	1.00E+00	3.17E-01	1.00E+00	9.47E-01	1.00E+00	8.61E-01	1.00E+00	natural killer cell mediated immunity	P
GO:0002245	452	9.00E-01	1.00E+00	8.19E-01	1.00E+00	9.82E-01	1.00E+00	8.51E-01	1.00E+00	9.91E-01	1.00E+00	9.26E-01	1.00E+00	1.41E-01	1.00E+00	1.87E-01	1.00E+00	physiological response to wounding	P
GO:0002250	160	4.69E-01	1.00E+00	4.43E-01	1.00E+00	7.14E-01	1.00E+00	1.52E-01	1.00E+00	8.86E-01	1.00E+00	8.96E-01	1.00E+00	8.30E-02	1.00E+00	3.41E-01	1.00E+00	adaptive immune response	P
GO:0002252	194	3.53E-01	1.00E+00	5.88E-01	1.00E+00	5.42E-01	1.00E+00	2.94E-01	1.00E+00	9.05E-01	1.00E+00	8.34E-01	1.00E+00	3.50E-02	8.38E-01	5.13E-01	1.00E+00	immune effector process	P
GO:0002253	81	5.92E-01	1.00E+00	5.72E-01	1.00E+00	7.21E-01	1.00E+00	6.43E-01	1.00E+00	9.56E-01	1.00E+00	6.27E-01	1.00E+00	2.79E-01	1.00E+00	4.50E-01	1.00E+00	activation of immune response	P
GO:0002260	29	6.31E-02	1.00E+00	1.88E-02	1.00E+00	9.02E-02	1.00E+00	1.60E-01	1.00E+00	5.25E-01	1.00E+00	3.47E-03	1.51E-01	3.78E-02	8.38E-01	1.95E-01	1.00E+00	lymphocyte homeostasis	P
GO:0002263	19	1.08E-02	6.08E-01	7.01E-03	3.12E-01	5.43E-02	1.00E+00	1.07E-02	5.72E-01	3.26E-01	1.00E+00	1.84E-01	1.00E+00	5.32E-03	2.23E-01	1.88E-02	7.36E-01	cell activation during immune response	P
GO:0002274	33	1.27E-01	1.00E+00	5.52E-01	1.00E+00	4.99E-01	1.00E+00	5.97E-01	1.00E+00	8.11E-01	1.00E+00	9.52E-01	1.00E+00	3.92E-03	2.23E-01	1.55E-01	1.00E+00	myeloid leukocyte activation	P
GO:0002285	17	3.60E-02	1.00E+00	3.19E-02	1.00E+00	5.72E-02	1.00E+00	3.92E-02	1.00E+00	4.97E-01	1.00E+00	2.10E-01	1.00E+00	1.32E-02	4.78E-01	7.59E-02	1.00E+00	lymphocyte activation during immune respo	P
GO:0002286	15	5.81E-02	1.00E+00	5.62E-02	1.00E+00	1.27E-01	1.00E+00	6.42E-02	1.00E+00	4.41E-01	1.00E+00	2.76E-01	1.00E+00	2.25E-02	6.36E-01	1.38E-01	1.00E+00	T cell activation during immune response	P
GO:0002292	13	5.99E-02	1.00E+00	7.42E-02	1.00E+00	1.44E-01	1.00E+00	9.56E-02	1.00E+00	4.31E-01	1.00E+00	3.97E-01	1.00E+00	1.36E-02	4.78E-01	1.14E-01	1.00E+00	T cell differentiation during immune respons	P
GO:0002293	13	5.99E-02	1.00E+00	7.42E-02	1.00E+00	1.44E-01	1.00E+00	9.56E-02	1.00E+00	4.31E-01	1.00E+00	3.97E-01	1.00E+00	1.36E-02	4.78E-01	1.14E-01	1.00E+00	alpha-beta T cell differentiation during immu	P
GO:0002294	13	5.99E-02	1.00E+00	7.42E-02	1.00E+00	1.44E-01	1.00E+00	9.56E-02	1.00E+00	4.31E-01	1.00E+00	3.97E-01	1.00E+00	1.36E-02	4.78E-01	1.14E-01	1.00E+00	CD4-positive, alpha-beta T cell differentiatic	P
GO:0002366	19	1.08E-02	6.08E-01	7.01E-03	3.12E-01	5.43E-02	1.00E+00	1.07E-02	5.72E-01	3.26E-01	1.00E+00	1.84E-01	1.00E+00	5.32E-03	2.23E-01	1.88E-02	7.36E-01	leukocyte activation during immune respons	P
GO:0002367	10	8.51E-01	1.00E+00	9.26E-01	1.00E+00	8.80E-01	1.00E+00	9.98E-01	1.00E+00	6.99E-01	1.00E+00	6.57E-01	1.00E+00	6.79E-01	1.00E+00	6.56E-01	1.00E+00	cytokine production during immune respons	P
GO:0002376	859	4.00E-02	1.00E+00	3.05E-02	1.00E+00	7.07E-02	1.00E+00	1.28E-01	1.00E+00	8.60E-01	1.00E+00	1.93E-01	1.00E+00	1.27E-04	8.00E-03	6.85E-03	4.28E-01	immune system process	P
GO:0002377	43	1.53E-01	1.00E+00	1.28E-02	6.07E-01	4.95E-01	1.00E+00	3.24E-02	1.00E+00	4.06E-01	1.00E+00	3.19E-01	1.00E+00	3.72E-02	8.38E-01	2.52E-02	9.99E-01	immunoglobulin production	P
GO:0002381	27	2.13E-01	1.00E+00	5.40E-03	3.08E-01	5.25E-01	1.00E+00	2.15E-03	1.39E-01	3.02E-01	1.00E+00	4.28E-01	1.00E+00	1.59E-01	1.00E+00	3.75E-02	1.00E+00	immunoglobulin production during immune	P
GO:0002429	40	7.64E-01	1.00E+00	2.59E-01	1.00E+00	5.73E-01	1.00E+00	6.27E-01	1.00E+00	9.30E-01	1.00E+00	3.25E-02	1.00E+00	6.60E-01	1.00E+00	6.36E-01	1.00E+00	immune response-activating cell surface re	P
GO:0002437	66	9.65E-01	1.00E+00	7.92E-01	1.00E+00	7.91E-01	1.00E+00	4.87E-01	1.00E+00	9.98E-01	1.00E+00	8.14E-01	1.00E+00	7.66E-01	1.00E+00	8.00E-01	1.00E+00	inflammatory response to antigenic stimulus	P
GO:0002438	59	9.95E-01	1.00E+00	9.40E-01	1.00E+00	9.62E-01	1.00E+00	7.83E-01	1.00E+00	9.99E-01	1.00E+00	9.63E-01	1.00E+00	8.31E-01	1.00E+00	8.56E-01	1.00E+00	acute inflammatory response to antigenic st	P
GO:0002440	48	2.22E-01	1.00E+00	3.24E-02	1.00E+00	6.45E-01	1.00E+00	8.09E-02	1.00E+00	3.71E-01	1.00E+00	3.63E-01	1.00E+00	9.18E-02	1.00E+00	3.35E-02	1.00E+00	production of molecular mediator of immune	P
GO:0002443	172	4.88E-01	1.00E+00	6.14E-01	1.00E+00	6.40E-01	1.00E+00	2.18E-01	1.00E+00	9.25E-01	1.00E+00	8.74E-01	1.00E+00	6.65E-02	1.00E+00	6.45E-01	1.00E+00	leukocyte mediated immunity	P
GO:0002444	16	3.12E-01	1.00E+00	5.24E-01	1.00E+00	4.97E-01	1.00E+00	6.40E-01	1.00E+00	6.84E-01	1.00E+00	7.66E-01	1.00E+00	1.25E-01	1.00E+00	1.54E-01	1.00E+00	myeloid leukocyte mediated immunity	P
GO:0002449	162	6.19E-01	1.00E+00	6.31E-01	1.00E+00	7.13E-01	1.00E+00	1.91E-01	1.00E+00	9.20E-01	1.00E+00	8.58E-01	1.00E+00	1.87E-01	1.00E+00	7.57E-01	1.00E+00	lymphocyte mediated immunity	P
GO:0002455	34	5.72E-01	1.00E+00	8.61E-01	1.00E+00	7.54E-01	1.00E+00	5.96E-01	1.00E+00	8.73E-01	1.00E+00	9.98E-01	1.00E+00	2.39E-01	1.00E+00	4.82E-01	1.00E+00	humoral immune response mediated by circ	P
GO:0002456	18	2.03E-01	1.00E+00	8.63E-02	1.00E+00	4.83E-01	1.00E+00	2.01E-01	1.00E+00	1.97E-01	1.00E+00	4.56E-02	1.00E+00	1.21E-01	1.00E+00	2.05E-01	1.00E+00	T cell mediated immunity	P
GO:0002460	160	4.69E-01	1.00E+00	4.43E-01	1.00E+00	7.14E-01	1.00E+00	1.52E-01	1.00E+00	8.86E-01	1.00E+00	8.96E-01	1.00E+00	8.30E-02	1.00E+00	3.41E-01	1.00E+00	adaptive immune response (sensu Gnathos	P

GO:0002474	18	4.28E-01	1.00E+00	7.55E-01	1.00E+00	2.16E-02	1.00E+00	6.44E-01	1.00E+00	5.95E-01	1.00E+00	1.92E-01	1.00E+00	7.56E-01	1.00E+00	9.96E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0002478	18	2.65E-02	1.00E+00	1.49E-01	1.00E+00	1.11E-01	1.00E+00	1.81E-01	1.00E+00	1.71E-01	1.00E+00	7.71E-02	1.00E+00	1.36E-01	1.00E+00	7.20E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0002495	16	2.93E-02	1.00E+00	8.09E-02	1.00E+00	1.52E-01	1.00E+00	1.14E-01	1.00E+00	1.90E-01	1.00E+00	6.31E-02	1.00E+00	6.99E-02	1.00E+00	6.58E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0002504	18	8.65E-02	1.00E+00	1.40E-01	1.00E+00	2.61E-01	1.00E+00	2.04E-01	1.00E+00	1.95E-01	1.00E+00	7.57E-02	1.00E+00	1.75E-01	1.00E+00	7.02E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0002520	319	3.32E-04	3.10E-02	2.32E-03	1.71E-01	1.75E-04	1.16E-02	2.85E-03	1.61E-01	3.29E-01	1.00E+00	1.87E-01	1.00E+00	5.74E-05	8.00E-03	5.08E-03	2.01E-01	immune system development	P
GO:0002521	164	6.99E-02	1.00E+00	4.75E-02	1.00E+00	7.45E-02	1.00E+00	1.43E-01	1.00E+00	6.34E-01	1.00E+00	3.87E-01	1.00E+00	1.50E-02	4.78E-01	2.95E-02	9.99E-01	leukocyte differentiation	P
GO:0002524	59	9.95E-01	1.00E+00	9.40E-01	1.00E+00	9.62E-01	1.00E+00	7.83E-01	1.00E+00	9.99E-01	1.00E+00	9.63E-01	1.00E+00	8.31E-01	1.00E+00	8.56E-01	1.00E+00	hypersensitivity	P
GO:0002526	128	9.85E-01	1.00E+00	9.95E-01	1.00E+00	9.57E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.45E-01	1.00E+00	8.98E-01	1.00E+00	acute inflammatory response	P
GO:0002541	37	4.69E-01	1.00E+00	9.22E-01	1.00E+00	6.47E-01	1.00E+00	6.12E-01	1.00E+00	9.21E-01	1.00E+00	9.97E-01	1.00E+00	2.22E-01	1.00E+00	5.94E-01	1.00E+00	activation of plasma proteins during acute i	P
GO:0002562	28	2.24E-01	1.00E+00	2.21E-03	1.71E-01	4.26E-01	1.00E+00	3.86E-03	2.88E-01	3.51E-01	1.00E+00	2.21E-01	1.00E+00	1.50E-01	1.00E+00	1.51E-02	6.56E-01	somatic diversification of immune receptors	P
GO:0002573	54	1.62E-01	1.00E+00	5.54E-01	1.00E+00	1.17E-01	1.00E+00	4.21E-01	1.00E+00	4.45E-01	1.00E+00	6.01E-01	1.00E+00	1.76E-01	1.00E+00	9.05E-01	1.00E+00	myeloid leukocyte differentiation	P
GO:0002673	10	9.79E-01	1.00E+00	4.97E-01	1.00E+00	9.56E-01	1.00E+00	5.48E-01	1.00E+00	8.61E-01	1.00E+00	5.35E-01	1.00E+00	9.24E-01	1.00E+00	3.69E-01	1.00E+00	regulation of acute inflammatory response	P
GO:0002682	127	5.52E-01	1.00E+00	5.28E-01	1.00E+00	7.02E-01	1.00E+00	6.31E-01	1.00E+00	9.64E-01	1.00E+00	7.48E-01	1.00E+00	1.17E-01	1.00E+00	1.61E-01	1.00E+00	regulation of immune system process	P
GO:0002683	12	9.42E-02	1.00E+00	1.83E-01	1.00E+00	6.21E-02	1.00E+00	5.68E-02	1.00E+00	2.27E-01	1.00E+00	4.86E-01	1.00E+00	3.08E-01	1.00E+00	1.39E-01	1.00E+00	negative regulation of immune system proc	P
GO:0002684	108	6.19E-01	1.00E+00	7.26E-01	1.00E+00	7.97E-01	1.00E+00	8.17E-01	1.00E+00	9.68E-01	1.00E+00	6.79E-01	1.00E+00	1.99E-01	1.00E+00	5.55E-01	1.00E+00	positive regulation of immune system proce	P
GO:0002697	25	9.99E-01	1.00E+00	7.93E-01	1.00E+00	9.90E-01	1.00E+00	8.02E-01	1.00E+00	9.99E-01	1.00E+00	7.18E-01	1.00E+00	7.79E-01	1.00E+00	7.19E-01	1.00E+00	regulation of immune effector process	P
GO:0002699	21	1.00E+00	1.00E+00	9.15E-01	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	1.00E+00	1.00E+00	8.42E-01	1.00E+00	6.97E-01	1.00E+00	8.17E-01	1.00E+00	positive regulation of immune effector proce	P
GO:0002703	24	9.99E-01	1.00E+00	7.63E-01	1.00E+00	9.83E-01	1.00E+00	7.58E-01	1.00E+00	9.99E-01	1.00E+00	6.85E-01	1.00E+00	7.49E-01	1.00E+00	7.23E-01	1.00E+00	regulation of leukocyte mediated immunity	P
GO:0002705	20	1.00E+00	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	6.61E-01	1.00E+00	8.20E-01	1.00E+00	positive regulation of leukocyte mediated im	P
GO:0002706	24	9.99E-01	1.00E+00	7.63E-01	1.00E+00	9.83E-01	1.00E+00	7.58E-01	1.00E+00	9.99E-01	1.00E+00	6.85E-01	1.00E+00	7.49E-01	1.00E+00	7.23E-01	1.00E+00	regulation of lymphocyte mediated immunity	P
GO:0002708	20	1.00E+00	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	6.61E-01	1.00E+00	8.20E-01	1.00E+00	positive regulation of lymphocyte mediated	P
GO:0002712	14	9.93E-01	1.00E+00	9.34E-01	1.00E+00	8.53E-01	1.00E+00	7.95E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	8.51E-01	1.00E+00	7.84E-01	1.00E+00	regulation of B cell mediated immunity	P
GO:0002714	11	9.97E-01	1.00E+00	8.93E-01	1.00E+00	9.96E-01	1.00E+00	8.26E-01	1.00E+00	9.97E-01	1.00E+00	9.31E-01	1.00E+00	7.45E-01	1.00E+00	6.61E-01	1.00E+00	positive regulation of B cell mediated immu	P
GO:0002757	44	6.71E-01	1.00E+00	2.05E-01	1.00E+00	6.74E-01	1.00E+00	5.96E-01	1.00E+00	8.57E-01	1.00E+00	6.16E-02	1.00E+00	4.86E-01	1.00E+00	3.51E-01	1.00E+00	immune response-activating signal transdu	P
GO:0002761	24	2.87E-01	1.00E+00	5.08E-01	1.00E+00	1.91E-01	1.00E+00	5.04E-01	1.00E+00	3.67E-01	1.00E+00	3.90E-01	1.00E+00	4.76E-01	1.00E+00	8.99E-01	1.00E+00	regulation of myeloid leukocyte differentiatio	P
GO:0002762	10	5.31E-01	1.00E+00	6.93E-01	1.00E+00	3.78E-01	1.00E+00	7.56E-01	1.00E+00	5.92E-01	1.00E+00	7.00E-01	1.00E+00	5.73E-01	1.00E+00	6.54E-01	1.00E+00	negative regulation of myeloid leukocyte dif	P
GO:0002763	11	5.09E-01	1.00E+00	8.04E-01	1.00E+00	5.52E-01	1.00E+00	5.69E-01	1.00E+00	4.10E-01	1.00E+00	6.93E-01	1.00E+00	5.20E-01	1.00E+00	9.92E-01	1.00E+00	positive regulation of myeloid leukocyte diffe	P
GO:0002764	47	6.92E-01	1.00E+00	2.27E-01	1.00E+00	7.01E-01	1.00E+00	5.41E-01	1.00E+00	8.78E-01	1.00E+00	7.56E-02	1.00E+00	4.18E-01	1.00E+00	4.41E-01	1.00E+00	immune response-regulating signal transdu	P
GO:0002768	43	7.82E-01	1.00E+00	2.85E-01	1.00E+00	6.06E-01	1.00E+00	5.70E-01	1.00E+00	9.42E-01	1.00E+00	4.19E-02	1.00E+00	5.84E-01	1.00E+00	7.26E-01	1.00E+00	immune response-regulating cell surface re	P
GO:0002790	49	2.56E-01	1.00E+00	1.51E-01	1.00E+00	4.38E-01	1.00E+00	4.81E-01	1.00E+00	5.26E-01	1.00E+00	3.21E-01	1.00E+00	3.56E-02	8.38E-01	1.29E-02	4.76E-01	peptide secretion	P
GO:0002819	26	5.04E-01	1.00E+00	3.54E-01	1.00E+00	8.48E-01	1.00E+00	3.59E-01	1.00E+00	4.22E-01	1.00E+00	4.92E-01	1.00E+00	3.48E-01	1.00E+00	2.30E-01	1.00E+00	regulation of adaptive immune response	P
GO:0002821	20	5.98E-01	1.00E+00	5.09E-01	1.00E+00	9.51E-01	1.00E+00	5.34E-01	1.00E+00	5.65E-01	1.00E+00	5.75E-01	1.00E+00	2.69E-01	1.00E+00	3.75E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002822	26	5.04E-01	1.00E+00	3.54E-01	1.00E+00	8.48E-01	1.00E+00	3.59E-01	1.00E+00	4.22E-01	1.00E+00	4.92E-01	1.00E+00	3.48E-01	1.00E+00	2.30E-01	1.00E+00	regulation of adaptive immune response (se	P
GO:0002824	20	5.98E-01	1.00E+00	5.09E-01	1.00E+00	9.51E-01	1.00E+00	5.34E-01	1.00E+00	5.65E-01	1.00E+00	5.75E-01	1.00E+00	2.69E-01	1.00E+00	3.75E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002861	14	7.39E-01	1.00E+00	2.43E-01	1.00E+00	5.87E-01	1.00E+00	1.87E-01	1.00E+00	7.23E-01	1.00E+00	2.99E-01	1.00E+00	8.50E-01	1.00E+00	2.75E-01	1.00E+00	regulation of inflammatory response to antig	P
GO:0002863	10	9.90E-01	1.00E+00	4.98E-01	1.00E+00	9.95E-01	1.00E+00	4.93E-01	1.00E+00	8.97E-01	1.00E+00	4.76E-01	1.00E+00	9.08E-01	1.00E+00	5.02E-01	1.00E+00	positive regulation of inflammatory respons	P
GO:0002864	10	9.79E-01	1.00E+00	4.97E-01	1.00E+00	9.56E-01	1.00E+00	5.48E-01	1.00E+00	8.61E-01	1.00E+00	5.35E-01	1.00E+00	9.24E-01	1.00E+00	3.69E-01	1.00E+00	regulation of acute inflammatory response t	P
GO:0002883	10	9.79E-01	1.00E+00	4.97E-01	1.00E+00	9.56E-01	1.00E+00	5.48E-01	1.00E+00	8.61E-01	1.00E+00	5.35E-01	1.00E+00	9.24E-01	1.00E+00	3.69E-01	1.00E+00	regulation of hypersensitivity	P
GO:0002889	14	9.93E-01	1.00E+00	9.34E-01	1.00E+00	8.53E-01	1.00E+00	7.95E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	8.51E-01	1.00E+00	7.84E-01	1.00E+00	regulation of immunoglobulin mediated imm	P
GO:0002891	11	9.97E-01	1.00E+00	8.93E-01	1.00E+00	9.96E-01	1.00E+00	8.26E-01	1.00E+00	9.97E-01	1.00E+00	9.31E-01	1.00E+00	7.45E-01	1.00E+00	6.61E-01	1.00E+00	positive regulation of immunoglobulin media	P
GO:0003674	17517	5.36E-36	0.00E+00	0.00E+00	0.00E+00	8.06E-39	0.00E+00	0.00E+00	0.00E+00	1.10E-29	0.00E+00	0.00E+00	0.00E+00	2.97E-04	2.29E-02	8.15E-40	0.00E+00	molecular_function	F
GO:0003676	3584	1.22E-39	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.04E-27	0.00E+00	3.41E-30	0.00E+00	4.24E-05	8.00E-03	1.32E-08	0.00E+00	nucleic acid binding	F
GO:0003677	2339	6.52E-21	0.00E+00	1.72E-21	0.00E+00	3.07E-24	0.00E+00	5.41E-25	0.00E+00	7.43E-13	0.00E+00	2.81E-13	6.20E-04	3.46E-04	2.29E-02	3.14E-06	2.00E-03	DNA binding	F
GO:0003678	25	7.36E-03	3.15E-01	3.48E-05	7.00E-03	2.83E-03	1.35E-01	3.54E-04	4.20E-02	4.20E-02	1.00E+00	9.95E-05	1.10E-02	1.46E-01	1.00E+00	5.11E-02	1.00E+00	DNA helicase activity	F
GO:0003682	132	1.55E-06	2.76E-03	2.98E-07	3.92E-03	2.11E-06	2.00E-03	3.71E-07	2.89E-03	2.87E-03	2.13E-01	5.31E-04	3.20E-02	1.50E-03	6.14E-02	3.89E-04	3.00E-02	chromatin binding	F
GO:0003684	35	2.30E-01	1.00E+00	8.87E-03	4.69E-01	2.00E-01	1.00E+00	3.83E-03	2.88E-01	1.47E-01	1.00E+00	1.97E-01	1.00E+00	6.94E-01	1.00E+00	1.53E-02	6.56E-01	damaged DNA binding	F
GO:0003690	43	1.84E-02	1.00E+00	1.11E-01	1.00E+00	1.18E-02	6.53E-01	1.47E-01	1.00E+00	1.53E-01	1.00E+00	1.41E-01	1.00E+00	6.37E-02	1.00E+00	2.56E-01	1.00E+00	double-stranded DNA binding	F
GO:0003697	40	1.97E-04	1.72E-02	1.82E-04	1.80E-02	6.04E-05	9.82E-03	6.35E-05	1.30E-02	1.59E-02	6.92E-01	1.41E-02	6.68E-01	3.02E-02	8.38E-01	2.12E-01	1.00E+00	single-stranded DNA binding	F
GO:0003700	927	2.52E-03	2.12E-01	1.69E-02	7.63E-01	1.51E-02	6.53E-01	3.71E-02	1.00E+00	5.07E-02	1.00E+00	1.46E-01	1.00E+00	6.46E-03	2.75E-01	1.69E-02	6.56E-01	transcription factor activity	F
GO:0003702	100	2.09E-01	1.00E+00	1.57E-01	1.00E+00	1.10E-01	1.00E+00	7.77E-02	1.00E+00	6.48E-01	1.00E+00	2.67E-01	1.00E+00	2.93E-01	1.00E+00	7.23E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003705	28	9.98E-01	1.00E+00	9.34E-01	1.00E+00	9.96E-01	1.00E+00	9.39E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	6.70E-01	1.00E+00	6.98E-01	1.00E+00	RNA polymerase II transcription factor activ	F
GO:0003707	53	5.06E-01	1.00E+00	3.66E-01	1.00E+00	6.56E-01	1.00E+00	5.41E-01	1.00E+00	4.59E-01	1.00E+00	4.57E-01	1.00E+00	4.76E-01	1.00E+00	1.79E-01	1.00E+00	steroid hormone receptor activity	F
GO:0003708	25	8.33E-01	1.00E+00	5.31E-01	1.00E+00	4.26E-01	1.00E+00	3.42E-01	1.00E+00	8.04E-01	1.00E+00	6.83E-01	1.00E+00	9.40E-01	1.00E+00	6.51E-01	1.00E+00	retinoic acid receptor activity	F
GO:0003711	13	9.04E-04	8.86E-02	1.89E-01	1.00E+00	3.14E-02	1.00E+00	1.39E-01	1.00E+00	2.53E-02	1.00E+00	1.24E-01	1.00E+00	7.26E-03	2.75E-01	8.95E-01	1.00E+00	transcriptional elongation regulator activity	F
GO:0003712	172	1.92E-07	2.57E-03	2.56E-11	0.00E+00	8.73E-09	9.80E-04	2.63E-09	0.00E+00	7.14E-04	1.20E-01	4.44E-06	2.90E-03	6.24E-03	2.75E-01	9.96E-06	7.00E-03	transcription cofactor activity	F
GO:0003713	96	2.58E-04	1.90E-02	3.10E-08	9.59E-04	9.21E-06	2.91E-03	2.05E-06	2.89E-03	3.09E-03	2.13E-01	3.73E-05	9.66E-03	2.49E-01	1.00E+00	5.29E-04	3.00E-02	transcription coactivator activity	F
GO:0003714	64	3.80E-04	3.10E-02	2.77E-04	4.40E-02	1.36E-03	7.90E-02	1.41E-03	9.40E-02	2.78E-02	1.00E+00	9.38E-03	5.03E-01	9.02E-03	2.75E-01	5.30E-03	2.01E-01	transcription corepressor activity	F
GO:0003723	675	8.08E-35	0.00E+00	1.39E-35	0.00E+00	6.41E-32	0.00E+00	2.33E-33	0.00E+00	3.71E-21	0.00E+00	5.12E-20	0.00E+00	2.04E-11	0.00E+00	1.61E-10	0.00E+00	RNA binding	F
GO:0003725	37	1.20E-03	8.86E-02	8.47E-03	4.69E-01	2.04E-02	1.00E+00	3.60E-02	1.00E+00	1.38E-02	6.92E-01	6.97E-02	1.00E+00	1.83E-02	6.36E-01	1.15E-02	4.76E-01	double-stranded RNA binding	F
GO:0003727	20	1.33E-03	8.86E-02	1.84E-02	1.00E+00	1.04E-03	7.90E-02	1.22E-01	1.00E+00	1.60E-01	1.00E+00	9.34E-02	1.00E+00	4.34E-02	1.00E+00	2.41E-03	7.90E-02	single-stranded RNA binding	F
GO:0003729	45	5.89E-02	1.00E+00	1.34E-02	6.07E-01	3.32E-02	1.00E+00	4.62E-03	2.88E-01	1.15E-01	1.00E+00	4.47E-02	1.00E+00	3.45E-01	1.00E+00	4.68E-01	1.00E+00	mRNA binding	F
GO:0003735	453	3.27E-09	2.57E-03	1.36E-02	6.07E-01	2.16E-09	9.80E-04	1.72E-02	6.47E-01	4.14E-07	9.59E-04	7.08E-03	4.21E-01	1.77E-03	8.40E-02	2.42E-01	1.00E+00	structural constituent of ribosome	F
GO:0003743	89	6.18E-07	2.76E-03	1.47E-10	0.00E+00	2.41E-10	7.95E-04	1.15E-07	2.89E-03	3.77E-04	4.90E-02	1.00E-08	8.78E-04	2.65E-02	8.38E-01	1.31E-03	6.00E-02	translation initiation factor activity	F
GO:0003746	37	1.46E-01	1.00E+00	2.44E-02	1.00E+00	5.27E-02	1.00E+00	5.01E-02	1.00E+00	1.81E-01	1.00E+00	6.90E-02	1.00E+00	6.18E-01	1.00E+00	6.39E-02	1.00E+00	translation elongation factor activity	F
GO:0003755	38	8.39E-05	1.43E-02	4.11E-03	1.88E-01	8.61E-03	6.53E-01	2.24E-03	1.39E-01	3.53E-04	4.90E-02	1.56E-01	1.00E+00	9.14E-04	3.44E-02	4.83E-02	1.00E+00	peptidyl-prolyl cis-trans isomerase activity	F
GO:0003774	167	6.42E-04	8.86E-02	5.60E-05	7.00E-03	3.33E-03	2.03E-01	3.12E-03	1.61E-01	6.15E-02	1.00E+00	9.58E-03	5.03E-01	4.01E-04	2.40E-02	9.00E-05	1.60E-02	motor activity	F
GO:0003777	81	2.15E-03	2.12E-01	9.67E-04	8.70E-02	4.09E-04	4.00E-02	4.49E-03	2.88E-01	7.28E-02	1.00E+00	9.17E-03	5.03E-01	1.90E-02	6.36E-01	1.91E-02	7.36E-01	microtubule motor activity	F
GO:0003779	309	2.33E-06	3.00E-03	3.86E-11	0.00E+00	1.88E-02	1.00E+00	2.69E-05	9.57E-03	2.57E-03	1.29E-01	1.41E-05	5.87E-03	9.26E-08	0.00E+00	3.01E-11	0.00E+00	actin binding	F
GO:0003796	11	4.88E-01	1.00E+00	6.20E-01	1.00E+00	8.02E-01	1.00E+00	8.97E-01	1.00E+00	2.45E-01	1.00E+00	6.84E-02	1.00E+00	8.01E-01	1.00E+00	9.68E-01	1.00E+00	lysozyme activity	F
GO:0003810	11	9.98E-01	1.00E+00	6.89E-01	1.00E+00	9.92E-01	1.00E+00	8.87E-01	1.00E+00	9.25E-01	1.00E+00	2.24E-01	1.00E+00	9.52E-01	1.00E+00	8.80E-01	1.00E+00	protein-glutamine gamma-glutamyltransfera	F
GO:0003823	54	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen binding	F
GO:0003824	5977	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.24E-42	0.00E+00	0.00E+00	0.00E+00	3.64E-33	0.00E+00	0.00E+00	0.00E+00	2.30E-12	0.00E+00	1.48E-37	0.00E+00	catalytic activity	F
GO:0003854	20	7.70E-01	1.00E+00	8.41E-01	1.00E+00	9.90E-01	1.00E+00	5.73E-01	1.00E+00	2.50E-01	1.00E+00	7.71E-01	1.00E+00	7.48E-01	1.00E+00	8.18E-01	1.00E+00	3-beta-hydroxy-delta5-steroid dehydrogena	F
GO:0003887	32	1.84E-02	1.00E+00	2.16E-01	1.00E+00	1.15E-02	6.53E-01	8.34E-02	1.00E+00	4.57E-02	1.00E+00	4.48E-01	1.00E+00	1.38E-01	1.00E+00	5.87E-01	1.00E+00	DNA-directed DNA polymerase activity	F
GO:0003899	39	6.76E-06	3.62E-03	9.35E-05	1.50E-02	1.89E-09	9.80E-04	1.87E-06	2.89E-03	6.49E-04	1.20E-01	9.23E-03	5.03E-01	1.14E-01	1.00E+00	5.37E-02	1.00E+00	DNA-directed RNA polymerase activity	F

GO:0003916	21	6.50E-02	1.00E+00	7.29E-02	1.00E+00	1.47E-02	6.53E-01	8.35E-02	1.00E+00	4.90E-02	1.00E+00	2.21E-01	1.00E+00	9.93E-01	1.00E+00	1.83E-01	1.00E+00	DNA topoisomerase activity	F
GO:0003918	17	6.82E-02	1.00E+00	3.04E-02	1.00E+00	1.78E-02	1.00E+00	1.37E-01	1.00E+00	7.63E-02	1.00E+00	1.83E-01	1.00E+00	9.61E-01	1.00E+00	3.56E-02	1.00E+00	DNA topoisomerase (ATP-hydrolyzing) activ	F
GO:0003924	241	1.33E-03	8.86E-02	3.93E-06	4.51E-03	1.99E-03	9.50E-02	4.31E-04	4.20E-02	1.50E-03	1.20E-01	5.67E-05	9.66E-03	8.19E-02	1.00E+00	2.32E-04	2.33E-02	GTPase activity	F
GO:0003950	19	4.84E-04	4.40E-02	7.14E-03	3.12E-01	1.37E-02	6.53E-01	1.39E-02	6.47E-01	3.56E-03	2.13E-01	2.48E-03	1.27E-01	5.23E-02	1.00E+00	3.21E-01	1.00E+00	NAD+ ADP-ribosyltransferase activity	F
GO:0003954	45	9.45E-02	1.00E+00	3.41E-01	1.00E+00	1.58E-01	1.00E+00	5.05E-01	1.00E+00	1.48E-01	1.00E+00	2.78E-01	1.00E+00	2.71E-01	1.00E+00	4.47E-01	1.00E+00	NADH dehydrogenase activity	F
GO:0003993	16	1.75E-01	1.00E+00	2.98E-02	1.00E+00	2.55E-01	1.00E+00	1.27E-02	6.47E-01	1.60E-01	1.00E+00	1.19E-01	1.00E+00	1.94E-01	1.00E+00	1.10E-01	1.00E+00	acid phosphatase activity	F
GO:0003995	17	1.59E-02	1.00E+00	4.54E-02	1.00E+00	5.83E-02	1.00E+00	7.82E-02	1.00E+00	1.99E-02	7.90E-01	4.74E-02	1.00E+00	2.35E-01	1.00E+00	2.94E-01	1.00E+00	acyl-CoA dehydrogenase activity	F
GO:0004003	14	4.32E-02	1.00E+00	9.56E-04	8.70E-02	4.24E-02	1.00E+00	4.49E-02	1.00E+00	3.44E-02	1.00E+00	1.71E-04	2.33E-02	2.53E-01	1.00E+00	1.59E-01	1.00E+00	ATP-dependent DNA helicase activity	F
GO:0004012	16	9.81E-01	1.00E+00	6.80E-01	1.00E+00	8.54E-01	1.00E+00	5.51E-01	1.00E+00	1.00E+00	1.00E+00	5.68E-01	1.00E+00	8.80E-01	1.00E+00	8.71E-01	1.00E+00	phospholipid-translocating ATPase activity	F
GO:0004016	11	5.43E-01	1.00E+00	2.53E-01	1.00E+00	8.45E-01	1.00E+00	6.01E-01	1.00E+00	4.79E-01	1.00E+00	2.39E-01	1.00E+00	4.08E-01	1.00E+00	1.59E-01	1.00E+00	adenylate cyclase activity	F
GO:0004022	35	8.94E-01	1.00E+00	5.11E-01	1.00E+00	8.21E-01	1.00E+00	8.28E-01	1.00E+00	8.67E-01	1.00E+00	2.53E-01	1.00E+00	6.23E-01	1.00E+00	2.99E-01	1.00E+00	alcohol dehydrogenase activity	F
GO:0004033	11	1.62E-01	1.00E+00	4.17E-01	1.00E+00	2.92E-01	1.00E+00	5.50E-01	1.00E+00	4.29E-02	1.00E+00	1.76E-01	1.00E+00	5.26E-01	1.00E+00	8.11E-01	1.00E+00	aldo-keto reductase activity	F
GO:0004089	19	5.21E-01	1.00E+00	3.68E-01	1.00E+00	4.90E-01	1.00E+00	8.12E-01	1.00E+00	3.32E-01	1.00E+00	1.87E-01	1.00E+00	9.65E-01	1.00E+00	3.40E-01	1.00E+00	carbonate dehydratase activity	F
GO:0004091	37	9.79E-01	1.00E+00	7.48E-01	1.00E+00	9.46E-01	1.00E+00	6.87E-01	1.00E+00	9.11E-01	1.00E+00	7.21E-01	1.00E+00	9.69E-01	1.00E+00	5.12E-01	1.00E+00	carboxylesterase activity	F
GO:0004104	18	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	8.24E-01	1.00E+00	cholinesterase activity	F
GO:0004112	27	9.60E-01	1.00E+00	8.91E-01	1.00E+00	9.20E-01	1.00E+00	8.98E-01	1.00E+00	9.76E-01	1.00E+00	9.66E-01	1.00E+00	9.74E-01	1.00E+00	6.62E-01	1.00E+00	cyclic-nucleotide phosphodiesterase activity	F
GO:0004114	25	9.86E-01	1.00E+00	9.74E-01	1.00E+00	9.66E-01	1.00E+00	9.79E-01	1.00E+00	9.97E-01	1.00E+00	9.78E-01	1.00E+00	9.66E-01	1.00E+00	8.38E-01	1.00E+00	3',5'-cyclic-nucleotide phosphodiesterase a	F
GO:0004129	30	1.65E-01	1.00E+00	2.39E-01	1.00E+00	8.87E-02	1.00E+00	5.95E-02	1.00E+00	2.03E-01	1.00E+00	2.69E-01	1.00E+00	5.78E-01	1.00E+00	6.57E-01	1.00E+00	cytochrome-c oxidase activity	F
GO:0004143	15	2.93E-01	1.00E+00	7.91E-01	1.00E+00	3.31E-01	1.00E+00	5.75E-01	1.00E+00	6.26E-01	1.00E+00	9.83E-01	1.00E+00	1.84E-01	1.00E+00	4.30E-01	1.00E+00	diacylglycerol kinase activity	F
GO:0004175	511	4.76E-01	1.00E+00	2.05E-01	1.00E+00	7.98E-01	1.00E+00	3.08E-01	1.00E+00	4.19E-01	1.00E+00	4.46E-01	1.00E+00	2.63E-01	1.00E+00	2.13E-02	9.99E-01	endopeptidase activity	F
GO:0004176	17	2.70E-01	1.00E+00	4.97E-01	1.00E+00	4.14E-01	1.00E+00	4.22E-01	1.00E+00	2.13E-01	1.00E+00	4.71E-01	1.00E+00	3.50E-01	1.00E+00	3.67E-01	1.00E+00	ATP-dependent peptidase activity	F
GO:0004177	42	1.90E-01	1.00E+00	1.08E-01	1.00E+00	4.58E-02	1.00E+00	3.09E-01	1.00E+00	1.70E-01	1.00E+00	4.30E-02	1.00E+00	7.82E-01	1.00E+00	2.93E-01	1.00E+00	aminopeptidase activity	F
GO:0004179	12	6.85E-01	1.00E+00	3.04E-01	1.00E+00	3.38E-01	1.00E+00	4.29E-01	1.00E+00	7.26E-01	1.00E+00	3.24E-01	1.00E+00	8.29E-01	1.00E+00	1.54E-01	1.00E+00	membrane alanyl aminopeptidase activity	F
GO:0004180	47	8.32E-01	1.00E+00	8.12E-01	1.00E+00	4.11E-01	1.00E+00	6.00E-01	1.00E+00	9.66E-01	1.00E+00	9.33E-01	1.00E+00	5.23E-01	1.00E+00	4.85E-01	1.00E+00	carboxypeptidase activity	F
GO:0004181	33	8.06E-01	1.00E+00	5.70E-01	1.00E+00	7.62E-01	1.00E+00	5.32E-01	1.00E+00	9.65E-01	1.00E+00	6.34E-01	1.00E+00	2.05E-01	1.00E+00	2.43E-01	1.00E+00	metallocarboxypeptidase activity	F
GO:0004182	30	8.15E-01	1.00E+00	5.73E-01	1.00E+00	8.02E-01	1.00E+00	6.87E-01	1.00E+00	9.85E-01	1.00E+00	5.36E-01	1.00E+00	1.60E-01	1.00E+00	2.14E-01	1.00E+00	carboxypeptidase A activity	F
GO:0004190	33	2.13E-01	1.00E+00	9.87E-02	1.00E+00	3.20E-01	1.00E+00	3.58E-01	1.00E+00	6.25E-02	1.00E+00	3.02E-01	1.00E+00	4.58E-01	1.00E+00	3.01E-02	9.99E-01	aspartic-type endopeptidase activity	F
GO:0004197	97	2.28E-01	1.00E+00	7.58E-02	1.00E+00	3.13E-01	1.00E+00	6.77E-02	1.00E+00	3.45E-01	1.00E+00	3.18E-01	1.00E+00	2.27E-01	1.00E+00	5.21E-02	1.00E+00	cysteine-type endopeptidase activity	F
GO:0004198	16	4.10E-01	1.00E+00	1.85E-01	1.00E+00	6.19E-01	1.00E+00	3.88E-01	1.00E+00	6.01E-01	1.00E+00	1.92E-01	1.00E+00	1.01E-01	1.00E+00	2.60E-01	1.00E+00	calpain activity	F
GO:0004221	67	3.65E-02	1.00E+00	5.97E-05	7.00E-03	3.39E-03	2.03E-01	1.01E-05	2.89E-03	1.08E-01	1.00E+00	9.49E-03	5.03E-01	7.20E-01	1.00E+00	2.46E-03	7.90E-02	ubiquitin thiolesterase activity	F
GO:0004222	119	7.08E-01	1.00E+00	8.09E-01	1.00E+00	9.74E-01	1.00E+00	8.07E-01	1.00E+00	6.53E-01	1.00E+00	7.58E-01	1.00E+00	1.81E-01	1.00E+00	5.98E-01	1.00E+00	metalloendopeptidase activity	F
GO:0004252	233	6.93E-01	1.00E+00	4.46E-01	1.00E+00	8.88E-01	1.00E+00	5.66E-01	1.00E+00	6.72E-01	1.00E+00	5.74E-01	1.00E+00	4.47E-01	1.00E+00	7.05E-02	1.00E+00	serine-type endopeptidase activity	F
GO:0004263	15	7.38E-01	1.00E+00	4.18E-01	1.00E+00	8.50E-01	1.00E+00	6.13E-01	1.00E+00	3.11E-01	1.00E+00	2.51E-01	1.00E+00	8.55E-01	1.00E+00	3.48E-01	1.00E+00	chymotrypsin activity	F
GO:0004289	21	9.13E-01	1.00E+00	7.05E-01	1.00E+00	7.77E-01	1.00E+00	8.36E-01	1.00E+00	9.78E-01	1.00E+00	8.66E-01	1.00E+00	8.75E-01	1.00E+00	4.81E-01	1.00E+00	subtilase activity	F
GO:0004293	13	1.00E+00	1.00E+00	3.17E-02	1.00E+00	1.00E+00	1.00E+00	1.38E-10	0.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.26E-04	3.44E-02	2.62E-03	8.32E-02	tissue kallikrein activity	F
GO:0004295	19	9.53E-01	1.00E+00	7.24E-01	1.00E+00	9.64E-01	1.00E+00	7.66E-01	1.00E+00	6.63E-01	1.00E+00	5.56E-01	1.00E+00	9.13E-01	1.00E+00	5.55E-01	1.00E+00	trypsin activity	F
GO:0004298	22	2.97E-01	1.00E+00	2.04E-01	1.00E+00	8.71E-02	1.00E+00	1.74E-01	1.00E+00	6.50E-01	1.00E+00	2.51E-02	1.00E+00	7.06E-01	1.00E+00	8.92E-01	1.00E+00	threonine endopeptidase activity	F
GO:0004303	10	2.01E-01	1.00E+00	1.61E-01	1.00E+00	4.47E-01	1.00E+00	4.10E-01	1.00E+00	1.78E-01	1.00E+00	2.15E-01	1.00E+00	1.35E-01	1.00E+00	4.16E-02	1.00E+00	estradiol 17-beta-dehydrogenase activity	F
GO:0004364	29	6.80E-01	1.00E+00	8.33E-01	1.00E+00	4.72E-01	1.00E+00	9.71E-01	1.00E+00	3.77E-01	1.00E+00	8.70E-02	1.00E+00	9.83E-01	1.00E+00	9.83E-01	1.00E+00	glutathione transferase activity	F
GO:0004365	30	9.82E-01	1.00E+00	8.65E-01	1.00E+00	8.79E-01	1.00E+00	9.74E-01	1.00E+00	9.99E-01	1.00E+00	4.98E-01	1.00E+00	8.81E-01	1.00E+00	7.42E-01	1.00E+00	glyceraldehyde-3-phosphate dehydrogenas	F
GO:0004383	11	2.37E-01	1.00E+00	5.99E-01	1.00E+00	7.45E-01	1.00E+00	4.87E-01	1.00E+00	1.16E-01	1.00E+00	8.29E-01	1.00E+00	2.61E-02	8.38E-01	4.90E-01	1.00E+00	guanylate cyclase activity	F
GO:0004386	145	3.57E-09	2.57E-03	3.86E-11	0.00E+00	1.51E-09	9.80E-04	1.68E-11	0.00E+00	7.21E-05	2.40E-02	4.57E-07	1.65E-03	6.84E-02	1.00E+00	1.90E-04	1.60E-02	helicase activity	F
GO:0004396	10	3.80E-03	2.12E-01	8.92E-04	8.70E-02	1.19E-01	1.00E+00	4.74E-02	1.00E+00	1.70E-02	6.92E-01	1.39E-02	6.68E-01	2.53E-03	8.40E-02	1.60E-01	1.00E+00	hexokinase activity	F
GO:0004402	21	2.14E-02	1.00E+00	4.05E-04	4.74E-02	7.33E-02	1.00E+00	6.28E-04	4.20E-02	8.93E-02	1.00E+00	7.77E-03	4.21E-01	4.18E-01	1.00E+00	4.48E-03	2.01E-01	histone acetyltransferase activity	F
GO:0004407	19	1.64E-02	1.00E+00	2.10E-02	1.00E+00	6.81E-02	1.00E+00	1.55E-02	6.47E-01	2.69E-02	1.00E+00	2.10E-01	1.00E+00	5.94E-02	1.00E+00	2.01E-01	1.00E+00	histone deacetylase activity	F
GO:0004428	35	3.32E-03	2.12E-01	1.43E-03	9.65E-02	4.83E-02	1.00E+00	2.64E-03	1.61E-01	1.35E-02	6.92E-01	1.50E-02	6.68E-01	1.53E-02	4.88E-01	8.78E-03	4.28E-01	inositol or phosphatidylinositol kinase activit	F
GO:0004434	16	4.15E-01	1.00E+00	2.24E-01	1.00E+00	6.40E-01	1.00E+00	5.64E-01	1.00E+00	2.82E-01	1.00E+00	2.99E-01	1.00E+00	6.22E-01	1.00E+00	1.25E-01	1.00E+00	inositol or phosphatidylinositol phosphodies	F
GO:0004435	16	4.15E-01	1.00E+00	2.24E-01	1.00E+00	6.40E-01	1.00E+00	5.64E-01	1.00E+00	2.82E-01	1.00E+00	2.99E-01	1.00E+00	6.22E-01	1.00E+00	1.25E-01	1.00E+00	phosphoinositide phospholipase C activity	F
GO:0004437	34	1.21E-01	1.00E+00	5.07E-02	1.00E+00	1.45E-01	1.00E+00	4.37E-02	1.00E+00	1.08E-01	1.00E+00	1.09E-01	1.00E+00	5.90E-01	1.00E+00	1.21E-01	1.00E+00	inositol or phosphatidylinositol phosphatase	F
GO:0004467	13	1.37E-01	1.00E+00	2.46E-02	1.00E+00	2.14E-01	1.00E+00	4.90E-02	1.00E+00	3.90E-01	1.00E+00	2.40E-01	1.00E+00	1.98E-02	6.36E-01	6.40E-02	1.00E+00	long-chain-fatty-acid-CoA ligase activity	F
GO:0004468	21	2.14E-02	1.00E+00	4.05E-04	4.74E-02	7.33E-02	1.00E+00	6.28E-04	4.20E-02	8.93E-02	1.00E+00	7.77E-03	4.21E-01	4.18E-01	1.00E+00	4.48E-03	2.01E-01	lysine N-acetyltransferase activity	F
GO:0004497	177	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.66E-01	1.00E+00	monooxygenase activity	F
GO:0004499	23	9.30E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.07E-01	1.00E+00	6.23E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	9.88E-01	1.00E+00	dimethylaniline monooxygenase (N-oxide-fo	F
GO:0004518	162	2.06E-03	2.12E-01	3.46E-04	4.40E-02	6.85E-03	4.69E-01	1.29E-02	6.47E-01	3.74E-03	2.13E-01	9.27E-03	5.03E-01	2.89E-01	1.00E+00	6.92E-04	6.00E-02	nuclease activity	F
GO:0004519	104	9.52E-03	6.08E-01	2.46E-02	1.00E+00	2.03E-02	1.00E+00	1.54E-01	1.00E+00	1.53E-02	6.92E-01	6.54E-02	1.00E+00	2.49E-01	1.00E+00	2.02E-02	7.36E-01	endonuclease activity	F
GO:0004520	15	3.15E-01	1.00E+00	1.29E-01	1.00E+00	3.28E-01	1.00E+00	7.51E-02	1.00E+00	8.78E-01	1.00E+00	7.19E-01	1.00E+00	1.23E-01	1.00E+00	1.05E-01	1.00E+00	endodeoxyribonuclease activity	F
GO:0004521	47	2.61E-01	1.00E+00	4.53E-01	1.00E+00	7.82E-01	1.00E+00	9.55E-01	1.00E+00	1.32E-01	1.00E+00	2.38E-01	1.00E+00	2.67E-01	1.00E+00	1.65E-01	1.00E+00	endoribonuclease activity	F
GO:0004522	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	7.36E-01	1.00E+00	9.75E-01	1.00E+00	9.92E-01	1.00E+00	pancreatic ribonuclease activity	F
GO:0004526	11	1.33E-01	1.00E+00	6.52E-02	1.00E+00	4.97E-01	1.00E+00	2.77E-01	1.00E+00	1.50E-01	1.00E+00	2.42E-01	1.00E+00	1.75E-01	1.00E+00	2.21E-02	9.99E-01	ribonuclease P activity	F
GO:0004527	55	1.55E-01	1.00E+00	2.99E-03	1.88E-01	1.81E-01	1.00E+00	2.72E-02	1.00E+00	2.43E-01	1.00E+00	1.66E-02	6.68E-01	5.97E-01	1.00E+00	4.10E-03	2.01E-01	exonuclease activity	F
GO:0004532	13	1.10E-01	1.00E+00	8.64E-02	1.00E+00	5.42E-02	1.00E+00	2.49E-01	1.00E+00	2.50E-01	1.00E+00	2.71E-02	1.00E+00	5.10E-01	1.00E+00	1.93E-01	1.00E+00	exoribonuclease activity	F
GO:0004536	26	3.81E-01	1.00E+00	3.97E-02	1.00E+00	3.85E-01	1.00E+00	1.30E-02	6.47E-01	4.50E-01	1.00E+00	5.43E-01	1.00E+00	6.46E-01	1.00E+00	1.18E-01	1.00E+00	deoxyribonuclease activity	F
GO:0004540	66	1.56E-01	1.00E+00	8.49E-02	1.00E+00	4.19E-01	1.00E+00	7.38E-01	1.00E+00	1.48E-01	1.00E+00	1.88E-02	6.68E-01	3.04E-01	1.00E+00	4.39E-02	1.00E+00	ribonuclease activity	F
GO:0004549	14	5.43E-02	1.00E+00	5.83E-02	1.00E+00	2.48E-01	1.00E+00	4.94E-01	1.00E+00	9.24E-02	1.00E+00	1.43E-01	1.00E+00	1.32E-01	1.00E+00	4.14E-02	1.00E+00	tRNA-specific ribonuclease activity	F
GO:0004550	12	6.11E-02	1.00E+00	2.24E-03	1.71E-01	1.03E-01	1.00E+00	3.15E-02	1.00E+00	1.82E-02	7.90E-01	3.47E-03	1.51E-01	5.60E-01	1.00E+00	8.52E-02	1.00E+00	nucleoside diphosphate kinase activity	F
GO:0004553	113	6.87E-02	1.00E+00	1.86E-01	1.00E+00	3.21E-02	1.00E+00	5.40E-01	1.00E+00	3.43E-02	1.00E+00	3.71E-02	1.00E+00	4.95E-01	1.00E+00	3.74E-01	1.00E+00	hydrolase activity, hydrolyzing O-glycosyl co	F
GO:0004568	10	9.17E-01	1.00E+00	9.67E-01	1.00E+00	9.78E-01	1.00E+00	8.76E-01	1.00E+00	5.79E-01	1.00E+00	9.75E-01	1.00E+00	9.85E-01	1.00E+00	9.38E-01	1.00E+00	chitinase activity	F
GO:0004601	50	3.52E-02	1.00E+00	1.16E-01	1.00E+00	7.08E-02	1.00E+00	1.02E-01	1.00E+00	1.92E-01	1.00E+00	2.13E-01	1.00E+00	1.59E-02	4.88E-01	2.48E-01	1.00E+00	peroxidase activity	F
GO:0004602	10	1.20E-01	1.00E+00	2.55E-01	1.00E+00	2.54E-01	1.00E+00	1.85E-01	1.00E+00	1.65E-01	1.00E+00	4.04E-01	1.00E+00	7.86E-02	1.00E+00	3.32E-01	1.00E+00	glutathione peroxidase activity	F
GO:0004620	59	5.32E-02	1.00E+00	1.50E-02	7.63E-01	2.21E-01	1.00E+00	4.86E-01	1.00E+00	4.74E-02	1.00E+00	1.32E-01	1.00E+00	1.25E-01	1.00E+00	7.80E-03	4.28E-01	phospholipase activity	F
GO:0004623	29	8.99E-02	1.00E+00	1.74E-01	1.00E+00	3.83E-01	1.00E+00	7.35E-01	1.00E+00	9.14E-02	1.00E+00	1.62E-01	1.00E+00	1.00E-01	1.00E+00	1.41E-01	1.00E+00	phospholipase A2 activity	F
GO:0004629	20	4.35E-01	1.00E+00	3.73E-01	1.00E+00	6.46E-01	1.00E+00	5.82E-01	1.00E+00	2.86E-01	1.00E+00	5.13E-01	1.00E+00	6.14E-01	1.00E+00	2.43E-01	1.00E+00	phospholipase C activity	F
GO:0004653	15	9.75E-01	1.00E+00	6.14E-01	1.00E+00	9.94E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	8.57E-01	1.00E+00	4.41E-01	1.00E+00	4.12E-02	1.00E+00	polypeptide N-acetylgalactosaminyltransfer	F
GO:0004659	20	6.84E-02	1.00E+00	2.32E-01	1.00E+00	9.68E-02	1.00E+00	4.63E-01	1.00E+00	1.28E-01	1.00E+00	2.02E-01	1.00E+00	2.96E-01	1.00E+00	2.32E-01	1.00E+00	prenyltransferase activity	F
GO:0004672	688	1.37E-04	1.43E-02	1.59E-12	0.00E+00	3.52E-05	9.82E-03	4.51E-09	8.93E-04	1.87E-03	1.20E-01	1.25E-07	1.65E-03	1.23E-01	1.00E+00	1.65E-08	0.00E+00	protein kinase activity	F

GO:0004673	30	6.50E-01	1.00E+00	5.25E-01	1.00E+00	8.19E-01	1.00E+00	5.37E-01	1.00E+00	4.53E-01	1.00E+00	6.59E-01	1.00E+00	6.76E-01	1.00E+00	1.93E-01	1.00E+00	protein histidine kinase activity	F
GO:0004674	562	2.22E-07	2.57E-03	6.51E-18	0.00E+00	1.80E-08	9.80E-04	1.56E-13	0.00E+00	3.43E-05	6.33E-03	1.01E-10	6.20E-04	7.49E-02	1.00E+00	2.82E-10	0.00E+00	protein serine/threonine kinase activity	F
GO:0004675	13	1.38E-01	1.00E+00	1.75E-01	1.00E+00	8.11E-02	1.00E+00	2.53E-01	1.00E+00	2.42E-01	1.00E+00	1.02E-01	1.00E+00	7.38E-01	1.00E+00	3.58E-01	1.00E+00	transmembrane receptor protein serine/thre	F
GO:0004683	22	1.60E-01	1.00E+00	1.41E-02	6.07E-01	1.52E-01	1.00E+00	7.77E-02	1.00E+00	2.89E-01	1.00E+00	4.65E-02	1.00E+00	1.34E-01	1.00E+00	2.79E-02	9.99E-01	calmodulin regulated protein kinase activity	F
GO:0004689	15	5.34E-01	1.00E+00	3.77E-02	1.00E+00	5.92E-01	1.00E+00	2.13E-01	1.00E+00	5.99E-01	1.00E+00	2.20E-02	1.00E+00	4.89E-01	1.00E+00	6.90E-02	1.00E+00	phosphorylase kinase activity	F
GO:0004693	31	4.41E-03	2.14E-01	1.18E-04	1.50E-02	3.76E-04	4.00E-02	5.01E-06	2.89E-03	6.34E-02	1.00E+00	2.51E-02	1.00E+00	3.61E-01	1.00E+00	1.90E-02	7.36E-01	cyclin-dependent protein kinase activity	F
GO:0004697	15	4.66E-01	1.00E+00	2.28E-01	1.00E+00	2.42E-01	1.00E+00	2.39E-01	1.00E+00	6.81E-01	1.00E+00	1.71E-01	1.00E+00	4.10E-01	1.00E+00	6.31E-01	1.00E+00	protein kinase C activity	F
GO:0004702	55	2.63E-03	2.12E-01	1.31E-03	9.65E-02	1.44E-03	7.90E-02	1.21E-02	6.47E-01	7.22E-03	6.92E-01	3.89E-03	1.84E-01	3.24E-01	1.00E+00	9.52E-02	1.00E+00	receptor signaling protein serine/threonine k	F
GO:0004707	18	1.65E-02	1.00E+00	1.23E-04	1.50E-02	1.21E-02	6.53E-01	2.86E-05	9.57E-03	1.06E-02	6.92E-01	2.58E-02	1.00E+00	5.73E-01	1.00E+00	1.04E-01	1.00E+00	MAP kinase activity	F
GO:0004709	17	1.23E-01	1.00E+00	4.37E-01	1.00E+00	2.84E-01	1.00E+00	9.92E-01	1.00E+00	1.24E-01	1.00E+00	2.04E-01	1.00E+00	2.10E-01	1.00E+00	2.74E-01	1.00E+00	MAP kinase kinase kinase activity	F
GO:0004712	10	3.87E-01	1.00E+00	3.23E-01	1.00E+00	5.27E-01	1.00E+00	5.16E-01	1.00E+00	4.93E-01	1.00E+00	2.24E-01	1.00E+00	1.72E-01	1.00E+00	4.37E-01	1.00E+00	protein threonine/tyrosine kinase activity	F
GO:0004713	570	3.23E-04	3.10E-02	1.05E-12	0.00E+00	4.09E-05	9.82E-03	2.72E-08	8.93E-04	4.88E-03	3.75E-01	5.61E-08	1.65E-03	1.63E-01	1.00E+00	5.31E-10	0.00E+00	protein-tyrosine kinase activity	F
GO:0004714	111	9.73E-01	1.00E+00	8.41E-01	1.00E+00	9.72E-01	1.00E+00	9.93E-01	1.00E+00	8.89E-01	1.00E+00	8.66E-01	1.00E+00	7.62E-01	1.00E+00	8.06E-02	1.00E+00	transmembrane receptor protein tyrosine ki	F
GO:0004715	38	3.50E-01	1.00E+00	1.11E-03	9.65E-02	4.34E-01	1.00E+00	2.09E-02	9.37E-01	2.23E-01	1.00E+00	7.58E-03	4.21E-01	6.28E-01	1.00E+00	6.15E-04	3.00E-02	non-membrane spanning protein tyrosine ki	F
GO:0004721	161	4.71E-04	4.40E-02	3.49E-05	7.00E-03	8.17E-04	4.90E-02	1.98E-04	1.30E-02	4.30E-02	1.00E+00	1.01E-02	5.03E-01	6.26E-04	3.44E-02	8.67E-04	6.00E-02	phosphoprotein phosphatase activity	F
GO:0004722	37	8.77E-03	6.08E-01	6.24E-05	7.00E-03	1.26E-03	7.90E-02	1.57E-04	1.30E-02	1.10E-01	1.00E+00	4.43E-03	2.66E-01	1.79E-01	1.00E+00	1.17E-02	4.76E-01	protein serine/threonine phosphatase activit	F
GO:0004725	112	3.68E-02	1.00E+00	9.64E-03	4.69E-01	6.50E-02	1.00E+00	4.33E-02	1.00E+00	3.05E-01	1.00E+00	5.93E-02	1.00E+00	5.06E-03	2.23E-01	2.82E-02	9.99E-01	protein tyrosine phosphatase activity	F
GO:0004745	10	6.17E-01	1.00E+00	2.60E-01	1.00E+00	9.31E-01	1.00E+00	2.02E-01	1.00E+00	2.11E-01	1.00E+00	2.59E-01	1.00E+00	7.23E-01	1.00E+00	6.56E-01	1.00E+00	retinol dehydrogenase activity	F
GO:0004765	12	4.80E-02	1.00E+00	3.15E-02	1.00E+00	6.99E-02	1.00E+00	1.36E-01	1.00E+00	3.90E-02	1.00E+00	7.92E-02	1.00E+00	1.29E-01	1.00E+00	9.28E-02	1.00E+00	shikimate kinase activity	F
GO:0004806	15	6.06E-01	1.00E+00	6.93E-01	1.00E+00	7.62E-01	1.00E+00	6.67E-01	1.00E+00	3.39E-01	1.00E+00	5.76E-01	1.00E+00	5.73E-01	1.00E+00	4.89E-01	1.00E+00	triacylglycerol lipase activity	F
GO:0004812	70	1.01E-05	7.00E-03	7.63E-05	1.50E-02	1.64E-04	1.16E-02	6.87E-05	1.30E-02	1.08E-04	2.70E-02	2.03E-04	2.33E-02	2.53E-02	8.38E-01	1.20E-01	1.00E+00	aminoacyl-tRNA ligase activity	F
GO:0004835	16	5.24E-01	1.00E+00	1.17E-01	1.00E+00	9.14E-01	1.00E+00	5.73E-02	1.00E+00	6.74E-01	1.00E+00	7.92E-01	1.00E+00	1.07E-01	1.00E+00	5.94E-02	1.00E+00	tubulin-tyrosine ligase activity	F
GO:0004842	151	6.91E-09	2.57E-03	2.60E-12	0.00E+00	4.15E-09	9.80E-04	2.59E-10	0.00E+00	1.42E-05	5.00E-03	3.81E-09	8.78E-04	4.16E-03	2.23E-01	9.61E-05	1.60E-02	ubiquitin-protein ligase activity	F
GO:0004843	69	2.01E-02	1.00E+00	4.28E-05	7.00E-03	1.04E-03	7.90E-02	3.60E-06	2.89E-03	9.77E-02	1.00E+00	1.02E-02	5.03E-01	7.16E-01	1.00E+00	3.04E-03	1.27E-01	ubiquitin-specific protease activity	F
GO:0004857	306	9.42E-01	1.00E+00	7.79E-01	1.00E+00	9.60E-01	1.00E+00	7.84E-01	1.00E+00	9.92E-01	1.00E+00	6.73E-01	1.00E+00	2.46E-01	1.00E+00	7.23E-01	1.00E+00	enzyme inhibitor activity	F
GO:0004859	11	1.95E-01	1.00E+00	2.97E-01	1.00E+00	3.35E-01	1.00E+00	8.55E-01	1.00E+00	5.39E-01	1.00E+00	2.14E-01	1.00E+00	9.39E-02	1.00E+00	1.48E-01	1.00E+00	phospholipase inhibitor activity	F
GO:0004860	23	3.10E-01	1.00E+00	8.11E-03	4.16E-01	1.40E-01	1.00E+00	7.21E-03	4.92E-01	8.57E-01	1.00E+00	1.70E-02	6.68E-01	4.07E-01	1.00E+00	1.39E-01	1.00E+00	protein kinase inhibitor activity	F
GO:0004864	19	2.13E-01	1.00E+00	1.20E-01	1.00E+00	3.69E-01	1.00E+00	1.08E-01	1.00E+00	1.91E-01	1.00E+00	3.31E-01	1.00E+00	2.49E-01	1.00E+00	4.42E-02	1.00E+00	protein phosphatase inhibitor activity	F
GO:0004866	205	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.89E-01	1.00E+00	9.99E-01	1.00E+00	endopeptidase inhibitor activity	F
GO:0004867	143	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	8.56E-01	1.00E+00	9.94E-01	1.00E+00	serine-type endopeptidase inhibitor activity	F
GO:0004869	42	9.41E-01	1.00E+00	9.97E-01	1.00E+00	3.94E-01	1.00E+00	9.75E-01	1.00E+00	9.94E-01	1.00E+00	9.78E-01	1.00E+00	9.21E-01	1.00E+00	9.57E-01	1.00E+00	cysteine protease inhibitor activity	F
GO:0004871	3625	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	signal transducer activity	F
GO:0004872	3284	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	receptor activity	F
GO:0004879	177	3.60E-03	2.12E-01	8.13E-05	1.50E-02	1.77E-02	1.00E+00	3.36E-04	4.20E-02	2.89E-03	2.13E-01	1.57E-04	2.33E-02	3.40E-01	1.00E+00	3.34E-02	1.00E+00	ligand-dependent nuclear receptor activity	F
GO:0004887	19	1.11E-01	1.00E+00	3.07E-01	1.00E+00	1.64E-01	1.00E+00	7.13E-01	1.00E+00	1.99E-01	1.00E+00	2.43E-01	1.00E+00	1.85E-01	1.00E+00	1.47E-01	1.00E+00	thyroid hormone receptor activity	F
GO:0004888	2484	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	transmembrane receptor activity	F
GO:0004889	17	1.44E-01	1.00E+00	3.60E-01	1.00E+00	6.57E-01	1.00E+00	4.14E-01	1.00E+00	3.02E-01	1.00E+00	5.78E-01	1.00E+00	1.29E-02	4.78E-01	1.95E-01	1.00E+00	nicotinic acetylcholine-activated cation-sele	F
GO:0004890	33	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	GABA-A receptor activity	F
GO:0004896	81	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	4.94E-01	1.00E+00	4.14E-01	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0004907	50	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.92E-01	1.00E+00	5.93E-01	1.00E+00	5.44E-01	1.00E+00	interleukin receptor activity	F
GO:0004908	27	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	interleukin-1 receptor activity	F
GO:0004918	10	5.47E-02	1.00E+00	5.04E-02	1.00E+00	7.92E-01	1.00E+00	8.03E-01	1.00E+00	4.44E-01	1.00E+00	9.22E-02	1.00E+00	1.40E-02	4.78E-01	9.93E-03	4.76E-01	interleukin-8 receptor activity	F
GO:0004926	12	5.46E-02	1.00E+00	1.36E-01	1.00E+00	2.18E-01	1.00E+00	1.22E-01	1.00E+00	1.38E-02	6.92E-01	3.52E-01	1.00E+00	6.21E-01	1.00E+00	8.52E-02	1.00E+00	non-G-protein coupled 7TM receptor activit	F
GO:0004930	2114	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor activity	F
GO:0004932	15	9.25E-01	1.00E+00	9.63E-01	1.00E+00	8.33E-01	1.00E+00	9.86E-01	1.00E+00	9.73E-01	1.00E+00	8.83E-01	1.00E+00	8.20E-01	1.00E+00	6.95E-01	1.00E+00	mating-type factor pheromone receptor acti	F
GO:0004935	41	9.97E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.72E-01	1.00E+00	9.84E-01	1.00E+00	6.02E-01	1.00E+00	4.26E-01	1.00E+00	adrenoceptor activity	F
GO:0004936	15	6.18E-01	1.00E+00	5.34E-01	1.00E+00	9.13E-01	1.00E+00	5.26E-01	1.00E+00	5.29E-01	1.00E+00	8.16E-01	1.00E+00	2.20E-01	1.00E+00	2.51E-01	1.00E+00	alpha-adrenergic receptor activity	F
GO:0004942	25	5.91E-01	1.00E+00	3.78E-02	1.00E+00	1.00E+00	1.00E+00	2.19E-01	1.00E+00	6.83E-01	1.00E+00	7.40E-02	1.00E+00	1.78E-02	5.17E-01	1.56E-02	6.56E-01	anaphylatoxin receptor activity	F
GO:0004943	12	7.07E-01	1.00E+00	7.79E-02	1.00E+00	1.00E+00	1.00E+00	4.16E-01	1.00E+00	6.52E-01	1.00E+00	7.42E-02	1.00E+00	4.65E-02	1.00E+00	7.89E-02	1.00E+00	C3a anaphylatoxin receptor activity	F
GO:0004945	62	5.03E-01	1.00E+00	3.97E-01	1.00E+00	9.89E-01	1.00E+00	9.30E-01	1.00E+00	2.90E-01	1.00E+00	8.90E-02	1.00E+00	1.40E-01	1.00E+00	4.62E-01	1.00E+00	angiotensin type II receptor activity	F
GO:0004946	18	9.07E-01	1.00E+00	9.35E-01	1.00E+00	9.97E-01	1.00E+00	9.42E-01	1.00E+00	9.31E-01	1.00E+00	8.82E-01	1.00E+00	2.63E-01	1.00E+00	8.19E-01	1.00E+00	bombesin receptor activity	F
GO:0004947	39	6.89E-01	1.00E+00	5.18E-01	1.00E+00	9.85E-01	1.00E+00	6.98E-01	1.00E+00	4.22E-01	1.00E+00	3.16E-01	1.00E+00	2.96E-01	1.00E+00	4.25E-01	1.00E+00	bradykinin receptor activity	F
GO:0004949	102	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cannabinoid receptor activity	F
GO:0004950	48	7.77E-01	1.00E+00	8.62E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	6.86E-01	1.00E+00	5.59E-01	1.00E+00	1.44E-01	1.00E+00	3.22E-01	1.00E+00	chemokine receptor activity	F
GO:0004952	61	2.86E-01	1.00E+00	1.03E-01	1.00E+00	1.80E-01	1.00E+00	9.11E-02	1.00E+00	6.46E-01	1.00E+00	3.02E-01	1.00E+00	1.62E-01	1.00E+00	6.65E-02	1.00E+00	dopamine receptor activity	F
GO:0004953	15	4.15E-01	1.00E+00	4.91E-01	1.00E+00	8.36E-01	1.00E+00	6.11E-01	1.00E+00	5.56E-01	1.00E+00	7.16E-01	1.00E+00	6.07E-02	1.00E+00	3.85E-01	1.00E+00	icosanoid receptor activity	F
GO:0004954	15	4.15E-01	1.00E+00	4.91E-01	1.00E+00	8.36E-01	1.00E+00	6.11E-01	1.00E+00	5.56E-01	1.00E+00	7.16E-01	1.00E+00	6.07E-02	1.00E+00	3.85E-01	1.00E+00	prostanoid receptor activity	F
GO:0004955	15	4.15E-01	1.00E+00	4.91E-01	1.00E+00	8.36E-01	1.00E+00	6.11E-01	1.00E+00	5.56E-01	1.00E+00	7.16E-01	1.00E+00	6.07E-02	1.00E+00	3.85E-01	1.00E+00	prostaglandin receptor activity	F
GO:0004957	11	7.75E-01	1.00E+00	7.99E-01	1.00E+00	8.98E-01	1.00E+00	7.41E-01	1.00E+00	7.42E-01	1.00E+00	8.25E-01	1.00E+00	5.21E-01	1.00E+00	9.55E-01	1.00E+00	prostaglandin E receptor activity	F
GO:0004965	45	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	GABA-B receptor activity	F
GO:0004966	47	2.71E-01	1.00E+00	3.65E-01	1.00E+00	4.99E-01	1.00E+00	6.40E-01	1.00E+00	3.27E-01	1.00E+00	3.85E-01	1.00E+00	2.00E-01	1.00E+00	2.56E-01	1.00E+00	galanin receptor activity	F
GO:0004969	48	9.02E-06	7.00E-03	4.44E-04	4.74E-02	8.23E-04	4.90E-02	9.87E-04	9.40E-02	6.60E-05	2.40E-02	2.39E-03	1.27E-01	1.29E-02	4.78E-01	1.42E-02	4.76E-01	histamine receptor activity	F
GO:0004970	18	9.78E-01	1.00E+00	9.91E-01	1.00E+00	9.80E-01	1.00E+00	9.22E-01	1.00E+00	9.17E-01	1.00E+00	9.99E-01	1.00E+00	8.63E-01	1.00E+00	6.97E-01	1.00E+00	ionotropic glutamate receptor activity	F
GO:0004974	20	3.98E-01	1.00E+00	4.20E-01	1.00E+00	6.54E-01	1.00E+00	1.05E-01	1.00E+00	2.56E-01	1.00E+00	5.72E-01	1.00E+00	7.57E-01	1.00E+00	9.57E-01	1.00E+00	leukotriene receptor activity	F
GO:0004977	483	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	melanocortin receptor activity	F
GO:0004981	18	9.83E-01	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	8.83E-01	1.00E+00	9.41E-01	1.00E+00	muscarinic acetylcholine receptor activity	F
GO:0004982	40	8.75E-01	1.00E+00	6.36E-01	1.00E+00	9.81E-01	1.00E+00	8.79E-01	1.00E+00	6.05E-01	1.00E+00	2.33E-01	1.00E+00	5.15E-01	1.00E+00	6.50E-01	1.00E+00	N-formyl peptide receptor activity	F
GO:0004983	95	9.72E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.10E-01	1.00E+00	9.84E-01	1.00E+00	1.49E-01	1.00E+00	6.01E-01	1.00E+00	neuropeptide Y receptor activity	F
GO:0004984	1122	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	olfactory receptor activity	F
GO:0004985	17	5.36E-01	1.00E+00	8.49E-01	1.00E+00	9.37E-01	1.00E+00	5.80E-01	1.00E+00	1.85E-01	1.00E+00	7.08E-01	1.00E+00	6.06E-01	1.00E+00	1.00E+00	1.00E+00	opioid receptor activity	F
GO:0004989	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	octopamine receptor activity	F
GO:0004992	24	9.29E-01	1.00E+00	8.70E-01	1.00E+00	9.90E-01	1.00E+00	9.81E-01	1.00E+00	8.07E-01	1.00E+00	5.10E-01	1.00E+00	7.21E-01	1.00E+00	8.68E-01	1.00E+00	platelet activating factor receptor activity	F
GO:0004994	19	5.14E-01	1.00E+00	8.37E-01	1.00E+00	7.99E-01	1.00E+00	7.92E-01	1.00E+00	2.29E-01	1.00E+00	5.68E-01	1.00E+00	8.25E-01	1.00E+00	9.95E-01	1.00E+00	somatostatin receptor activity	F
GO:0005000	17	9.40E-01	1.00E+00	7.61E-01	1.00E+00	8.17E-01	1.00E+00	6.20E-01	1.00E+00	8.68E-01	1.00E+00	8.15E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	vasopressin receptor activity	F
GO:0005003	14	5.72E-01	1.00E+00	7.19E-01	1.00E+00	8.26E-01	1.00E+00	9.76E-01	1.00E+00	3.30E-01	1.00E+00	7.01E-01	1.00E+00	6.00E-01	1.00E+00	2.95E-01	1.00E+00	ephrin receptor activity	F

GO:0005021	65	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	9.07E-01	1.00E+00	4.98E-01	1.00E+00	vascular endothelial growth factor receptor	F
GO:0005024	13	1.38E-01	1.00E+00	1.75E-01	1.00E+00	8.11E-02	1.00E+00	2.53E-01	1.00E+00	2.42E-01	1.00E+00	1.02E-01	1.00E+00	7.38E-01	1.00E+00	3.58E-01	1.00E+00	transforming growth factor beta receptor ac	F
GO:0005044	35	7.88E-01	1.00E+00	4.68E-01	1.00E+00	9.11E-01	1.00E+00	7.56E-01	1.00E+00	9.68E-01	1.00E+00	8.57E-01	1.00E+00	1.85E-01	1.00E+00	6.01E-02	1.00E+00	scavenger receptor activity	F
GO:0005048	10	7.60E-02	1.00E+00	1.29E-02	6.07E-01	5.09E-02	1.00E+00	1.07E-01	1.00E+00	8.21E-01	1.00E+00	6.37E-02	1.00E+00	1.95E-01	1.00E+00	1.44E-03	6.00E-02	signal sequence binding	F
GO:0005057	108	9.95E-04	8.86E-02	5.93E-04	5.90E-02	1.96E-03	9.50E-02	1.71E-02	6.47E-01	1.19E-02	6.92E-01	4.29E-03	2.66E-01	1.97E-02	6.36E-01	9.84E-03	4.76E-01	receptor signaling protein activity	F
GO:0005070	17	1.20E-01	1.00E+00	3.92E-02	1.00E+00	2.30E-01	1.00E+00	4.02E-02	1.00E+00	1.79E-01	1.00E+00	1.94E-01	1.00E+00	2.70E-01	1.00E+00	2.27E-02	9.99E-01	SH3/SH2 adaptor activity	F
GO:0005083	216	4.31E-03	2.14E-01	2.18E-09	8.90E-04	2.36E-02	1.00E+00	1.46E-05	2.89E-03	2.66E-01	1.00E+00	9.32E-08	1.65E-03	4.76E-03	2.23E-01	8.44E-05	1.60E-02	small GTPase regulator activity	F
GO:0005085	157	2.21E-01	1.00E+00	5.88E-03	3.08E-01	5.61E-01	1.00E+00	1.91E-02	9.37E-01	5.02E-01	1.00E+00	2.27E-02	1.00E+00	6.19E-02	1.00E+00	1.93E-02	7.36E-01	guanyl-nucleotide exchange factor activity	F
GO:0005086	17	8.95E-01	1.00E+00	4.24E-01	1.00E+00	8.90E-01	1.00E+00	5.60E-01	1.00E+00	9.76E-01	1.00E+00	3.31E-01	1.00E+00	5.98E-01	1.00E+00	3.76E-01	1.00E+00	ARF guanyl-nucleotide exchange factor act	F
GO:0005088	84	2.12E-01	1.00E+00	6.42E-04	5.90E-02	4.41E-01	1.00E+00	3.74E-02	1.00E+00	8.36E-01	1.00E+00	5.36E-03	3.43E-01	3.58E-02	8.38E-01	2.65E-04	3.00E-02	Ras guanyl-nucleotide exchange factor acti	F
GO:0005089	74	5.35E-01	1.00E+00	1.99E-03	1.30E-01	6.29E-01	1.00E+00	7.14E-02	1.00E+00	9.72E-01	1.00E+00	1.69E-02	6.68E-01	1.55E-01	1.00E+00	1.05E-03	6.00E-02	Rho guanyl-nucleotide exchange factor acti	F
GO:0005096	200	1.21E-01	1.00E+00	4.76E-05	7.00E-03	1.11E-01	1.00E+00	3.58E-03	2.57E-01	6.12E-01	1.00E+00	2.51E-05	5.87E-03	1.15E-01	1.00E+00	2.70E-02	9.99E-01	GTPase activator activity	F
GO:0005097	44	1.60E-02	1.00E+00	1.67E-03	9.65E-02	4.09E-02	1.00E+00	9.20E-03	5.72E-01	1.29E-01	1.00E+00	1.48E-03	9.30E-02	1.18E-01	1.00E+00	1.86E-01	1.00E+00	Rab GTPase activator activity	F
GO:0005099	67	1.37E-02	6.08E-01	2.86E-04	4.40E-02	5.31E-02	1.00E+00	1.82E-03	1.24E-01	1.36E-01	1.00E+00	4.02E-04	2.33E-02	8.66E-02	1.00E+00	2.03E-01	1.00E+00	Ras GTPase activator activity	F
GO:0005100	17	3.51E-01	1.00E+00	9.96E-02	1.00E+00	4.39E-01	1.00E+00	2.20E-01	1.00E+00	6.40E-01	1.00E+00	6.85E-02	1.00E+00	1.57E-01	1.00E+00	3.51E-01	1.00E+00	Rho GTPase activator activity	F
GO:0005102	810	5.05E-01	1.00E+00	2.02E-01	1.00E+00	8.23E-01	1.00E+00	5.60E-01	1.00E+00	6.42E-01	1.00E+00	3.88E-01	1.00E+00	8.76E-02	1.00E+00	2.85E-02	9.99E-01	receptor binding	F
GO:0005118	11	4.10E-01	1.00E+00	6.93E-01	1.00E+00	2.96E-01	1.00E+00	6.50E-01	1.00E+00	7.71E-01	1.00E+00	5.37E-01	1.00E+00	3.90E-01	1.00E+00	8.42E-01	1.00E+00	sevenless binding	F
GO:0005125	259	9.96E-01	1.00E+00	8.44E-01	1.00E+00	9.71E-01	1.00E+00	8.78E-01	1.00E+00	9.95E-01	1.00E+00	9.51E-01	1.00E+00	8.85E-01	1.00E+00	2.43E-01	1.00E+00	cytokine activity	F
GO:0005126	61	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.54E-01	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0005149	13	9.55E-01	1.00E+00	9.33E-01	1.00E+00	9.47E-01	1.00E+00	9.68E-01	1.00E+00	9.86E-01	1.00E+00	9.88E-01	1.00E+00	5.29E-01	1.00E+00	7.63E-01	1.00E+00	interleukin-1 receptor binding	F
GO:0005158	18	5.61E-01	1.00E+00	7.20E-01	1.00E+00	9.60E-01	1.00E+00	7.99E-01	1.00E+00	6.11E-01	1.00E+00	6.41E-01	1.00E+00	1.22E-01	1.00E+00	7.23E-01	1.00E+00	insulin receptor binding	F
GO:0005160	11	1.86E-01	1.00E+00	6.02E-01	1.00E+00	2.70E-01	1.00E+00	5.24E-01	1.00E+00	3.56E-01	1.00E+00	6.53E-01	1.00E+00	1.52E-01	1.00E+00	4.94E-01	1.00E+00	transforming growth factor beta receptor bir	F
GO:0005164	33	2.57E-01	1.00E+00	7.82E-02	1.00E+00	3.17E-01	1.00E+00	2.14E-01	1.00E+00	4.13E-01	1.00E+00	6.72E-02	1.00E+00	1.54E-01	1.00E+00	1.64E-01	1.00E+00	tumor necrosis factor receptor binding	F
GO:0005178	29	6.96E-01	1.00E+00	1.06E-01	1.00E+00	7.67E-01	1.00E+00	5.74E-01	1.00E+00	6.88E-01	1.00E+00	2.04E-01	1.00E+00	3.53E-01	1.00E+00	3.65E-02	1.00E+00	integrin binding	F
GO:0005179	170	4.98E-01	1.00E+00	7.24E-01	1.00E+00	8.90E-01	1.00E+00	9.24E-01	1.00E+00	4.94E-01	1.00E+00	5.07E-01	1.00E+00	1.09E-01	1.00E+00	5.29E-01	1.00E+00	hormone activity	F
GO:0005184	18	1.64E-01	1.00E+00	6.04E-02	1.00E+00	2.00E-01	1.00E+00	3.08E-01	1.00E+00	3.70E-01	1.00E+00	2.86E-02	1.00E+00	7.45E-02	1.00E+00	8.16E-02	1.00E+00	neuropeptide hormone activity	F
GO:0005198	1009	2.06E-07	2.57E-03	6.40E-04	5.90E-02	1.54E-05	3.00E-03	5.94E-03	2.88E-01	2.86E-06	1.69E-03	2.66E-03	1.44E-01	8.63E-04	3.44E-02	2.77E-03	1.27E-01	structural molecule activity	F
GO:0005199	60	1.88E-02	1.00E+00	6.62E-03	3.12E-01	6.55E-02	1.00E+00	2.30E-03	1.39E-01	1.75E-02	7.90E-01	2.25E-02	1.00E+00	2.59E-01	1.00E+00	1.19E-01	1.00E+00	structural constituent of cell wall	F
GO:0005200	51	1.46E-01	1.00E+00	6.51E-02	1.00E+00	1.90E-01	1.00E+00	2.41E-01	1.00E+00	1.51E-01	1.00E+00	2.13E-01	1.00E+00	3.22E-01	1.00E+00	1.78E-02	6.56E-01	structural constituent of cytoskeleton	F
GO:0005201	52	5.01E-01	1.00E+00	3.42E-01	1.00E+00	6.46E-01	1.00E+00	2.24E-01	1.00E+00	6.95E-01	1.00E+00	5.40E-01	1.00E+00	2.23E-01	1.00E+00	3.41E-01	1.00E+00	extracellular matrix structural constituent	F
GO:0005212	20	2.93E-01	1.00E+00	4.04E-01	1.00E+00	5.57E-01	1.00E+00	6.05E-01	1.00E+00	4.05E-01	1.00E+00	2.12E-01	1.00E+00	1.83E-01	1.00E+00	4.40E-01	1.00E+00	structural constituent of eye lens	F
GO:0005215	1570	9.32E-05	1.43E-02	2.33E-11	0.00E+00	7.03E-03	4.69E-01	1.65E-06	2.89E-03	1.12E-02	6.92E-01	2.47E-06	2.90E-03	1.70E-04	8.00E-03	9.07E-11	0.00E+00	transporter activity	F
GO:0005216	443	6.32E-01	1.00E+00	2.81E-01	1.00E+00	9.58E-01	1.00E+00	7.91E-01	1.00E+00	9.33E-01	1.00E+00	5.49E-01	1.00E+00	1.60E-02	4.88E-01	4.49E-03	2.01E-01	ion channel activity	F
GO:0005217	12	8.64E-01	1.00E+00	5.14E-01	1.00E+00	9.54E-01	1.00E+00	6.22E-01	1.00E+00	9.53E-01	1.00E+00	5.73E-01	1.00E+00	9.47E-02	1.00E+00	2.78E-01	1.00E+00	intracellular ligand-gated ion channel activit	F
GO:0005230	75	9.48E-01	1.00E+00	9.85E-01	1.00E+00	9.69E-01	1.00E+00	9.71E-01	1.00E+00	8.86E-01	1.00E+00	9.75E-01	1.00E+00	7.77E-01	1.00E+00	7.33E-01	1.00E+00	extracellular ligand-gated ion channel activi	F
GO:0005231	49	4.35E-01	1.00E+00	6.26E-01	1.00E+00	7.24E-01	1.00E+00	5.76E-01	1.00E+00	6.84E-01	1.00E+00	6.77E-01	1.00E+00	1.28E-01	1.00E+00	4.70E-01	1.00E+00	excitatory extracellular ligand-gated ion cha	F
GO:0005234	19	9.85E-01	1.00E+00	9.95E-01	1.00E+00	9.69E-01	1.00E+00	9.09E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	9.10E-01	1.00E+00	7.57E-01	1.00E+00	glutamate-gated ion channel activity	F
GO:0005242	19	9.95E-01	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	3.89E-01	1.00E+00	8.88E-01	1.00E+00	inward rectifier potassium channel activity	F
GO:0005244	269	4.46E-01	1.00E+00	1.31E-01	1.00E+00	7.63E-01	1.00E+00	6.05E-01	1.00E+00	8.13E-01	1.00E+00	3.21E-01	1.00E+00	3.97E-02	1.00E+00	7.91E-03	4.28E-01	voltage-gated ion channel activity	F
GO:0005245	40	4.49E-01	1.00E+00	1.08E-01	1.00E+00	7.71E-01	1.00E+00	3.28E-01	1.00E+00	5.11E-01	1.00E+00	4.13E-01	1.00E+00	1.73E-01	1.00E+00	1.75E-02	6.56E-01	voltage-gated calcium channel activity	F
GO:0005246	13	4.05E-01	1.00E+00	2.04E-01	1.00E+00	4.99E-01	1.00E+00	2.35E-01	1.00E+00	8.52E-01	1.00E+00	1.14E-01	1.00E+00	3.81E-02	8.38E-01	3.56E-01	1.00E+00	calcium channel regulator activity	F
GO:0005247	19	2.88E-01	1.00E+00	1.38E-01	1.00E+00	6.41E-01	1.00E+00	1.83E-01	1.00E+00	3.40E-01	1.00E+00	7.32E-01	1.00E+00	2.23E-01	1.00E+00	1.38E-01	1.00E+00	voltage-gated chloride channel activity	F
GO:0005248	13	8.76E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.75E-01	1.00E+00	1.00E+00	1.00E+00	1.11E-01	1.00E+00	7.20E-02	1.00E+00	voltage-gated sodium channel activity	F
GO:0005249	204	5.39E-01	1.00E+00	3.55E-01	1.00E+00	7.46E-01	1.00E+00	7.66E-01	1.00E+00	8.69E-01	1.00E+00	3.18E-01	1.00E+00	8.93E-02	1.00E+00	7.89E-02	1.00E+00	voltage-gated potassium channel activity	F
GO:0005253	67	9.52E-01	1.00E+00	7.26E-01	1.00E+00	9.90E-01	1.00E+00	8.10E-01	1.00E+00	8.91E-01	1.00E+00	9.06E-01	1.00E+00	7.73E-01	1.00E+00	2.95E-01	1.00E+00	anion channel activity	F
GO:0005254	62	9.74E-01	1.00E+00	9.61E-01	1.00E+00	9.95E-01	1.00E+00	9.74E-01	1.00E+00	9.27E-01	1.00E+00	9.98E-01	1.00E+00	8.06E-01	1.00E+00	4.72E-01	1.00E+00	chloride channel activity	F
GO:0005261	339	2.96E-01	1.00E+00	6.41E-02	1.00E+00	7.82E-01	1.00E+00	4.70E-01	1.00E+00	7.90E-01	1.00E+00	1.49E-01	1.00E+00	2.60E-03	8.40E-02	2.50E-03	7.90E-02	cation channel activity	F
GO:0005262	89	4.29E-01	1.00E+00	7.93E-03	4.16E-01	6.76E-01	1.00E+00	1.17E-01	1.00E+00	6.59E-01	1.00E+00	1.52E-01	1.00E+00	7.03E-02	1.00E+00	9.48E-04	6.00E-02	calcium channel activity	F
GO:0005267	226	7.16E-01	1.00E+00	5.22E-01	1.00E+00	8.78E-01	1.00E+00	8.71E-01	1.00E+00	9.56E-01	1.00E+00	3.85E-01	1.00E+00	9.34E-02	1.00E+00	1.07E-01	1.00E+00	potassium channel activity	F
GO:0005272	28	6.47E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	7.64E-01	1.00E+00	5.58E-01	1.00E+00	9.97E-01	1.00E+00	7.38E-02	1.00E+00	5.99E-01	1.00E+00	sodium channel activity	F
GO:0005275	74	5.60E-01	1.00E+00	1.61E-01	1.00E+00	4.05E-01	1.00E+00	4.55E-01	1.00E+00	5.47E-01	1.00E+00	1.75E-01	1.00E+00	6.85E-01	1.00E+00	1.61E-01	1.00E+00	amine transporter activity	F
GO:0005279	20	7.01E-01	1.00E+00	6.68E-01	1.00E+00	8.75E-01	1.00E+00	6.93E-01	1.00E+00	6.35E-01	1.00E+00	3.98E-01	1.00E+00	4.57E-01	1.00E+00	8.17E-01	1.00E+00	amino acid-polyamine transporter activity	F
GO:0005283	15	7.90E-01	1.00E+00	6.20E-01	1.00E+00	7.00E-01	1.00E+00	5.44E-01	1.00E+00	9.10E-01	1.00E+00	3.14E-01	1.00E+00	6.63E-01	1.00E+00	9.75E-01	1.00E+00	sodium:amino acid symporter activity	F
GO:0005310	71	8.11E-01	1.00E+00	6.67E-01	1.00E+00	9.37E-01	1.00E+00	9.13E-01	1.00E+00	7.72E-01	1.00E+00	5.44E-01	1.00E+00	5.42E-01	1.00E+00	3.90E-01	1.00E+00	dicarboxylic acid transporter activity	F
GO:0005313	10	4.76E-01	1.00E+00	2.15E-01	1.00E+00	3.92E-01	1.00E+00	1.70E-01	1.00E+00	4.82E-01	1.00E+00	4.94E-01	1.00E+00	5.29E-01	1.00E+00	3.47E-01	1.00E+00	L-glutamate transporter activity	F
GO:0005319	61	2.41E-02	1.00E+00	1.06E-01	1.00E+00	2.37E-02	1.00E+00	7.15E-02	1.00E+00	2.76E-02	1.00E+00	6.26E-01	1.00E+00	2.80E-01	1.00E+00	6.31E-02	1.00E+00	lipid transporter activity	F
GO:0005326	32	9.03E-01	1.00E+00	5.30E-01	1.00E+00	8.95E-01	1.00E+00	9.48E-01	1.00E+00	9.67E-01	1.00E+00	3.65E-01	1.00E+00	5.22E-01	1.00E+00	1.42E-01	1.00E+00	neurotransmitter transporter activity	F
GO:0005328	30	9.49E-01	1.00E+00	5.53E-01	1.00E+00	9.68E-01	1.00E+00	9.15E-01	1.00E+00	9.64E-01	1.00E+00	4.06E-01	1.00E+00	5.79E-01	1.00E+00	1.72E-01	1.00E+00	neurotransmitter:sodium symporter activity	F
GO:0005337	14	3.40E-01	1.00E+00	5.25E-01	1.00E+00	6.89E-01	1.00E+00	5.81E-01	1.00E+00	2.92E-01	1.00E+00	5.05E-01	1.00E+00	2.77E-01	1.00E+00	2.79E-01	1.00E+00	nucleoside transporter activity	F
GO:0005342	140	6.68E-01	1.00E+00	2.31E-01	1.00E+00	5.71E-01	1.00E+00	5.09E-01	1.00E+00	5.92E-01	1.00E+00	2.16E-01	1.00E+00	8.04E-01	1.00E+00	2.62E-01	1.00E+00	organic acid transporter activity	F
GO:0005343	89	8.58E-01	1.00E+00	4.44E-01	1.00E+00	8.78E-01	1.00E+00	5.82E-01	1.00E+00	8.32E-01	1.00E+00	3.53E-01	1.00E+00	8.21E-01	1.00E+00	4.70E-01	1.00E+00	organic acid:sodium symporter activity	F
GO:0005344	12	7.36E-01	1.00E+00	1.65E-01	1.00E+00	3.02E-01	1.00E+00	6.50E-02	1.00E+00	1.00E+00	1.00E+00	1.80E-01	1.00E+00	4.83E-01	1.00E+00	5.59E-01	1.00E+00	oxygen transporter activity	F
GO:0005351	44	1.32E-01	1.00E+00	3.40E-02	1.00E+00	3.75E-01	1.00E+00	1.80E-01	1.00E+00	1.02E-01	1.00E+00	4.57E-02	1.00E+00	1.89E-01	1.00E+00	6.92E-02	1.00E+00	sugar porter activity	F
GO:0005355	12	1.20E-01	1.00E+00	2.80E-02	1.00E+00	3.61E-01	1.00E+00	3.14E-01	1.00E+00	1.63E-01	1.00E+00	1.04E-02	5.03E-01	3.14E-02	8.38E-01	6.05E-02	1.00E+00	glucose transporter activity	F
GO:0005372	11	4.91E-01	1.00E+00	1.57E-01	1.00E+00	2.94E-01	1.00E+00	2.81E-02	1.00E+00	4.79E-01	1.00E+00	3.93E-01	1.00E+00	8.32E-01	1.00E+00	5.17E-01	1.00E+00	water transporter activity	F
GO:0005385	12	5.07E-03	2.72E-01	7.57E-04	8.10E-02	3.37E-03	2.03E-01	2.83E-03	1.61E-01	1.02E-01	1.00E+00	7.43E-02	1.00E+00	3.02E-01	1.00E+00	1.27E-02	4.76E-01	zinc ion transporter activity	F
GO:0005386	438	1.72E-01	1.00E+00	7.33E-03	3.12E-01	2.47E-01	1.00E+00	4.83E-02	1.00E+00	8.77E-02	1.00E+00	2.67E-02	1.00E+00	7.19E-01	1.00E+00	2.87E-02	9.99E-01	carrier activity	F
GO:0005416	18	6.97E-01	1.00E+00	6.28E-01	1.00E+00	8.56E-01	1.00E+00	6.69E-01	1.00E+00	7.96E-01	1.00E+00	4.05E-01	1.00E+00	3.40E-01	1.00E+00	7.47E-01	1.00E+00	cation:amino acid symporter activity	F
GO:0005451	19	1.93E-01	1.00E+00	2.71E-01	1.00E+00	1.77E-01	1.00E+00	3.23E-01	1.00E+00	9.20E-02	1.00E+00	4.93E-01	1.00E+00	4.57E-01	1.00E+00	1.06E-01	1.00E+00	monovalent cation:proton antiporter activity	F
GO:0005452	16	3.32E-01	1.00E+00	5.41E-02	1.00E+00	7.10E-01	1.00E+00	2.28E-02	9.37E-01	1.97E-01	1.00E+00	5.89E-01	1.00E+00	3.02E-01	1.00E+00	2.03E-02	7.36E-01	inorganic anion exchanger activity	F
GO:0005478	29	2.71E-02	1.00E+00	7.14E-04	5.90E-02	6.28E-02	1.00E+00	1.14E-02	6.47E-01	1.22E-02	6.92E-01	4.92E-03	2.66E-01	3.50E-01	1.00E+00	1.04E-02	4.76E-01	intracellular transporter activity	F
GO:0005484	22	1.12E-01	1.00E+00	2.42E-02	1.00E+00	1.07E-01	1.00E+00	1.12E-01	1.00E+00	6.17E-02	1.00E+00	1.80E-02	6.68E-01	6.70E-01	1.00E+00	5.33E-02	1.00E+00	SNAP receptor activity	F
GO:0005488	13193	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.29E-17	0.00E+00	0.00E+00	0.00E+00	binding	F
GO:0005496	67	1.46E-01	1.00E+00	2.48E-01	1.00E+00	4.76E-01	1.00E+00	3.97E-01	1.00E+00	1.69E-01	1.00E+00	2.00E-01	1.00E+00	1.06E-01	1.00E+00	2.34E-01	1.00E+00	steroid binding	F
GO:0005501	17	8.88E-01	1.00E+00	3.85E-01	1.00E+00	9.70E-01	1.00E+00	3.88E-01	1.00E+00	9.72E-01	1.00E+00	6.26E-01	1.00E+00	4.33E-01	1.00E+00	1.53E-01	1.00E+00	retinoid binding	F

GO:0005504	20	1.48E-01	1.00E+00	1.06E-01	1.00E+00	3.50E-01	1.00E+00	6.00E-01	1.00E+00	1.71E-01	1.00E+00	6.54E-01	1.00E+00	2.12E-01	1.00E+00	9.00E-03	4.28E-01	fatty acid binding	F
GO:0005506	375	9.31E-01	1.00E+00	6.41E-01	1.00E+00	9.51E-01	1.00E+00	7.48E-01	1.00E+00	9.92E-01	1.00E+00	5.14E-01	1.00E+00	5.02E-01	1.00E+00	4.17E-01	1.00E+00	iron ion binding	F
GO:0005507	79	7.54E-01	1.00E+00	7.86E-01	1.00E+00	9.37E-01	1.00E+00	8.48E-01	1.00E+00	7.74E-01	1.00E+00	6.69E-01	1.00E+00	3.28E-01	1.00E+00	8.92E-01	1.00E+00	copper ion binding	F
GO:0005509	1021	8.87E-01	1.00E+00	1.61E-01	1.00E+00	9.99E-01	1.00E+00	8.81E-01	1.00E+00	8.69E-01	1.00E+00	7.86E-01	1.00E+00	1.05E-01	1.00E+00	1.59E-05	7.00E-03	calcium ion binding	F
GO:0005515	7049	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.06E-43	0.00E+00	0.00E+00	0.00E+00	protein binding	F
GO:0005516	120	1.35E-01	1.00E+00	1.32E-03	9.65E-02	5.17E-01	1.00E+00	2.55E-02	1.00E+00	2.92E-01	1.00E+00	3.98E-03	1.84E-01	3.21E-02	8.38E-01	2.88E-03	1.27E-01	calmodulin binding	F
GO:0005520	24	9.14E-01	1.00E+00	7.51E-01	1.00E+00	9.01E-01	1.00E+00	9.48E-01	1.00E+00	6.79E-01	1.00E+00	7.94E-01	1.00E+00	8.62E-01	1.00E+00	1.95E-01	1.00E+00	insulin-like growth factor binding	F
GO:0005524	1555	1.06E-27	0.00E+00	5.98E-43	0.00E+00	1.35E-26	0.00E+00	7.65E-31	0.00E+00	2.56E-15	0.00E+00	1.97E-27	0.00E+00	1.39E-08	0.00E+00	2.77E-20	0.00E+00	ATP binding	F
GO:0005525	379	4.84E-07	2.57E-03	3.20E-09	8.90E-04	2.81E-05	3.00E-03	5.72E-07	2.89E-03	2.13E-06	1.69E-03	3.17E-07	1.65E-03	2.98E-03	8.70E-02	3.15E-04	3.00E-02	GTP binding	F
GO:0005529	240	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.87E-01	1.00E+00	4.69E-01	1.00E+00	sugar binding	F
GO:0005537	15	6.04E-01	1.00E+00	3.67E-01	1.00E+00	7.13E-01	1.00E+00	2.73E-01	1.00E+00	5.35E-01	1.00E+00	8.78E-01	1.00E+00	4.52E-01	1.00E+00	2.24E-01	1.00E+00	mannose binding	F
GO:0005539	83	6.81E-01	1.00E+00	6.88E-01	1.00E+00	6.38E-01	1.00E+00	7.58E-01	1.00E+00	5.95E-01	1.00E+00	8.16E-01	1.00E+00	7.54E-01	1.00E+00	3.93E-01	1.00E+00	glycosaminoglycan binding	F
GO:0005540	17	2.82E-01	1.00E+00	6.02E-01	1.00E+00	4.03E-01	1.00E+00	1.84E-01	1.00E+00	1.74E-01	1.00E+00	8.28E-01	1.00E+00	5.01E-01	1.00E+00	8.76E-01	1.00E+00	hyaluronic acid binding	F
GO:0005542	11	1.49E-01	1.00E+00	2.13E-01	1.00E+00	2.15E-01	1.00E+00	1.72E-01	1.00E+00	2.45E-01	1.00E+00	3.37E-01	1.00E+00	8.86E-02	1.00E+00	6.27E-01	1.00E+00	folic acid binding	F
GO:0005543	128	7.08E-05	1.41E-02	1.26E-09	8.90E-04	1.10E-02	6.53E-01	2.09E-07	2.89E-03	8.17E-04	1.20E-01	4.15E-06	2.90E-03	1.76E-03	8.40E-02	3.47E-05	7.00E-03	phospholipid binding	F
GO:0005544	23	3.26E-01	1.00E+00	7.07E-02	1.00E+00	4.29E-01	1.00E+00	5.70E-01	1.00E+00	7.00E-01	1.00E+00	1.19E-02	5.03E-01	1.60E-01	1.00E+00	2.16E-01	1.00E+00	calcium-dependent phospholipid binding	F
GO:0005545	10	3.71E-01	1.00E+00	8.91E-02	1.00E+00	4.63E-01	1.00E+00	1.28E-01	1.00E+00	1.83E-01	1.00E+00	8.38E-02	1.00E+00	9.43E-01	1.00E+00	1.64E-01	1.00E+00	phosphatidylinositol binding	F
GO:0005548	19	9.55E-01	1.00E+00	3.62E-01	1.00E+00	7.87E-01	1.00E+00	3.98E-01	1.00E+00	9.95E-01	1.00E+00	2.80E-01	1.00E+00	7.12E-01	1.00E+00	6.24E-01	1.00E+00	phospholipid transporter activity	F
GO:0005549	41	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	odorant binding	F
GO:0005550	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.97E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	pheromone binding	F
GO:0005575	16829	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.91E-10	0.00E+00	9.53E-44	0.00E+00	cellular_component	C
GO:0005576	2619	7.27E-01	1.00E+00	9.52E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	8.49E-01	1.00E+00	9.95E-01	1.00E+00	7.05E-03	2.75E-01	3.18E-03	1.27E-01	extracellular region	C
GO:0005578	319	7.82E-01	1.00E+00	6.13E-01	1.00E+00	9.81E-01	1.00E+00	9.66E-01	1.00E+00	7.29E-01	1.00E+00	5.07E-01	1.00E+00	1.74E-01	1.00E+00	7.22E-02	1.00E+00	extracellular matrix (sensu Metazoa)	C
GO:0005581	21	9.17E-01	1.00E+00	7.76E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	9.25E-01	1.00E+00	8.70E-01	1.00E+00	3.53E-01	1.00E+00	1.89E-01	1.00E+00	collagen	C
GO:0005604	72	9.29E-01	1.00E+00	7.50E-01	1.00E+00	9.92E-01	1.00E+00	8.18E-01	1.00E+00	8.56E-01	1.00E+00	7.38E-01	1.00E+00	3.51E-01	1.00E+00	2.68E-01	1.00E+00	basement membrane	C
GO:0005605	26	9.15E-01	1.00E+00	9.52E-01	1.00E+00	9.59E-01	1.00E+00	8.09E-01	1.00E+00	8.36E-01	1.00E+00	8.48E-01	1.00E+00	4.28E-01	1.00E+00	9.95E-01	1.00E+00	basal lamina	C
GO:0005615	1830	2.57E-01	1.00E+00	4.02E-01	1.00E+00	8.85E-01	1.00E+00	9.20E-01	1.00E+00	5.71E-01	1.00E+00	7.73E-01	1.00E+00	5.22E-04	3.44E-02	1.15E-03	6.00E-02	extracellular space	C
GO:0005622	10505	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	intracellular	C
GO:0005623	15412	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.20E-45	0.00E+00	0.00E+00	0.00E+00	1.04E-09	0.00E+00	8.07E-43	0.00E+00	cell	C
GO:0005624	512	1.01E-01	1.00E+00	5.33E-04	4.74E-02	1.20E-01	1.00E+00	7.84E-03	4.92E-01	1.70E-01	1.00E+00	4.34E-03	2.66E-01	3.04E-01	1.00E+00	1.02E-03	6.00E-02	membrane fraction	C
GO:0005625	100	2.02E-03	2.12E-01	4.47E-04	4.74E-02	3.01E-03	1.35E-01	1.24E-04	1.30E-02	6.69E-03	6.92E-01	1.53E-02	6.68E-01	4.31E-02	1.00E+00	2.69E-02	9.99E-01	soluble fraction	C
GO:0005626	21	1.24E-02	6.08E-01	3.99E-03	1.88E-01	5.80E-02	1.00E+00	3.88E-02	1.00E+00	1.30E-02	6.92E-01	1.40E-02	6.68E-01	1.93E-02	6.36E-01	1.66E-02	6.56E-01	insoluble fraction	C
GO:0005634	4585	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.76E-17	0.00E+00	8.27E-30	0.00E+00	nucleus	C
GO:0005635	169	3.10E-09	2.57E-03	1.24E-14	0.00E+00	9.01E-07	2.00E-03	1.48E-11	0.00E+00	1.72E-06	1.69E-03	6.51E-09	8.78E-04	1.26E-03	6.14E-02	4.05E-05	7.00E-03	nuclear envelope	C
GO:0005637	17	2.14E-02	1.00E+00	7.21E-03	3.12E-01	1.06E-02	6.53E-01	2.50E-03	1.39E-01	1.75E-01	1.00E+00	4.31E-02	1.00E+00	1.04E-01	1.00E+00	1.02E-01	1.00E+00	nuclear inner membrane	C
GO:0005640	11	2.11E-01	1.00E+00	4.22E-02	1.00E+00	2.55E-01	1.00E+00	1.41E-01	1.00E+00	2.81E-01	1.00E+00	8.10E-02	1.00E+00	2.32E-01	1.00E+00	1.83E-01	1.00E+00	nuclear outer membrane	C
GO:0005643	57	9.00E-09	2.57E-03	9.67E-13	0.00E+00	1.17E-07	2.00E-03	2.56E-11	0.00E+00	6.00E-06	1.69E-03	1.01E-05	5.87E-03	4.92E-02	1.00E+00	8.54E-05	1.60E-02	nuclear pore	C
GO:0005654	531	1.23E-24	0.00E+00	2.54E-27	0.00E+00	1.29E-21	0.00E+00	5.54E-25	0.00E+00	9.39E-15	0.00E+00	1.35E-15	0.00E+00	7.59E-09	0.00E+00	1.56E-09	0.00E+00	nucleoplasm	C
GO:0005657	29	6.66E-06	3.62E-03	2.01E-07	3.92E-03	5.62E-05	9.82E-03	6.67E-09	8.93E-04	1.75E-05	5.37E-03	3.61E-03	1.80E-01	8.87E-03	2.75E-01	1.14E-02	4.76E-01	replication fork	C
GO:0005667	270	2.89E-06	3.02E-03	5.12E-07	3.92E-03	1.17E-04	1.16E-02	3.22E-06	2.89E-03	5.51E-04	4.90E-02	4.81E-04	2.33E-02	1.00E-03	3.62E-02	2.37E-05	7.00E-03	transcription factor complex	C
GO:0005669	20	4.00E-03	2.12E-01	7.18E-02	1.00E+00	5.81E-03	4.69E-01	1.11E-01	1.00E+00	2.91E-02	1.00E+00	1.00E-01	1.00E+00	5.73E-02	1.00E+00	2.00E-01	1.00E+00	transcription factor TFIID complex	C
GO:0005681	128	3.68E-13	0.00E+00	1.09E-10	0.00E+00	1.32E-10	7.95E-04	3.34E-11	0.00E+00	6.42E-10	0.00E+00	6.48E-06	5.87E-03	2.18E-04	1.20E-02	8.26E-03	4.28E-01	spliceosome complex	C
GO:0005689	14	1.70E-02	1.00E+00	1.42E-02	6.07E-01	1.90E-02	1.00E+00	2.38E-03	1.39E-01	3.03E-03	2.13E-01	2.12E-02	7.56E-01	7.63E-01	1.00E+00	9.78E-01	1.00E+00	minor (U12-dependent) spliceosome compl	C
GO:0005694	505	3.23E-10	2.57E-03	4.25E-11	0.00E+00	1.99E-13	7.08E-04	4.13E-16	0.00E+00	7.38E-06	2.00E-03	5.98E-05	9.66E-03	5.96E-03	2.75E-01	4.93E-04	3.00E-02	chromosome	C
GO:0005720	28	2.26E-04	1.72E-02	3.68E-03	1.88E-01	2.23E-04	2.10E-02	3.27E-03	1.76E-01	1.38E-02	6.92E-01	1.67E-02	6.68E-01	1.50E-02	4.78E-01	8.93E-02	1.00E+00	nuclear heterochromatin	C
GO:0005730	153	2.99E-10	2.57E-03	9.64E-07	3.92E-03	5.73E-11	7.08E-04	1.34E-07	2.89E-03	4.80E-08	9.59E-04	1.03E-03	9.00E-02	1.96E-02	6.36E-01	2.03E-02	7.36E-01	nucleolus	C
GO:0005732	14	9.76E-03	6.08E-01	1.67E-01	1.00E+00	4.57E-02	1.00E+00	1.63E-01	1.00E+00	8.26E-03	6.92E-01	3.58E-01	1.00E+00	2.14E-02	6.36E-01	8.33E-02	1.00E+00	small nucleolar ribonucleoprotein complex	C
GO:0005737	6418	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	cytoplasm	C
GO:0005739	994	7.04E-29	0.00E+00	3.64E-25	0.00E+00	8.87E-20	0.00E+00	1.01E-17	0.00E+00	8.87E-20	0.00E+00	5.55E-22	0.00E+00	2.86E-13	0.00E+00	2.28E-06	2.00E-03	mitochondrion	C
GO:0005740	420	7.63E-14	0.00E+00	1.05E-12	0.00E+00	5.01E-09	9.80E-04	8.64E-11	0.00E+00	4.85E-12	0.00E+00	5.60E-10	6.20E-04	2.19E-06	8.23E-04	4.46E-04	3.00E-02	mitochondrial envelope	C
GO:0005741	67	1.83E-03	2.12E-01	4.98E-06	4.51E-03	2.62E-02	1.00E+00	1.66E-04	1.30E-02	9.45E-03	6.92E-01	3.25E-04	2.33E-02	2.21E-03	8.40E-02	4.57E-03	2.01E-01	mitochondrial outer membrane	C
GO:0005743	315	4.24E-09	2.57E-03	4.69E-08	9.59E-04	1.22E-06	2.00E-03	4.58E-06	2.89E-03	2.05E-08	9.59E-04	4.39E-06	2.90E-03	1.36E-03	6.14E-02	5.11E-04	3.00E-02	mitochondrial inner membrane	C
GO:0005746	67	1.17E-02	6.08E-01	1.60E-02	7.63E-01	1.26E-01	1.00E+00	2.30E-02	9.37E-01	2.26E-02	1.00E+00	6.01E-02	1.00E+00	3.26E-02	8.38E-01	9.30E-02	1.00E+00	mitochondrial electron transport chain	C
GO:0005747	15	2.39E-02	1.00E+00	3.52E-02	1.00E+00	4.42E-02	1.00E+00	1.49E-01	1.00E+00	2.25E-01	1.00E+00	1.09E-01	1.00E+00	5.82E-02	1.00E+00	6.71E-02	1.00E+00	respiratory chain complex I (sensu Eukaryo	C
GO:0005758	26	2.15E-02	1.00E+00	6.18E-02	1.00E+00	9.34E-02	1.00E+00	1.49E-01	1.00E+00	1.23E-02	6.92E-01	3.52E-02	1.00E+00	5.40E-02	1.00E+00	3.17E-01	1.00E+00	mitochondrial intermembrane space	C
GO:0005759	156	2.60E-06	3.02E-03	8.58E-05	1.50E-02	2.61E-05	3.00E-03	8.57E-03	4.92E-01	4.11E-03	2.13E-01	1.24E-04	1.30E-02	2.59E-03	8.40E-02	2.42E-02	9.99E-01	mitochondrial matrix	C
GO:0005761	46	1.34E-04	1.43E-02	9.54E-03	4.69E-01	5.17E-05	9.82E-03	8.81E-02	1.00E+00	3.53E-03	2.13E-01	1.96E-03	1.27E-01	1.53E-01	1.00E+00	1.96E-01	1.00E+00	mitochondrial ribosome	C
GO:0005762	24	3.30E-02	1.00E+00	1.42E-01	1.00E+00	1.47E-02	6.53E-01	1.40E-01	1.00E+00	2.92E-02	1.00E+00	1.41E-01	1.00E+00	5.22E-01	1.00E+00	4.59E-01	1.00E+00	mitochondrial large ribosomal subunit	C
GO:0005763	14	1.63E-05	7.00E-03	2.75E-02	1.00E+00	1.44E-03	7.90E-02	1.12E-01	1.00E+00	1.07E-02	6.92E-01	1.04E-02	5.03E-01	1.46E-01	1.00E+00	9.73E-02	1.00E+00	mitochondrial small ribosomal subunit	C
GO:0005764	201	1.66E-06	2.76E-03	3.09E-07	3.92E-03	1.98E-03	9.50E-02	1.48E-04	1.30E-02	3.25E-04	4.90E-02	2.95E-05	9.52E-03	1.41E-04	8.00E-03	5.56E-04	3.00E-02	lysosome	C
GO:0005765	54	1.17E-03	8.86E-02	8.97E-06	4.51E-03	5.48E-02	1.00E+00	4.87E-03	2.88E-01	2.30E-02	1.00E+00	8.46E-04	4.48E-02	2.93E-02	8.38E-01	2.54E-03	7.90E-02	lysosomal membrane	C
GO:0005768	205	5.41E-08	2.57E-03	9.36E-14	0.00E+00	4.50E-06	2.91E-03	2.57E-10	0.00E+00	1.35E-04	2.70E-02	1.71E-08	8.78E-04	9.78E-05	8.00E-03	3.04E-05	7.00E-03	endosome	C
GO:0005769	61	4.71E-04	4.40E-02	3.31E-05	7.00E-03	1.08E-03	7.90E-02	2.78E-04	4.20E-02	1.22E-03	1.20E-01	3.19E-04	2.33E-02	1.78E-01	1.00E+00	5.73E-02	1.00E+00	early endosome	C
GO:0005770	60	6.85E-06	3.62E-03	2.70E-05	7.00E-03	4.16E-04	4.00E-02	1.05E-03	9.40E-02	1.64E-03	1.20E-01	4.79E-03	2.66E-01	5.91E-03	2.75E-01	3.64E-03	1.27E-01	late endosome	C
GO:0005771	11	1.63E-02	1.00E+00	4.75E-03	2.61E-01	3.90E-02	1.00E+00	2.91E-02	1.00E+00	1.59E-01	1.00E+00	7.14E-02	1.00E+00	2.99E-01	1.00E+00	5.18E-02	1.00E+00	multivesicular body	C
GO:0005773	222	1.26E-07	2.57E-03	7.50E-07	3.92E-03	2.60E-04	4.00E-02	1.35E-04	1.30E-02	5.65E-05	2.40E-02	3.68E-05	9.66E-03	1.98E-04	1.20E-02	1.95E-03	7.90E-02	vacuole	C
GO:0005774	66	2.88E-04	1.90E-02	2.89E-05	7.00E-03	2.25E-02	1.00E+00	5.41E-03	2.88E-01	1.23E-02	6.92E-01	5.90E-04	3.20E-02	1.50E-02	4.78E-01	9.34E-03	4.28E-01	vacuolar membrane	C
GO:0005777	99	7.41E-03	3.15E-01	1.60E-03	9.65E-02	7.21E-02	1.00E+00	1.60E-02	6.47E-01	9.66E-03	6.92E-01	3.42E-03	1.51E-01	4.98E-02	1.00E+00	4.62E-02	1.00E+00	peroxisome	C
GO:0005778	40	1.67E-03	2.12E-01	1.05E-02	4.69E-01	5.02E-02	1.00E+00	2.61E-02	1.00E+00	1.35E-02	6.92E-01	5.79E-02	1.00E+00	2.82E-03	8.40E-02	1.61E-02	6.56E-01	peroxisomal membrane	C
GO:0005783	848	3.26E-09	2.57E-03	1.03E-10	0.00E+00	3.97E-06	2.91E-03	1.05E-07	2.89E-03	2.87E-07	9.59E-04	6.37E-09	8.78E-04	2.12E-04	1.20E-02	3.33E-04	3.00E-02	endoplasmic reticulum	C
GO:0005788	60	4.61E-02	1.00E+00	3.00E-02	1.00E+00	1.16E-01	1.00E+00	2.51E-02	1.00E+00	2.59E-02	1.00E+00	1.87E-02	6.68E-01	1.13E-01	1.00E+00	3.03E-01	1.00E+00	endoplasmic reticulum lumen	C
GO:0005789	469	4.54E-06	3.02E-03	1.31E-06	3.92E-03	7.78E-04	4.90E-02	6.97E-05	1.30E-02	2.06E-04	4.90E-02	3.21E-05	9.52E-03	4.37E-04	2.40E-02	1.40E-03	6.00E-02	endoplasmic reticulum membrane	C
GO:0005791	16	1.15E-01	1.00E+00	1.84E-01	1.00E+00	1.81E-01	1.00E+00	1.27E-01	1.00E+00	2.69E-01	1.00E+00	1.23E-01	1.00E+00	6.72E-02	1.00E+00	6.90E-01	1.00E+00	rough endoplasmic reticulum	C
GO:0005792	177	7.97E-01	1.00E+00	3.99E-01	1.00E+00	8.28E-01	1.00E+00	7.74E-01	1.00E+00	4.53E-01	1.00E+00	2.03E-01	1.00E+00	8.97E-01	1.00E+00	1.61E-01	1.00E+00	microsome	C
GO:0005793	25	8.26E-02	1.00E+00	1.38E-02	6.07E-01	5.37E-02	1.00E+00	2.66E-02	1.00E+00	5.78E-02	1.00E+00	2.09E-02	7.56E-01	5.59E-01	1.00E+00	1.55E-01	1.00E+00	ER-Golgi intermediate compartment	C

GO:0005794	653	1.78E-14	0.00E+00	2.47E-16	0.00E+00	5.97E-09	9.80E-04	1.15E-12	0.00E+00	2.88E-11	0.00E+00	1.63E-09	8.78E-04	4.31E-06	1.00E-03	3.09E-08	0.00E+00	Golgi apparatus	C
GO:0005795	21	3.32E-02	1.00E+00	1.75E-03	9.65E-02	4.83E-03	3.08E-01	1.04E-02	5.72E-01	2.67E-01	1.00E+00	9.61E-03	5.03E-01	5.87E-01	1.00E+00	3.08E-02	9.99E-01	Golgi stack	C
GO:0005798	43	8.00E-06	3.62E-03	1.20E-05	4.51E-03	5.48E-03	4.69E-01	1.55E-04	1.30E-02	2.92E-04	4.90E-02	9.06E-05	1.10E-02	1.50E-03	6.14E-02	4.32E-03	2.01E-01	Golgi-associated vesicle	C
GO:0005801	12	3.10E-04	3.10E-02	3.70E-03	1.88E-01	6.17E-02	1.00E+00	1.83E-02	9.37E-01	2.31E-03	1.20E-01	1.39E-02	6.68E-01	5.16E-02	1.00E+00	4.70E-02	1.00E+00	Golgi cis face	C
GO:0005802	43	1.79E-06	3.00E-03	2.35E-05	7.00E-03	1.38E-03	7.90E-02	1.26E-04	1.30E-02	4.35E-04	4.90E-02	5.15E-03	2.66E-01	2.49E-04	1.20E-02	1.42E-02	4.76E-01	Golgi trans face	C
GO:0005811	12	1.69E-02	1.00E+00	1.17E-02	6.07E-01	2.91E-02	1.00E+00	5.65E-02	1.00E+00	2.19E-02	1.00E+00	6.58E-01	1.00E+00	4.21E-01	1.00E+00	6.44E-02	1.00E+00	lipid particle	C
GO:0005813	135	1.42E-06	2.76E-03	1.82E-07	3.92E-03	2.81E-06	2.91E-03	1.29E-05	2.89E-03	1.66E-04	4.90E-02	3.36E-05	9.52E-03	5.04E-03	2.23E-01	3.64E-03	1.27E-01	centrosome	C
GO:0005814	11	8.01E-02	1.00E+00	1.65E-01	1.00E+00	1.90E-01	1.00E+00	5.04E-01	1.00E+00	2.52E-02	1.00E+00	8.54E-02	1.00E+00	3.85E-01	1.00E+00	4.34E-01	1.00E+00	centriole	C
GO:0005815	153	2.80E-06	3.02E-03	2.66E-07	3.92E-03	6.60E-06	2.91E-03	1.62E-05	9.57E-03	3.31E-04	4.90E-02	2.52E-05	5.87E-03	4.76E-03	2.23E-01	4.54E-03	2.01E-01	microtubule organizing center	C
GO:0005819	87	5.64E-08	2.57E-03	8.02E-06	4.51E-03	7.40E-09	9.80E-04	6.68E-06	2.89E-03	4.39E-05	6.58E-03	3.97E-04	2.33E-02	1.75E-03	8.40E-02	8.90E-03	4.28E-01	spindle	C
GO:0005829	472	1.21E-11	2.57E-03	3.10E-15	0.00E+00	1.12E-10	7.95E-04	8.34E-12	0.00E+00	1.33E-06	1.69E-03	8.92E-14	6.20E-04	6.67E-04	3.44E-02	3.37E-04	3.00E-02	cytosol	C
GO:0005833	12	8.73E-01	1.00E+00	1.87E-01	1.00E+00	4.96E-01	1.00E+00	1.04E-01	1.00E+00	9.98E-01	1.00E+00	1.29E-01	1.00E+00	7.64E-01	1.00E+00	7.85E-01	1.00E+00	hemoglobin complex	C
GO:0005834	38	4.32E-01	1.00E+00	3.95E-01	1.00E+00	5.46E-01	1.00E+00	8.00E-01	1.00E+00	6.84E-01	1.00E+00	5.91E-01	1.00E+00	2.53E-01	1.00E+00	6.94E-02	1.00E+00	heterotrimeric G-protein complex	C
GO:0005839	21	3.41E-01	1.00E+00	1.96E-01	1.00E+00	1.41E-01	1.00E+00	1.86E-01	1.00E+00	6.04E-01	1.00E+00	1.73E-02	6.68E-01	6.71E-01	1.00E+00	8.58E-01	1.00E+00	proteasome core complex (sensu Eukaryot	C
GO:0005840	495	9.97E-11	2.57E-03	1.71E-03	9.65E-02	1.58E-11	7.08E-04	2.23E-03	1.39E-01	6.73E-08	9.59E-04	7.41E-04	4.48E-02	1.67E-03	8.40E-02	2.46E-01	1.00E+00	ribosome	C
GO:0005856	1130	4.37E-09	2.57E-03	4.25E-14	0.00E+00	5.73E-06	2.91E-03	7.68E-09	8.93E-04	4.86E-06	1.69E-03	3.15E-08	9.03E-04	3.66E-06	1.00E-03	5.55E-11	0.00E+00	cytoskeleton	C
GO:0005863	15	9.06E-01	1.00E+00	6.27E-01	1.00E+00	9.98E-01	1.00E+00	6.30E-01	1.00E+00	7.00E-01	1.00E+00	6.99E-01	1.00E+00	8.03E-01	1.00E+00	4.00E-01	1.00E+00	striated muscle thick filament	C
GO:0005865	12	3.56E-02	1.00E+00	1.44E-01	1.00E+00	1.21E-01	1.00E+00	3.49E-01	1.00E+00	9.44E-02	1.00E+00	2.10E-01	1.00E+00	5.82E-02	1.00E+00	1.65E-01	1.00E+00	striated muscle thin filament	C
GO:0005871	12	5.43E-02	1.00E+00	5.91E-02	1.00E+00	8.37E-02	1.00E+00	3.12E-02	1.00E+00	3.57E-01	1.00E+00	7.04E-02	1.00E+00	9.79E-02	1.00E+00	5.29E-01	1.00E+00	kinesin complex	C
GO:0005874	232	5.81E-09	2.57E-03	4.06E-09	8.90E-04	2.76E-09	9.80E-04	4.63E-08	2.89E-03	3.22E-04	4.90E-02	4.51E-05	9.66E-03	5.22E-06	1.00E-03	2.30E-04	2.33E-02	microtubule	C
GO:0005875	115	9.08E-05	1.43E-02	5.91E-05	7.00E-03	3.39E-05	9.82E-03	4.15E-04	4.20E-02	2.28E-02	1.00E+00	2.07E-03	1.27E-01	1.39E-03	6.14E-02	1.55E-02	6.56E-01	microtubule associated complex	C
GO:0005876	14	4.59E-05	9.52E-03	6.94E-03	3.12E-01	2.23E-03	1.03E-01	3.36E-02	1.00E+00	1.23E-05	3.00E-03	8.85E-02	1.00E+00	5.25E-03	2.23E-01	6.53E-03	4.28E-01	spindle microtubule	C
GO:0005882	164	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	intermediate filament	C
GO:0005884	36	2.35E-02	1.00E+00	4.36E-02	1.00E+00	1.83E-01	1.00E+00	2.23E-01	1.00E+00	6.07E-02	1.00E+00	4.71E-02	1.00E+00	1.07E-02	2.75E-01	1.09E-01	1.00E+00	actin filament	C
GO:0005886	3370	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	plasma membrane	C
GO:0005887	507	9.41E-01	1.00E+00	2.45E-01	1.00E+00	9.62E-01	1.00E+00	8.32E-01	1.00E+00	9.92E-01	1.00E+00	3.29E-01	1.00E+00	2.19E-01	1.00E+00	2.64E-03	8.32E-02	integral to plasma membrane	C
GO:0005891	27	8.60E-01	1.00E+00	6.92E-01	1.00E+00	9.90E-01	1.00E+00	9.82E-01	1.00E+00	9.91E-01	1.00E+00	8.27E-01	1.00E+00	2.29E-01	1.00E+00	7.14E-02	1.00E+00	voltage-gated calcium channel complex	C
GO:0005892	13	5.39E-01	1.00E+00	9.35E-01	1.00E+00	9.65E-01	1.00E+00	9.45E-01	1.00E+00	9.63E-01	1.00E+00	9.90E-01	1.00E+00	1.48E-02	4.78E-01	3.14E-01	1.00E+00	nicotinic acetylcholine-gated receptor-chan	C
GO:0005901	34	1.34E-02	6.08E-01	1.90E-03	1.30E-01	3.20E-02	1.00E+00	6.51E-03	3.33E-01	4.13E-02	1.00E+00	1.98E-02	7.56E-01	4.72E-02	1.00E+00	7.10E-03	4.28E-01	caveola	C
GO:0005902	18	3.48E-01	1.00E+00	4.96E-02	1.00E+00	3.96E-01	1.00E+00	1.09E-01	1.00E+00	5.36E-01	1.00E+00	6.21E-02	1.00E+00	1.60E-01	1.00E+00	2.50E-01	1.00E+00	microvillus	C
GO:0005903	29	5.37E-01	1.00E+00	5.06E-02	1.00E+00	8.44E-01	1.00E+00	2.25E-01	1.00E+00	4.12E-01	1.00E+00	5.26E-02	1.00E+00	4.76E-01	1.00E+00	1.31E-01	1.00E+00	brush border	C
GO:0005905	33	1.63E-02	1.00E+00	1.31E-06	3.92E-03	2.42E-02	1.00E+00	1.37E-04	1.30E-02	1.67E-01	1.00E+00	4.05E-04	2.33E-02	3.11E-02	8.38E-01	1.09E-03	6.00E-02	coated pit	C
GO:0005911	190	8.55E-03	6.08E-01	2.73E-02	1.00E+00	2.11E-01	1.00E+00	4.33E-01	1.00E+00	2.76E-01	1.00E+00	2.25E-01	1.00E+00	3.01E-04	2.29E-02	1.41E-04	1.60E-02	intercellular junction	C
GO:0005912	79	3.32E-03	2.12E-01	4.15E-03	1.88E-01	9.28E-02	1.00E+00	2.67E-02	1.00E+00	2.32E-03	1.20E-01	4.70E-02	1.00E+00	1.85E-02	6.36E-01	3.12E-03	1.27E-01	adherens junction	C
GO:0005913	30	5.95E-02	1.00E+00	8.46E-02	1.00E+00	1.48E-01	1.00E+00	6.59E-02	1.00E+00	5.28E-02	1.00E+00	2.71E-01	1.00E+00	4.15E-01	1.00E+00	2.48E-01	1.00E+00	cell-cell adherens junction	C
GO:0005921	31	4.76E-02	1.00E+00	6.49E-02	1.00E+00	2.71E-01	1.00E+00	3.89E-01	1.00E+00	2.51E-01	1.00E+00	1.28E-01	1.00E+00	1.70E-02	4.88E-01	2.81E-02	9.99E-01	gap junction	C
GO:0005922	25	9.27E-02	1.00E+00	1.64E-01	1.00E+00	5.64E-01	1.00E+00	6.04E-01	1.00E+00	3.25E-01	1.00E+00	3.61E-01	1.00E+00	1.99E-02	6.36E-01	2.98E-02	9.99E-01	connexon complex	C
GO:0005923	100	2.63E-02	1.00E+00	3.88E-02	1.00E+00	3.53E-01	1.00E+00	3.06E-01	1.00E+00	1.61E-01	1.00E+00	4.30E-01	1.00E+00	3.40E-03	2.23E-01	7.34E-04	6.00E-02	tight junction	C
GO:0005924	45	1.71E-02	1.00E+00	1.94E-02	1.00E+00	3.31E-01	1.00E+00	1.19E-01	1.00E+00	1.22E-02	6.92E-01	6.22E-02	1.00E+00	1.01E-02	2.75E-01	5.06E-03	2.01E-01	cell-substrate adherens junction	C
GO:0005925	41	1.76E-02	1.00E+00	3.58E-02	1.00E+00	2.60E-01	1.00E+00	1.51E-01	1.00E+00	1.40E-02	6.92E-01	9.96E-02	1.00E+00	1.45E-02	4.78E-01	1.24E-02	4.76E-01	focal adhesion	C
GO:0005929	100	1.32E-01	1.00E+00	4.55E-03	2.61E-01	4.82E-01	1.00E+00	8.32E-02	1.00E+00	4.65E-02	1.00E+00	7.87E-03	4.21E-01	2.20E-01	1.00E+00	3.31E-02	1.00E+00	cilium	C
GO:0005930	16	3.31E-01	1.00E+00	2.09E-01	1.00E+00	2.88E-01	1.00E+00	2.34E-01	1.00E+00	3.16E-01	1.00E+00	4.70E-01	1.00E+00	5.87E-01	1.00E+00	4.80E-02	1.00E+00	axoneme	C
GO:0005932	14	5.47E-01	1.00E+00	7.71E-01	1.00E+00	7.74E-01	1.00E+00	7.78E-01	1.00E+00	4.74E-01	1.00E+00	6.89E-01	1.00E+00	6.82E-01	1.00E+00	7.46E-01	1.00E+00	basal body	C
GO:0005938	92	9.96E-03	6.08E-01	8.69E-08	3.92E-03	1.71E-02	1.00E+00	8.32E-06	2.89E-03	1.31E-01	1.00E+00	1.12E-03	9.00E-02	5.57E-02	1.00E+00	1.34E-04	1.60E-02	cell cortex	C
GO:0005941	45	6.12E-01	1.00E+00	1.34E-01	1.00E+00	4.97E-01	1.00E+00	4.74E-01	1.00E+00	8.09E-01	1.00E+00	1.07E-01	1.00E+00	4.00E-01	1.00E+00	8.83E-02	1.00E+00	unlocalized protein complex	C
GO:0005942	18	6.08E-01	1.00E+00	2.63E-02	1.00E+00	4.70E-01	1.00E+00	3.88E-02	1.00E+00	8.44E-01	1.00E+00	5.42E-02	1.00E+00	5.87E-01	1.00E+00	4.67E-02	1.00E+00	phosphoinositide 3-kinase complex	C
GO:0005952	21	7.32E-01	1.00E+00	6.56E-01	1.00E+00	9.04E-01	1.00E+00	5.82E-01	1.00E+00	6.80E-01	1.00E+00	9.84E-01	1.00E+00	2.83E-01	1.00E+00	2.61E-01	1.00E+00	cAMP-dependent protein kinase complex	C
GO:0005964	15	5.34E-01	1.00E+00	3.77E-02	1.00E+00	5.92E-01	1.00E+00	2.13E-01	1.00E+00	5.99E-01	1.00E+00	2.20E-02	1.00E+00	4.89E-01	1.00E+00	6.90E-02	1.00E+00	phosphorylase kinase complex	C
GO:0005975	498	9.81E-04	8.86E-02	6.06E-06	4.51E-03	1.53E-03	9.50E-02	1.24E-03	9.40E-02	1.90E-03	1.20E-01	4.83E-07	2.00E-03	2.17E-01	1.00E+00	1.18E-02	4.76E-01	carbohydrate metabolism	P
GO:0005976	76	4.71E-01	1.00E+00	1.96E-01	1.00E+00	7.35E-01	1.00E+00	3.06E-01	1.00E+00	1.85E-01	1.00E+00	3.21E-01	1.00E+00	7.00E-01	1.00E+00	6.73E-02	1.00E+00	polysaccharide metabolism	P
GO:0005977	46	3.34E-01	1.00E+00	1.59E-01	1.00E+00	4.36E-01	1.00E+00	3.86E-01	1.00E+00	4.14E-01	1.00E+00	2.11E-01	1.00E+00	3.86E-01	1.00E+00	8.75E-02	1.00E+00	glycogen metabolism	P
GO:0005978	26	8.63E-01	1.00E+00	7.74E-02	1.00E+00	9.38E-01	1.00E+00	4.84E-01	1.00E+00	6.26E-01	1.00E+00	2.72E-02	1.00E+00	8.11E-01	1.00E+00	7.57E-02	1.00E+00	glycogen biosynthesis	P
GO:0005996	196	5.87E-04	8.86E-02	3.84E-05	7.00E-03	1.74E-03	9.50E-02	1.05E-02	5.72E-01	3.29E-02	1.00E+00	8.22E-07	2.00E-03	1.10E-02	3.39E-01	4.37E-02	1.00E+00	monosaccharide metabolism	P
GO:0006006	151	7.42E-03	3.15E-01	1.40E-03	9.65E-02	4.96E-03	3.08E-01	1.71E-01	1.00E+00	1.47E-01	1.00E+00	2.55E-05	5.87E-03	2.85E-02	8.38E-01	4.83E-02	1.00E+00	glucose metabolism	P
GO:0006007	74	2.35E-03	2.12E-01	7.85E-05	1.50E-02	1.27E-03	7.90E-02	4.09E-02	1.00E+00	1.01E-02	6.92E-01	4.25E-06	2.90E-03	3.27E-01	1.00E+00	3.54E-02	1.00E+00	glucose catabolism	P
GO:0006013	10	2.50E-02	1.00E+00	2.99E-02	1.00E+00	1.93E-01	1.00E+00	4.62E-02	1.00E+00	3.66E-02	1.00E+00	3.43E-02	1.00E+00	1.00E-01	1.00E+00	1.33E-01	1.00E+00	mannose metabolism	P
GO:0006020	12	1.76E-02	1.00E+00	7.63E-02	1.00E+00	2.81E-02	1.00E+00	7.01E-02	1.00E+00	5.66E-02	1.00E+00	8.66E-02	1.00E+00	1.41E-01	1.00E+00	7.67E-01	1.00E+00	myo-inositol metabolism	P
GO:0006022	31	7.34E-02	1.00E+00	2.91E-01	1.00E+00	5.12E-01	1.00E+00	4.54E-02	1.00E+00	6.70E-02	1.00E+00	3.61E-01	1.00E+00	9.46E-02	1.00E+00	8.31E-01	1.00E+00	aminoglycan metabolism	P
GO:0006023	15	2.19E-01	1.00E+00	2.97E-01	1.00E+00	6.41E-01	1.00E+00	9.86E-03	5.72E-01	1.64E-01	1.00E+00	4.69E-01	1.00E+00	3.11E-01	1.00E+00	9.39E-01	1.00E+00	aminoglycan biosynthesis	P
GO:0006024	15	2.19E-01	1.00E+00	2.97E-01	1.00E+00	6.41E-01	1.00E+00	9.86E-03	5.72E-01	1.64E-01	1.00E+00	4.69E-01	1.00E+00	3.11E-01	1.00E+00	9.39E-01	1.00E+00	glycosaminoglycan biosynthesis	P
GO:0006029	27	8.60E-01	1.00E+00	7.02E-01	1.00E+00	9.96E-01	1.00E+00	2.04E-01	1.00E+00	6.20E-01	1.00E+00	9.99E-01	1.00E+00	3.84E-01	1.00E+00	4.12E-01	1.00E+00	proteoglycan metabolism	P
GO:0006030	12	9.53E-01	1.00E+00	9.57E-01	1.00E+00	9.96E-01	1.00E+00	9.46E-01	1.00E+00	5.77E-01	1.00E+00	9.06E-01	1.00E+00	9.96E-01	1.00E+00	7.54E-01	1.00E+00	chitin metabolism	P
GO:0006032	10	9.17E-01	1.00E+00	9.67E-01	1.00E+00	9.78E-01	1.00E+00	8.76E-01	1.00E+00	5.79E-01	1.00E+00	9.75E-01	1.00E+00	9.85E-01	1.00E+00	9.38E-01	1.00E+00	chitin catabolism	P
GO:0006040	34	9.05E-01	1.00E+00	6.62E-01	1.00E+00	9.57E-01	1.00E+00	5.58E-01	1.00E+00	3.71E-01	1.00E+00	3.01E-01	1.00E+00	9.63E-01	1.00E+00	9.48E-01	1.00E+00	amino sugar metabolism	P
GO:0006041	26	6.62E-01	1.00E+00	4.51E-01	1.00E+00	8.38E-01	1.00E+00	4.07E-01	1.00E+00	1.56E-01	1.00E+00	2.34E-01	1.00E+00	8.10E-01	1.00E+00	8.89E-01	1.00E+00	glucosamine metabolism	P
GO:0006043	11	9.00E-01	1.00E+00	7.64E-01	1.00E+00	8.74E-01	1.00E+00	6.72E-01	1.00E+00	5.93E-01	1.00E+00	6.58E-01	1.00E+00	9.88E-01	1.00E+00	8.56E-01	1.00E+00	glucosamine catabolism	P
GO:0006044	26	6.62E-01	1.00E+00	4.51E-01	1.00E+00	8.38E-01	1.00E+00	4.07E-01	1.00E+00	1.56E-01	1.00E+00	2.34E-01	1.00E+00	8.10E-01	1.00E+00	8.89E-01	1.00E+00	N-acetylglucosamine metabolism	P
GO:0006046	10	9.17E-01	1.00E+00	9.67E-01	1.00E+00	9.78E-01	1.00E+00	8.76E-01	1.00E+00	5.79E-01	1.00E+00	9.75E-01	1.00E+00	9.85E-01	1.00E+00	9.38E-01	1.00E+00	N-acetylglucosamine catabolism	P
GO:0006066	397	3.49E-05	7.00E-03	9.79E-07	3.92E-03	3.31E-04	4.00E-02	9.15E-04	9.40E-02	3.25E-03	2.13E-01	1.81E-06	2.00E-03	8.35E-04	3.44E-02	6.62E-04	6.00E-02	alcohol metabolism	P
GO:0006071	34	1.33E-02	6.08E-01	3.29E-02	1.00E+00	3.09E-02	1.00E+00	2.04E-02	9.37E-01	5.71E-02	1.00E+00	1.62E-01	1.00E+00	1.05E-01	1.00E+00	1.99E-01	1.00E+00	glycerol metabolism	P
GO:0006072	19	1.81E-01	1.00E+00	8.55E-02	1.00E+00	2.32E-01	1.00E+00	2.34E-01	1.00E+00	2.89E-01	1.00E+00	1.20E-01	1.00E+00	2.23E-01	1.00E+00	1.49E-01	1.00E+00	glycerol-3-phosphate metabolism	P
GO:0006073	46	3.34E-01	1.00E+00	1.59E-01	1.00E+00	4.36E-01	1.00E+00	3.86E-01	1.00E+00	4.14E-01	1.00E+00	2.11E-01	1.00E+00	3.86E-01	1.00E+00	8.75E-02	1.00E+00	glucan metabolism	P
GO:0006081	16	3.85E-02	1.00E+00	2.23E-01	1.00E+00	2.25E-02	1.00E+00	2.39E-01	1.00E+00	1.11E-01	1.00E+00	1.67E-01	1.00E+00	2.13E-01	1.00E+00	5.03E-01	1.00E+00	aldehyde metabolism	P
GO:0006082	642	4.34E-06	3.02E-03	3.48E-10	0.00E+00	2.70E-04	4.00E-02	7.79E-06	2.89E-03	9.40E-04	1.20E-01	2.08E-08	8.78E-04	6.73E-05	8.00E-03	4.18E-06	2.91E-03	organic acid metabolism	P
GO:0006084	31	1.82E-02	1.00E+00	3.20E-02	1.00E+00	2.37E-02	1.00E+00	9.91E-02	1.00E+00	6.21E-02	1.00E+00	5.39E-02	1.00E+00	2.70E-01	1.00E+00	1.21E-01	1.00E+00	acetyl-CoA metabolism	P

GO:0006090	30	2.61E-01	1.00E+00	1.64E-01	1.00E+00	1.86E-01	1.00E+00	2.93E-01	1.00E+00	7.89E-01	1.00E+00	6.13E-01	1.00E+00	7.36E-02	1.00E+00	1.09E-01	1.00E+00	pyruvate metabolism	P
GO:0006091	269	4.23E-03	2.14E-01	2.15E-04	2.40E-02	3.32E-03	2.03E-01	1.97E-02	9.37E-01	3.41E-02	1.00E+00	1.02E-04	1.10E-02	2.94E-01	1.00E+00	8.62E-03	4.28E-01	generation of precursor metabolites and en	P
GO:0006092	123	9.68E-04	8.86E-02	1.12E-05	4.51E-03	3.36E-04	4.00E-02	1.57E-02	6.47E-01	2.34E-02	1.00E+00	3.96E-06	2.90E-03	1.61E-01	1.00E+00	1.16E-02	4.76E-01	main pathways of carbohydrate metabolism	P
GO:0006094	24	1.17E-01	1.00E+00	5.26E-02	1.00E+00	1.66E-01	1.00E+00	1.42E-01	1.00E+00	4.61E-01	1.00E+00	3.61E-01	1.00E+00	3.30E-02	8.38E-01	6.24E-02	1.00E+00	gluconeogenesis	P
GO:0006096	66	3.04E-02	1.00E+00	5.32E-04	4.74E-02	9.96E-03	6.53E-01	9.57E-02	1.00E+00	5.87E-02	1.00E+00	6.58E-05	9.66E-03	4.38E-01	1.00E+00	3.78E-02	1.00E+00	glycolysis	P
GO:0006099	23	1.64E-02	1.00E+00	4.20E-02	1.00E+00	3.05E-02	1.00E+00	9.14E-02	1.00E+00	3.60E-02	1.00E+00	4.66E-02	1.00E+00	3.47E-01	1.00E+00	1.82E-01	1.00E+00	tricarboxylic acid cycle	P
GO:0006100	19	6.15E-01	1.00E+00	9.14E-02	1.00E+00	4.87E-01	1.00E+00	2.00E-01	1.00E+00	8.35E-01	1.00E+00	7.24E-02	1.00E+00	6.75E-01	1.00E+00	2.03E-01	1.00E+00	tricarboxylic acid cycle intermediate metabc	P
GO:0006109	13	5.14E-01	1.00E+00	1.20E-01	1.00E+00	7.68E-01	1.00E+00	3.70E-01	1.00E+00	9.72E-01	1.00E+00	1.83E-01	1.00E+00	4.49E-02	1.00E+00	7.93E-02	1.00E+00	regulation of carbohydrate metabolism	P
GO:0006112	50	4.32E-01	1.00E+00	1.78E-01	1.00E+00	4.54E-01	1.00E+00	4.93E-01	1.00E+00	4.31E-01	1.00E+00	1.17E-01	1.00E+00	5.65E-01	1.00E+00	1.43E-01	1.00E+00	energy reserve metabolism	P
GO:0006118	42	9.79E-02	1.00E+00	2.56E-01	1.00E+00	2.12E-01	1.00E+00	2.51E-01	1.00E+00	1.27E-01	1.00E+00	2.38E-01	1.00E+00	2.61E-01	1.00E+00	3.85E-01	1.00E+00	electron transport	P
GO:0006119	76	2.29E-01	1.00E+00	4.03E-01	1.00E+00	2.07E-01	1.00E+00	2.88E-01	1.00E+00	2.43E-01	1.00E+00	3.83E-01	1.00E+00	7.55E-01	1.00E+00	6.45E-01	1.00E+00	oxidative phosphorylation	P
GO:0006120	17	1.76E-01	1.00E+00	5.68E-01	1.00E+00	2.31E-01	1.00E+00	6.73E-01	1.00E+00	2.37E-01	1.00E+00	4.89E-01	1.00E+00	1.81E-01	1.00E+00	2.89E-01	1.00E+00	mitochondrial electron transport, NADH to u	P
GO:0006139	3843	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.10E-40	0.00E+00	4.14E-38	0.00E+00	2.14E-10	0.00E+00	1.02E-15	0.00E+00	nucleobase, nucleoside, nucleotide and nuc	P
GO:0006140	18	4.82E-02	1.00E+00	7.11E-02	1.00E+00	2.25E-01	1.00E+00	1.78E-01	1.00E+00	5.08E-02	1.00E+00	1.18E-01	1.00E+00	3.81E-02	8.38E-01	4.47E-02	1.00E+00	regulation of nucleotide metabolism	P
GO:0006163	93	2.01E-03	2.12E-01	4.22E-04	4.74E-02	5.06E-03	3.08E-01	1.02E-03	9.40E-02	1.03E-03	1.20E-01	3.20E-03	1.51E-01	4.18E-01	1.00E+00	5.62E-02	1.00E+00	purine nucleotide metabolism	P
GO:0006164	77	2.40E-02	1.00E+00	1.63E-02	7.63E-01	2.97E-02	1.00E+00	1.18E-02	6.47E-01	8.79E-03	6.92E-01	5.46E-02	1.00E+00	8.09E-01	1.00E+00	2.29E-01	1.00E+00	purine nucleotide biosynthesis	P
GO:0006171	21	3.09E-01	1.00E+00	1.37E-01	1.00E+00	7.64E-01	1.00E+00	5.48E-01	1.00E+00	3.35E-01	1.00E+00	3.11E-01	1.00E+00	9.09E-02	1.00E+00	4.18E-02	1.00E+00	cAMP biosynthesis	P
GO:0006182	13	3.04E-01	1.00E+00	6.11E-01	1.00E+00	7.47E-01	1.00E+00	4.57E-01	1.00E+00	1.61E-01	1.00E+00	8.68E-01	1.00E+00	3.38E-01	1.00E+00	5.27E-01	1.00E+00	cGMP biosynthesis	P
GO:0006183	13	4.09E-02	1.00E+00	8.53E-04	8.70E-02	1.10E-01	1.00E+00	1.71E-02	6.47E-01	7.78E-03	6.92E-01	4.36E-03	2.66E-01	5.05E-01	1.00E+00	5.00E-02	1.00E+00	GTP biosynthesis	P
GO:0006206	10	3.65E-02	1.00E+00	5.96E-01	1.00E+00	6.09E-02	1.00E+00	3.55E-01	1.00E+00	1.56E-02	6.92E-01	9.26E-01	1.00E+00	2.68E-01	1.00E+00	3.85E-01	1.00E+00	pyrimidine base metabolism	P
GO:0006213	10	4.04E-01	1.00E+00	9.51E-01	1.00E+00	3.64E-01	1.00E+00	8.01E-01	1.00E+00	4.07E-01	1.00E+00	8.68E-01	1.00E+00	3.59E-01	1.00E+00	9.40E-01	1.00E+00	pyrimidine nucleoside metabolism	P
GO:0006220	25	7.21E-02	1.00E+00	8.79E-03	4.69E-01	7.90E-02	1.00E+00	8.37E-03	4.92E-01	3.89E-02	1.00E+00	1.23E-02	5.03E-01	3.02E-01	1.00E+00	1.57E-01	1.00E+00	pyrimidine nucleotide metabolism	P
GO:0006221	21	5.69E-02	1.00E+00	3.84E-03	1.88E-01	7.54E-02	1.00E+00	8.51E-03	4.92E-01	3.82E-02	1.00E+00	1.07E-02	5.03E-01	1.65E-01	1.00E+00	3.64E-02	1.00E+00	pyrimidine nucleotide biosynthesis	P
GO:0006228	12	6.11E-02	1.00E+00	2.24E-03	1.71E-01	1.03E-01	1.00E+00	3.15E-02	1.00E+00	1.82E-02	7.90E-01	3.47E-03	1.51E-01	5.60E-01	1.00E+00	8.52E-02	1.00E+00	UTP biosynthesis	P
GO:0006241	13	6.96E-02	1.00E+00	1.59E-03	9.65E-02	1.08E-01	1.00E+00	1.55E-02	6.47E-01	2.36E-02	1.00E+00	1.14E-02	5.03E-01	5.54E-01	1.00E+00	5.21E-02	1.00E+00	CTP biosynthesis	P
GO:0006259	811	6.55E-20	0.00E+00	8.36E-23	0.00E+00	1.61E-21	0.00E+00	3.05E-30	0.00E+00	9.04E-12	0.00E+00	1.91E-10	6.20E-04	1.86E-04	8.00E-03	2.32E-07	9.38E-04	DNA metabolism	P
GO:0006260	167	7.09E-08	2.57E-03	2.32E-07	3.92E-03	8.66E-06	2.91E-03	2.42E-06	2.89E-03	4.66E-06	1.69E-03	5.45E-05	9.66E-03	5.20E-03	2.23E-01	7.41E-04	6.00E-02	DNA replication	P
GO:0006261	74	1.21E-04	1.43E-02	1.22E-05	4.51E-03	1.29E-03	7.90E-02	7.93E-04	6.90E-02	1.38E-03	1.20E-01	5.34E-05	9.66E-03	6.93E-02	1.00E+00	4.09E-02	1.00E+00	DNA-dependent DNA replication	P
GO:0006265	23	8.70E-02	1.00E+00	8.30E-02	1.00E+00	2.70E-02	1.00E+00	8.92E-02	1.00E+00	5.72E-02	1.00E+00	2.34E-01	1.00E+00	9.98E-01	1.00E+00	2.08E-01	1.00E+00	DNA topological change	P
GO:0006268	12	1.02E-02	6.08E-01	4.52E-02	1.00E+00	9.88E-03	6.53E-01	1.62E-02	6.47E-01	1.42E-02	6.92E-01	8.81E-02	1.00E+00	2.18E-01	1.00E+00	8.67E-01	1.00E+00	DNA unwinding during replication	P
GO:0006270	20	9.00E-03	6.08E-01	1.82E-02	1.00E+00	6.45E-02	1.00E+00	2.14E-02	9.37E-01	2.13E-02	9.56E-01	4.17E-02	1.00E+00	3.29E-01	1.00E+00	2.17E-01	1.00E+00	DNA replication initiation	P
GO:0006275	30	1.02E-03	8.86E-02	1.37E-03	9.65E-02	2.37E-02	1.00E+00	5.16E-02	1.00E+00	5.59E-03	3.75E-01	6.59E-04	3.20E-02	1.94E-02	6.36E-01	1.01E-01	1.00E+00	regulation of DNA replication	P
GO:0006281	242	3.93E-11	2.57E-03	7.50E-13	0.00E+00	2.41E-10	7.95E-04	7.59E-12	0.00E+00	5.92E-08	9.59E-04	1.52E-06	2.00E-03	1.59E-02	4.88E-01	3.78E-05	7.00E-03	DNA repair	P
GO:0006284	23	5.20E-03	2.72E-01	5.08E-01	1.00E+00	1.31E-02	6.53E-01	7.14E-01	1.00E+00	4.32E-03	2.13E-01	6.17E-01	1.00E+00	6.34E-01	1.00E+00	1.27E-01	1.00E+00	base-excision repair	P
GO:0006289	33	7.93E-03	6.08E-01	9.74E-02	1.00E+00	8.71E-03	6.53E-01	1.75E-01	1.00E+00	1.25E-02	6.92E-01	4.34E-01	1.00E+00	1.84E-01	1.00E+00	3.90E-02	1.00E+00	nucleotide-excision repair	P
GO:0006298	14	5.64E-01	1.00E+00	5.02E-02	1.00E+00	4.08E-01	1.00E+00	2.89E-01	1.00E+00	8.55E-01	1.00E+00	3.00E-02	1.00E+00	5.11E-01	1.00E+00	2.97E-02	9.99E-01	mismatch repair	P
GO:0006302	32	1.35E-02	6.08E-01	1.52E-05	4.51E-03	6.17E-03	4.69E-01	2.86E-05	9.57E-03	3.93E-02	1.00E+00	9.28E-04	9.00E-02	3.30E-01	1.00E+00	1.10E-02	4.76E-01	double-strand break repair	P
GO:0006304	38	8.21E-01	1.00E+00	8.03E-01	1.00E+00	5.62E-01	1.00E+00	4.65E-01	1.00E+00	9.84E-01	1.00E+00	9.40E-01	1.00E+00	6.04E-01	1.00E+00	7.00E-01	1.00E+00	DNA modification	P
GO:0006305	37	8.07E-01	1.00E+00	8.17E-01	1.00E+00	5.14E-01	1.00E+00	4.86E-01	1.00E+00	9.80E-01	1.00E+00	9.23E-01	1.00E+00	6.45E-01	1.00E+00	7.67E-01	1.00E+00	DNA alkylation	P
GO:0006306	37	8.07E-01	1.00E+00	8.17E-01	1.00E+00	5.14E-01	1.00E+00	4.86E-01	1.00E+00	9.80E-01	1.00E+00	9.23E-01	1.00E+00	6.45E-01	1.00E+00	7.67E-01	1.00E+00	DNA methylation	P
GO:0006308	18	2.39E-03	2.12E-01	7.76E-04	8.10E-02	2.06E-03	9.50E-02	4.77E-04	4.20E-02	7.89E-03	6.92E-01	2.93E-03	1.44E-01	1.57E-01	1.00E+00	9.47E-02	1.00E+00	DNA catabolism	P
GO:0006309	10	7.01E-03	3.15E-01	2.36E-02	1.00E+00	1.18E-02	6.53E-01	1.24E-02	6.47E-01	2.13E-02	9.56E-01	3.32E-02	1.00E+00	3.27E-02	8.38E-01	3.73E-01	1.00E+00	DNA fragmentation during apoptosis	P
GO:0006310	86	1.70E-04	1.72E-02	6.88E-08	3.92E-03	1.30E-04	1.16E-02	3.75E-07	2.89E-03	2.90E-02	1.00E+00	3.21E-04	2.33E-02	1.49E-02	4.78E-01	2.87E-04	3.00E-02	DNA recombination	P
GO:0006323	377	2.76E-08	2.57E-03	1.15E-10	0.00E+00	2.73E-10	7.95E-04	5.45E-16	0.00E+00	8.25E-04	1.20E-01	1.19E-05	5.87E-03	2.61E-03	8.40E-02	1.33E-03	6.00E-02	DNA packaging	P
GO:0006325	375	4.30E-08	2.57E-03	2.79E-10	0.00E+00	4.63E-10	7.95E-04	1.77E-15	0.00E+00	1.01E-03	1.20E-01	1.76E-05	5.87E-03	2.71E-03	8.40E-02	2.13E-03	7.90E-02	establishment and/or maintenance of chron	P
GO:0006333	222	5.07E-02	1.00E+00	1.07E-01	1.00E+00	6.96E-03	4.69E-01	1.13E-03	9.40E-02	4.90E-01	1.00E+00	4.84E-01	1.00E+00	1.37E-01	1.00E+00	6.67E-01	1.00E+00	chromatin assembly or disassembly	P
GO:0006334	174	8.04E-01	1.00E+00	9.04E-01	1.00E+00	2.86E-01	1.00E+00	1.32E-01	1.00E+00	9.85E-01	1.00E+00	9.82E-01	1.00E+00	6.62E-01	1.00E+00	9.97E-01	1.00E+00	nucleosome assembly	P
GO:0006338	49	1.01E-08	2.57E-03	8.15E-11	0.00E+00	1.28E-07	2.00E-03	1.14E-10	0.00E+00	1.19E-04	2.70E-02	1.65E-05	5.87E-03	5.82E-05	8.00E-03	1.79E-06	2.00E-03	chromatin remodeling	P
GO:0006342	16	2.33E-03	2.12E-01	2.35E-03	1.71E-01	6.62E-03	4.69E-01	4.14E-03	2.88E-01	1.87E-02	7.90E-01	9.35E-02	1.00E+00	6.57E-03	2.75E-01	1.35E-02	4.76E-01	chromatin silencing	P
GO:0006350	2593	3.34E-26	0.00E+00	4.68E-34	0.00E+00	9.61E-28	0.00E+00	2.53E-36	0.00E+00	7.01E-19	0.00E+00	7.37E-23	0.00E+00	1.20E-05	3.63E-03	2.72E-09	0.00E+00	transcription	P
GO:0006351	2397	2.56E-22	0.00E+00	1.45E-28	0.00E+00	1.51E-23	0.00E+00	9.10E-32	0.00E+00	3.54E-17	0.00E+00	9.35E-20	0.00E+00	1.47E-04	8.00E-03	4.86E-07	1.92E-03	transcription, DNA-dependent	P
GO:0006352	64	9.53E-05	1.43E-02	9.59E-05	1.50E-02	2.92E-05	3.00E-03	2.32E-06	2.89E-03	5.25E-04	4.90E-02	2.88E-03	1.44E-01	7.32E-02	1.00E+00	1.10E-01	1.00E+00	transcription initiation	P
GO:0006354	11	1.60E-04	1.72E-02	4.44E-02	1.00E+00	1.45E-02	6.53E-01	2.00E-02	9.37E-01	2.19E-02	1.00E+00	4.66E-02	1.00E+00	8.11E-02	1.00E+00	8.69E-01	1.00E+00	RNA elongation	P
GO:0006355	2352	3.39E-21	0.00E+00	9.10E-28	0.00E+00	3.54E-22	0.00E+00	7.72E-30	0.00E+00	6.70E-16	0.00E+00	1.60E-19	0.00E+00	1.20E-04	8.00E-03	3.06E-07	1.00E-03	regulation of transcription, DNA-dependent	P
GO:0006357	531	4.00E-06	3.02E-03	7.84E-06	4.51E-03	2.54E-07	2.00E-03	9.36E-05	1.30E-02	2.76E-02	1.00E+00	5.96E-03	4.21E-01	2.18E-04	1.20E-02	4.33E-05	7.00E-03	regulation of transcription from RNA polyme	P
GO:0006364	69	1.68E-07	2.57E-03	1.16E-03	9.65E-02	1.18E-07	2.00E-03	6.44E-04	4.20E-02	1.70E-06	1.69E-03	1.90E-02	6.68E-01	6.90E-02	1.00E+00	2.27E-01	1.00E+00	rRNA processing	P
GO:0006366	579	8.36E-07	2.76E-03	2.67E-06	3.92E-03	1.67E-08	9.80E-04	2.80E-05	9.57E-03	1.17E-02	6.92E-01	1.89E-03	1.27E-01	4.10E-04	2.40E-02	1.56E-04	1.60E-02	transcription from RNA polymerase II promc	P
GO:0006367	23	2.67E-03	2.12E-01	1.63E-03	9.65E-02	7.28E-04	4.90E-02	6.24E-04	4.20E-02	1.13E-02	6.92E-01	2.29E-02	1.00E+00	1.56E-01	1.00E+00	1.61E-01	1.00E+00	transcription initiation from RNA polymerase	P
GO:0006376	10	6.39E-02	1.00E+00	8.07E-02	1.00E+00	1.11E-01	1.00E+00	7.90E-02	1.00E+00	8.71E-02	1.00E+00	2.02E-01	1.00E+00	1.33E-02	4.78E-01	2.61E-01	1.00E+00	mRNA splice site selection	P
GO:0006396	411	2.86E-29	0.00E+00	2.26E-25	0.00E+00	6.87E-27	0.00E+00	1.08E-23	0.00E+00	1.10E-17	0.00E+00	1.49E-13	6.20E-04	1.58E-09	0.00E+00	1.31E-07	9.38E-04	RNA processing	P
GO:0006397	244	3.46E-20	0.00E+00	2.03E-18	0.00E+00	7.38E-18	0.00E+00	8.94E-18	0.00E+00	5.56E-13	0.00E+00	9.19E-10	6.20E-04	2.01E-07	0.00E+00	9.62E-06	7.00E-03	mRNA processing	P
GO:0006399	127	3.62E-07	2.57E-03	1.32E-05	4.51E-03	3.40E-05	9.82E-03	4.60E-05	1.07E-02	2.95E-05	6.33E-03	1.35E-04	1.30E-02	1.00E-03	3.62E-02	4.98E-02	1.00E+00	tRNA metabolism	P
GO:0006400	11	1.10E-01	1.00E+00	4.65E-01	1.00E+00	3.87E-01	1.00E+00	8.80E-01	1.00E+00	1.28E-01	1.00E+00	7.75E-01	1.00E+00	1.10E-01	1.00E+00	1.47E-01	1.00E+00	tRNA modification	P
GO:0006401	35	2.49E-04	1.90E-02	1.06E-03	9.65E-02	1.55E-03	9.50E-02	1.26E-02	6.47E-01	2.08E-03	1.20E-01	2.33E-03	1.27E-01	2.70E-02	8.38E-01	2.86E-02	9.99E-01	RNA catabolism	P
GO:0006402	29	3.61E-04	3.10E-02	3.28E-03	1.88E-01	1.34E-03	7.90E-02	1.29E-02	6.47E-01	2.24E-03	1.20E-01	1.83E-02	6.68E-01	3.25E-02	8.38E-01	2.13E-02	9.99E-01	mRNA catabolism	P
GO:0006403	62	1.17E-06	2.76E-03	3.54E-10	0.00E+00	1.40E-05	3.00E-03	5.91E-10	0.00E+00	9.49E-06	2.00E-03	1.59E-05	5.87E-03	2.75E-01	1.00E+00	1.27E-03	6.00E-02	RNA localization	P
GO:0006405	21	9.33E-05	1.43E-02	2.24E-04	2.40E-02	1.29E-03	7.90E-02	1.20E-03	9.40E-02	9.30E-05	2.70E-02	1.33E-03	9.00E-02	8.22E-02	1.00E+00	1.16E-02	4.76E-01	RNA export from nucleus	P
GO:0006406	16	7.01E-04	8.86E-02	4.96E-04	4.74E-02	9.12E-03	6.53E-01	6.94E-04	4.20E-02	1.90E-04	4.90E-02	3.27E-03	1.51E-01	1.13E-01	1.00E+00	4.70E-02	1.00E+00	mRNA export from nucleus	P
GO:0006412	941	3.88E-17	0.00E+00	5.12E-13	0.00E+00	1.65E-15	0.00E+00	1.09E-09	0.00E+00	1.64E-11	0.00E+00	1.17E-09	6.20E-04	4.79E-07	8.23E-04	2.47E-06	2.00E-03	protein biosynthesis	P
GO:0006413	65	1.02E-05	7.00E-03	3.09E-07	3.92E-03	2.78E-07	2.00E-03	1.19E-05	2.89E-03	4.02E-04	4.90E-02	6.20E-06	5.87E-03	6.44E-02	1.00E+00	8.32E-03	4.28E-01	translational initiation	P
GO:0006414	24	2.05E-01	1.00E+00	5.18E-02	1.00E+00	2.00E-02	1.00E+00	8.73E-03	4.92E-01	1.88E-01	1.00E+00	2.45E-01	1.00E+00	7.74E-01	1.00E+00	2.01E-01	1.00E+00	translational elongation	P
GO:0006417	158	4.36E-03	2.14E-01	4.87E-05	7.00E-03	2.62E-02	1.00E+00	6.00E-03	2.88E-01	7.03E-02	1.00E+00	9.49E-03	5.03E-01	4.76E-03	2.23E-01	1.96E-04	1.60E-02	regulation of protein biosynthesis	P
GO:0006418	68	1.05E-05	7.00E-03	1.16E-04	1.50E-02	2.35E-04	2.10E-02	1.24E-04	1.30E-02	6.40E-05	2.40E-02	2.27E-04	2.33E-02	2.83E-02	8.38E-01	1.63E-01	1.00E+00	tRNA aminoacylation for protein translation	P
GO:0006445	31	8.54E-05	1.43E-02	1.64E-06	3.92E-03	9.13E-05	1.16E-02	6.17E-05	1.30E-02	8.32E-04	1.20E-01	1.24E-03	9.00E-02	1.15E-02	3.39E-01	1.87E-03	7.90E-02	regulation of translation	P
GO:0006446	22	2.77E-04	1.90E-02	4.87E-05	7.00E-03	9.45E-04	4.90E-02	8.38E-04	6.90E-02	1.26E-03	1.20E-01	3.21E-03	1.51E-01	1.13E-02	3.39E-01	1.42E-02	4.76E-01	regulation of translational initiation	P

GO:0006457	150	2.74E-11	2.57E-03	1.97E-11	0.00E+00	3.84E-08	9.80E-04	1.18E-11	0.00E+00	2.23E-08	9.59E-04	6.18E-06	5.87E-03	2.17E-05	4.00E-03	1.63E-03	6.00E-02	protein folding	P
GO:0006461	383	2.00E-02	1.00E+00	4.35E-03	1.88E-01	3.15E-03	1.35E-01	7.12E-05	1.30E-02	3.36E-01	1.00E+00	2.78E-02	1.00E+00	7.11E-02	1.00E+00	5.33E-01	1.00E+00	protein complex assembly	P
GO:0006464	1800	2.61E-24	0.00E+00	0.00E+00	0.00E+00	3.13E-23	0.00E+00	1.03E-39	0.00E+00	1.19E-15	0.00E+00	2.25E-31	0.00E+00	1.21E-06	8.23E-04	8.62E-24	0.00E+00	protein modification	P
GO:0006468	748	3.91E-04	3.10E-02	1.98E-12	0.00E+00	2.71E-04	4.00E-02	4.97E-08	2.89E-03	5.49E-03	3.75E-01	2.52E-08	9.03E-04	6.35E-02	1.00E+00	1.07E-08	0.00E+00	protein amino acid phosphorylation	P
GO:0006469	51	4.82E-02	1.00E+00	7.01E-06	4.51E-03	2.73E-02	1.00E+00	2.34E-04	1.30E-02	4.21E-01	1.00E+00	1.16E-04	1.30E-02	7.39E-02	1.00E+00	7.93E-04	6.00E-02	negative regulation of protein kinase activity	P
GO:0006470	135	7.71E-03	6.08E-01	1.49E-04	1.50E-02	7.04E-03	4.69E-01	7.87E-04	6.90E-02	3.11E-01	1.00E+00	2.51E-02	1.00E+00	2.74E-03	8.40E-02	1.88E-03	7.90E-02	protein amino acid dephosphorylation	P
GO:0006471	16	7.41E-03	3.15E-01	4.88E-02	1.00E+00	1.01E-01	1.00E+00	2.90E-01	1.00E+00	3.76E-02	1.00E+00	1.31E-01	1.00E+00	5.11E-02	1.00E+00	1.61E-01	1.00E+00	protein amino acid ADP-ribosylation	P
GO:0006473	16	1.66E-02	1.00E+00	1.51E-03	9.65E-02	1.74E-02	1.00E+00	5.41E-03	2.88E-01	2.54E-01	1.00E+00	4.57E-03	2.66E-01	5.33E-01	1.00E+00	1.51E-02	6.56E-01	protein amino acid acetylation	P
GO:0006476	19	1.24E-02	6.08E-01	7.48E-03	3.12E-01	4.74E-02	1.00E+00	1.21E-02	6.47E-01	2.24E-03	1.20E-01	6.00E-02	1.00E+00	1.65E-01	1.00E+00	1.72E-01	1.00E+00	protein amino acid deacetylation	P
GO:0006479	36	3.25E-05	7.00E-03	9.32E-08	3.92E-03	7.06E-05	1.07E-02	6.69E-07	2.89E-03	2.22E-03	1.20E-01	3.81E-05	9.66E-03	1.28E-02	4.78E-01	7.06E-04	6.00E-02	protein amino acid methylation	P
GO:0006486	88	4.97E-02	1.00E+00	1.74E-02	7.63E-01	1.46E-01	1.00E+00	9.59E-02	1.00E+00	2.60E-01	1.00E+00	6.15E-02	1.00E+00	6.71E-03	2.75E-01	6.35E-03	4.28E-01	protein amino acid glycosylation	P
GO:0006487	22	5.09E-03	2.72E-01	1.83E-02	1.00E+00	4.32E-02	1.00E+00	6.04E-02	1.00E+00	3.65E-02	1.00E+00	1.03E-01	1.00E+00	4.08E-02	1.00E+00	8.22E-03	4.28E-01	protein amino acid N-linked glycosylation	P
GO:0006493	15	7.08E-01	1.00E+00	1.01E-01	1.00E+00	5.56E-01	1.00E+00	2.67E-01	1.00E+00	9.11E-01	1.00E+00	2.31E-01	1.00E+00	5.56E-01	1.00E+00	5.53E-02	1.00E+00	protein amino acid O-linked glycosylation	P
GO:0006497	49	1.18E-01	1.00E+00	5.41E-02	1.00E+00	3.57E-01	1.00E+00	3.95E-02	1.00E+00	8.10E-02	1.00E+00	1.37E-01	1.00E+00	6.31E-01	1.00E+00	3.50E-01	1.00E+00	protein amino acid lipidation	P
GO:0006505	28	2.34E-02	1.00E+00	2.61E-02	1.00E+00	6.53E-02	1.00E+00	7.17E-02	1.00E+00	3.38E-02	1.00E+00	2.80E-02	1.00E+00	2.68E-01	1.00E+00	2.10E-01	1.00E+00	GPI anchor metabolism	P
GO:0006506	24	4.89E-02	1.00E+00	3.06E-02	1.00E+00	8.05E-02	1.00E+00	1.70E-02	6.47E-01	8.77E-02	1.00E+00	3.31E-02	1.00E+00	4.62E-01	1.00E+00	5.21E-01	1.00E+00	GPI anchor biosynthesis	P
GO:0006508	827	3.85E-02	1.00E+00	2.00E-04	2.40E-02	1.74E-02	1.00E+00	8.46E-04	6.90E-02	4.43E-01	1.00E+00	2.68E-02	1.00E+00	7.31E-02	1.00E+00	6.41E-05	7.00E-03	proteolysis	P
GO:0006509	13	1.28E-01	1.00E+00	2.70E-02	1.00E+00	1.48E-01	1.00E+00	2.76E-02	1.00E+00	3.20E-01	1.00E+00	5.37E-02	1.00E+00	2.43E-01	1.00E+00	3.69E-01	1.00E+00	membrane protein ectodomain proteolysis	P
GO:0006511	159	5.28E-05	9.52E-03	3.12E-09	8.90E-04	1.02E-06	2.00E-03	6.09E-10	0.00E+00	7.13E-03	6.92E-01	7.65E-06	5.87E-03	1.88E-01	1.00E+00	7.38E-04	6.00E-02	ubiquitin-dependent protein catabolism	P
GO:0006512	551	1.04E-18	0.00E+00	4.18E-30	0.00E+00	3.74E-20	0.00E+00	1.04E-27	0.00E+00	2.83E-14	0.00E+00	4.50E-21	0.00E+00	6.15E-03	2.75E-01	5.21E-09	0.00E+00	ubiquitin cycle	P
GO:0006515	12	3.24E-02	1.00E+00	4.06E-06	4.51E-03	3.91E-02	1.00E+00	4.08E-04	4.20E-02	7.25E-02	1.00E+00	4.36E-02	1.00E+00	2.47E-01	1.00E+00	7.16E-02	1.00E+00	misfolded or incompletely synthesized prote	P
GO:0006516	10	1.74E-01	1.00E+00	3.77E-01	1.00E+00	2.56E-01	1.00E+00	9.49E-02	1.00E+00	1.68E-01	1.00E+00	4.62E-01	1.00E+00	4.10E-01	1.00E+00	8.92E-01	1.00E+00	glycoprotein catabolism	P
GO:0006518	16	9.22E-01	1.00E+00	7.97E-01	1.00E+00	8.68E-01	1.00E+00	5.21E-01	1.00E+00	1.00E+00	1.00E+00	6.92E-01	1.00E+00	6.28E-01	1.00E+00	9.96E-01	1.00E+00	peptide metabolism	P
GO:0006519	463	7.17E-05	1.41E-02	3.50E-06	3.92E-03	1.16E-03	7.90E-02	5.03E-04	4.20E-02	3.74E-03	2.13E-01	1.25E-05	5.87E-03	1.18E-03	6.14E-02	4.74E-03	2.01E-01	amino acid and derivative metabolism	P
GO:0006520	374	3.61E-04	3.10E-02	4.15E-06	4.51E-03	6.26E-03	4.69E-01	1.16E-03	9.40E-02	1.24E-02	6.92E-01	8.94E-06	5.87E-03	8.59E-04	3.44E-02	1.61E-03	6.00E-02	amino acid metabolism	P
GO:0006521	97	8.85E-01	1.00E+00	5.11E-01	1.00E+00	9.32E-01	1.00E+00	7.98E-01	1.00E+00	9.86E-01	1.00E+00	5.13E-01	1.00E+00	1.60E-01	1.00E+00	1.32E-01	1.00E+00	regulation of amino acid metabolism	P
GO:0006536	10	2.73E-01	1.00E+00	1.96E-01	1.00E+00	3.84E-01	1.00E+00	4.07E-01	1.00E+00	2.84E-01	1.00E+00	1.37E-01	1.00E+00	4.48E-01	1.00E+00	4.03E-01	1.00E+00	glutamate metabolism	P
GO:0006541	18	3.93E-01	1.00E+00	9.23E-02	1.00E+00	3.52E-01	1.00E+00	1.04E-01	1.00E+00	6.58E-01	1.00E+00	3.35E-01	1.00E+00	2.98E-01	1.00E+00	3.94E-02	1.00E+00	glutamine metabolism	P
GO:0006544	12	7.71E-01	1.00E+00	1.72E-02	7.63E-01	7.96E-01	1.00E+00	9.19E-03	5.72E-01	6.47E-01	1.00E+00	5.01E-02	1.00E+00	7.04E-01	1.00E+00	7.90E-02	1.00E+00	glycine metabolism	P
GO:0006547	11	6.48E-01	1.00E+00	5.73E-01	1.00E+00	8.78E-01	1.00E+00	7.22E-01	1.00E+00	4.94E-01	1.00E+00	6.43E-01	1.00E+00	3.26E-01	1.00E+00	2.53E-01	1.00E+00	histidine metabolism	P
GO:0006548	11	6.48E-01	1.00E+00	5.73E-01	1.00E+00	8.78E-01	1.00E+00	7.22E-01	1.00E+00	4.94E-01	1.00E+00	6.43E-01	1.00E+00	3.26E-01	1.00E+00	2.53E-01	1.00E+00	histidine catabolism	P
GO:0006570	14	5.45E-01	1.00E+00	4.09E-01	1.00E+00	5.93E-01	1.00E+00	6.54E-01	1.00E+00	6.03E-01	1.00E+00	5.67E-01	1.00E+00	5.70E-01	1.00E+00	7.11E-02	1.00E+00	tyrosine metabolism	P
GO:0006575	156	6.58E-02	1.00E+00	1.08E-02	4.69E-01	1.06E-01	1.00E+00	5.25E-02	1.00E+00	1.93E-01	1.00E+00	1.65E-02	6.68E-01	1.20E-01	1.00E+00	9.92E-02	1.00E+00	amino acid derivative metabolism	P
GO:0006576	89	3.28E-01	1.00E+00	1.71E-01	1.00E+00	4.18E-01	1.00E+00	1.54E-01	1.00E+00	3.85E-01	1.00E+00	3.90E-01	1.00E+00	2.19E-01	1.00E+00	2.60E-01	1.00E+00	biogenic amine metabolism	P
GO:0006582	11	7.38E-01	1.00E+00	7.81E-01	1.00E+00	7.67E-01	1.00E+00	8.47E-01	1.00E+00	9.65E-01	1.00E+00	9.84E-01	1.00E+00	1.32E-01	1.00E+00	1.26E-01	1.00E+00	melanin metabolism	P
GO:0006584	36	7.24E-01	1.00E+00	5.99E-01	1.00E+00	7.29E-01	1.00E+00	6.39E-01	1.00E+00	5.18E-01	1.00E+00	6.43E-01	1.00E+00	7.56E-01	1.00E+00	3.81E-01	1.00E+00	catecholamine metabolism	P
GO:0006586	11	7.31E-01	1.00E+00	4.41E-01	1.00E+00	9.97E-01	1.00E+00	6.60E-01	1.00E+00	4.27E-01	1.00E+00	5.43E-01	1.00E+00	3.25E-01	1.00E+00	2.10E-01	1.00E+00	indolalkylamine metabolism	P
GO:0006595	21	4.27E-03	2.14E-01	6.88E-04	5.90E-02	2.20E-02	1.00E+00	3.00E-04	4.20E-02	1.06E-01	1.00E+00	3.36E-03	1.51E-01	1.02E-02	2.75E-01	1.29E-01	1.00E+00	polyamine metabolism	P
GO:0006596	12	2.60E-02	1.00E+00	6.08E-02	1.00E+00	1.82E-01	1.00E+00	4.06E-02	1.00E+00	1.72E-01	1.00E+00	1.10E-01	1.00E+00	1.37E-02	4.78E-01	1.65E-01	1.00E+00	polyamine biosynthesis	P
GO:0006605	228	2.10E-07	2.57E-03	2.82E-08	9.59E-04	7.95E-06	2.91E-03	1.63E-08	8.93E-04	7.26E-06	2.00E-03	4.58E-04	2.33E-02	2.47E-03	8.40E-02	9.75E-04	6.00E-02	protein targeting	P
GO:0006606	81	9.67E-05	1.43E-02	2.60E-07	3.92E-03	1.28E-04	1.16E-02	7.13E-06	2.89E-03	2.17E-03	1.20E-01	1.48E-03	9.30E-02	8.05E-02	1.00E+00	1.76E-04	1.60E-02	protein import into nucleus	P
GO:0006611	18	2.55E-02	1.00E+00	1.33E-03	9.65E-02	9.50E-02	1.00E+00	1.32E-03	9.40E-02	3.89E-02	1.00E+00	4.79E-02	1.00E+00	3.20E-01	1.00E+00	1.20E-02	4.76E-01	protein export from nucleus	P
GO:0006612	29	3.11E-03	2.12E-01	1.57E-02	7.63E-01	6.00E-02	1.00E+00	1.69E-02	6.47E-01	2.30E-03	1.20E-01	5.30E-02	1.00E+00	4.16E-02	1.00E+00	2.09E-01	1.00E+00	protein targeting to membrane	P
GO:0006613	19	4.50E-02	1.00E+00	1.78E-01	1.00E+00	5.10E-01	1.00E+00	1.71E-01	1.00E+00	2.50E-02	1.00E+00	1.87E-01	1.00E+00	1.27E-01	1.00E+00	3.36E-01	1.00E+00	cotranslational protein targeting to membrai	P
GO:0006614	16	2.77E-02	1.00E+00	1.97E-01	1.00E+00	5.23E-01	1.00E+00	1.80E-01	1.00E+00	1.45E-02	6.92E-01	2.83E-01	1.00E+00	7.80E-02	1.00E+00	2.50E-01	1.00E+00	SRP-dependent cotranslational protein targ	P
GO:0006625	10	7.33E-02	1.00E+00	1.37E-01	1.00E+00	2.06E-01	1.00E+00	1.49E-01	1.00E+00	1.06E-01	1.00E+00	3.02E-01	1.00E+00	1.31E-01	1.00E+00	7.62E-02	1.00E+00	protein targeting to peroxisome	P
GO:0006626	11	2.40E-01	1.00E+00	1.22E-01	1.00E+00	4.93E-01	1.00E+00	2.09E-01	1.00E+00	3.30E-01	1.00E+00	4.94E-01	1.00E+00	5.56E-02	1.00E+00	8.81E-02	1.00E+00	protein targeting to mitochondrion	P
GO:0006629	751	7.11E-07	2.76E-03	6.15E-13	0.00E+00	7.87E-05	1.16E-02	2.47E-07	2.89E-03	3.30E-05	6.33E-03	2.77E-08	9.03E-04	1.21E-04	8.00E-03	9.09E-11	0.00E+00	lipid metabolism	P
GO:0006631	189	4.20E-03	2.14E-01	1.59E-05	4.51E-03	2.41E-02	1.00E+00	6.39E-03	3.33E-01	2.63E-02	1.00E+00	5.60E-05	9.66E-03	7.01E-03	2.75E-01	4.70E-04	3.00E-02	fatty acid metabolism	P
GO:0006633	84	1.10E-02	6.08E-01	1.47E-03	9.65E-02	2.58E-02	1.00E+00	5.54E-02	1.00E+00	2.50E-02	1.00E+00	3.66E-03	1.80E-01	3.44E-02	8.38E-01	2.24E-03	7.90E-02	fatty acid biosynthesis	P
GO:0006635	16	9.75E-02	1.00E+00	4.79E-02	1.00E+00	6.84E-02	1.00E+00	3.01E-01	1.00E+00	1.51E-01	1.00E+00	9.28E-02	1.00E+00	6.65E-01	1.00E+00	1.06E-01	1.00E+00	fatty acid beta-oxidation	P
GO:0006637	16	7.46E-01	1.00E+00	3.59E-02	1.00E+00	7.76E-01	1.00E+00	2.03E-01	1.00E+00	5.68E-01	1.00E+00	5.44E-04	3.20E-02	7.96E-01	1.00E+00	3.30E-01	1.00E+00	acyl-CoA metabolism	P
GO:0006638	36	3.38E-03	2.12E-01	1.19E-02	6.07E-01	4.68E-02	1.00E+00	8.88E-03	4.92E-01	1.08E-02	6.92E-01	3.46E-01	1.00E+00	6.90E-03	2.75E-01	2.92E-03	1.27E-01	neutral lipid metabolism	P
GO:0006639	35	3.66E-03	2.12E-01	1.65E-02	7.63E-01	3.60E-02	1.00E+00	1.47E-02	6.47E-01	1.08E-02	6.92E-01	3.05E-01	1.00E+00	1.12E-02	3.39E-01	4.75E-03	2.01E-01	acylglycerol metabolism	P
GO:0006641	30	4.14E-04	3.10E-02	6.06E-03	3.08E-01	1.95E-02	1.00E+00	7.44E-03	4.92E-01	1.53E-03	1.20E-01	1.30E-01	1.00E+00	2.92E-03	8.70E-02	3.50E-03	1.27E-01	triacylglycerol metabolism	P
GO:0006643	207	2.90E-08	2.57E-03	1.11E-09	8.90E-04	3.14E-06	2.91E-03	7.34E-07	2.89E-03	2.74E-05	6.00E-03	7.15E-05	1.10E-02	7.59E-05	8.00E-03	4.29E-06	2.91E-03	membrane lipid metabolism	P
GO:0006644	164	5.41E-06	3.62E-03	6.35E-07	3.92E-03	7.76E-05	1.16E-02	3.49E-05	9.57E-03	5.31E-04	4.90E-02	2.81E-03	1.44E-01	1.66E-03	8.40E-02	1.25E-04	1.60E-02	phospholipid metabolism	P
GO:0006650	85	1.42E-04	1.43E-02	1.81E-05	4.51E-03	1.34E-03	7.90E-02	2.02E-04	1.30E-02	1.27E-03	1.20E-01	2.45E-03	1.27E-01	1.46E-02	4.78E-01	1.48E-03	6.00E-02	glycerophospholipid metabolism	P
GO:0006662	37	3.94E-03	2.12E-01	1.30E-02	6.07E-01	3.20E-02	1.00E+00	9.96E-03	5.72E-01	1.32E-02	6.92E-01	2.62E-01	1.00E+00	9.05E-03	2.75E-01	4.77E-03	2.01E-01	glycerol ether metabolism	P
GO:0006664	17	4.06E-02	1.00E+00	2.42E-03	1.71E-01	6.08E-02	1.00E+00	1.90E-01	1.00E+00	1.31E-01	1.00E+00	1.57E-03	1.22E-01	3.57E-02	8.38E-01	3.08E-02	9.99E-01	glycolipid metabolism	P
GO:0006665	56	1.74E-05	7.00E-03	9.61E-05	1.50E-02	7.25E-04	4.90E-02	6.34E-03	3.33E-01	1.53E-03	1.20E-01	1.33E-04	1.30E-02	9.85E-04	3.62E-02	4.94E-03	2.01E-01	sphingolipid metabolism	P
GO:0006672	30	8.12E-06	3.62E-03	2.51E-06	3.92E-03	2.41E-04	2.10E-02	3.57E-03	2.57E-01	1.26E-03	1.20E-01	8.31E-05	1.10E-02	2.69E-03	8.40E-02	2.64E-03	8.32E-02	ceramide metabolism	P
GO:0006684	10	1.89E-02	1.00E+00	1.29E-01	1.00E+00	7.59E-02	1.00E+00	3.33E-01	1.00E+00	3.34E-02	1.00E+00	2.28E-02	1.00E+00	5.62E-02	1.00E+00	5.27E-01	1.00E+00	sphingomyelin metabolism	P
GO:0006687	11	2.23E-02	1.00E+00	5.06E-03	2.79E-01	1.16E-02	6.53E-01	4.98E-02	1.00E+00	8.82E-02	1.00E+00	7.14E-03	4.21E-01	7.06E-02	1.00E+00	6.32E-02	1.00E+00	glycosphingolipid metabolism	P
GO:0006690	34	5.22E-01	1.00E+00	7.79E-02	1.00E+00	6.41E-01	1.00E+00	1.19E-01	1.00E+00	3.92E-01	1.00E+00	9.54E-02	1.00E+00	4.79E-01	1.00E+00	1.58E-01	1.00E+00	icosanoid metabolism	P
GO:0006691	20	6.16E-01	1.00E+00	3.80E-01	1.00E+00	8.31E-01	1.00E+00	5.14E-01	1.00E+00	2.95E-01	1.00E+00	2.02E-01	1.00E+00	6.25E-01	1.00E+00	7.46E-01	1.00E+00	leukotriene metabolism	P
GO:0006692	14	3.93E-01	1.00E+00	5.01E-02	1.00E+00	3.48E-01	1.00E+00	4.30E-02	1.00E+00	6.10E-01	1.00E+00	1.48E-01	1.00E+00	3.15E-01	1.00E+00	3.49E-02	1.00E+00	prostanoid metabolism	P
GO:0006693	14	3.93E-01	1.00E+00	5.01E-02	1.00E+00	3.48E-01	1.00E+00	4.30E-02	1.00E+00	6.10E-01	1.00E+00	1.48E-01	1.00E+00	3.15E-01	1.00E+00	3.49E-02	1.00E+00	prostaglandin metabolism	P
GO:0006694	93	2.29E-01	1.00E+00	5.15E-01	1.00E+00	4.40E-01	1.00E+00	5.16E-01	1.00E+00	9.91E-02	1.00E+00	3.86E-01	1.00E+00	3.19E-01	1.00E+00	4.35E-01	1.00E+00	steroid biosynthesis	P
GO:0006695	27	3.30E-02	1.00E+00	8.35E-02	1.00E+00	2.24E-02	1.00E+00	8.26E-02	1.00E+00	1.20E-01	1.00E+00	8.84E-02	1.00E+00	1.43E-01	1.00E+00	2.71E-01	1.00E+00	cholesterol biosynthesis	P
GO:0006700	15	9.30E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	9.99E-01	1.00E+00	7.34E-01	1.00E+00	9.79E-01	1.00E+00	7.92E-01	1.00E+00	1.00E+00	1.00E+00	C21-steroid hormone biosynthesis	P
GO:0006706	10	3.83E-01	1.00E+00	1.48E-01	1.00E+00	3.77E-01	1.00E+00	1.98E-01	1.00E+00	1.63E-01	1.00E+00	1.11E-02	5.03E-01	9.68E-01	1.00E+00	7.56E-01	1.00E+00	steroid catabolism	P
GO:0006720	34	7.59E-01	1.00E+00	4.28E-01	1.00E+00	4.55E-01	1.00E+00	5.98E-01	1.00E+00	8.11E-01	1.00E+00	5.04E-01	1.00E+00	7.09E-01	1.00E+00	1.16E-01	1.00E+00	isoprenoid metabolism	P
GO:0006725	176	1.32E-01	1.00E+00	4.42E-02	1.00E+00	3.01E-01	1.00E+00	3.84E-01	1.00E+00	4.65E-02	1.00E+00	5.33E-02	1.00E+00	5.75E-01	1.00E+00	3.91E-02	1.00E+00	aromatic compound metabolism	P
GO:0006730	127	2.96E-02	1.00E+00	4.08E-03	1.88E-01	1.53E-02	6.53E-01	1.14E-03	9.40E-02	9.67E-02	1.00E+00	1.54E-02	6.68E-01	1.71E-01	1.00E+00	8.24E-02	1.00E+00	one-carbon compound metabolism	P

GO:0006732	185	6.29E-06	3.62E-03	9.15E-05	1.50E-02	3.35E-05	9.82E-03	3.03E-03	1.61E-01	4.44E-05	6.58E-03	4.05E-05	9.66E-03	4.33E-02	1.00E+00	1.19E-01	1.00E+00	coenzyme metabolism	P
GO:0006733	35	9.07E-05	1.43E-02	1.00E-01	1.00E+00	1.62E-03	9.50E-02	3.48E-01	1.00E+00	3.42E-03	2.13E-01	4.06E-02	1.00E+00	1.66E-02	4.88E-01	3.62E-01	1.00E+00	oxidoreduction coenzyme metabolism	P
GO:0006739	14	3.45E-07	2.57E-03	1.43E-02	6.07E-01	9.57E-05	1.16E-02	1.85E-02	9.37E-01	8.18E-03	6.92E-01	1.38E-02	6.68E-01	9.62E-03	2.75E-01	5.81E-01	1.00E+00	NADP metabolism	P
GO:0006749	26	3.42E-03	2.12E-01	4.62E-03	2.61E-01	6.40E-03	4.69E-01	3.90E-02	1.00E+00	7.17E-03	6.92E-01	5.42E-04	3.20E-02	3.23E-02	8.38E-01	3.71E-01	1.00E+00	glutathione metabolism	P
GO:0006752	73	3.16E-02	1.00E+00	1.15E-01	1.00E+00	4.47E-02	1.00E+00	7.39E-02	1.00E+00	1.63E-02	6.92E-01	2.73E-01	1.00E+00	4.55E-01	1.00E+00	3.22E-01	1.00E+00	group transfer coenzyme metabolism	P
GO:0006753	44	1.54E-01	1.00E+00	4.91E-01	1.00E+00	1.27E-01	1.00E+00	4.12E-01	1.00E+00	6.56E-02	1.00E+00	5.35E-01	1.00E+00	9.21E-01	1.00E+00	6.59E-01	1.00E+00	nucleoside phosphate metabolism	P
GO:0006754	44	1.54E-01	1.00E+00	4.91E-01	1.00E+00	1.27E-01	1.00E+00	4.12E-01	1.00E+00	6.56E-02	1.00E+00	5.35E-01	1.00E+00	9.21E-01	1.00E+00	6.59E-01	1.00E+00	ATP biosynthesis	P
GO:0006760	16	1.48E-01	1.00E+00	7.24E-02	1.00E+00	3.45E-01	1.00E+00	8.23E-02	1.00E+00	2.06E-01	1.00E+00	1.26E-01	1.00E+00	1.37E-01	1.00E+00	5.54E-01	1.00E+00	folic acid and derivative metabolism	P
GO:0006766	77	3.19E-02	1.00E+00	1.29E-01	1.00E+00	2.25E-02	1.00E+00	1.77E-01	1.00E+00	6.42E-02	1.00E+00	2.50E-01	1.00E+00	5.04E-01	1.00E+00	1.87E-01	1.00E+00	vitamin metabolism	P
GO:0006767	48	1.15E-04	1.43E-02	5.68E-02	1.00E+00	1.39E-04	1.16E-02	1.01E-01	1.00E+00	3.82E-03	2.13E-01	1.04E-01	1.00E+00	3.67E-01	1.00E+00	3.53E-01	1.00E+00	water-soluble vitamin metabolism	P
GO:0006769	23	4.96E-04	4.40E-02	1.01E-01	1.00E+00	1.47E-02	6.53E-01	3.61E-01	1.00E+00	1.05E-02	6.92E-01	3.19E-02	1.00E+00	5.80E-02	1.00E+00	3.71E-01	1.00E+00	nicotinamide metabolism	P
GO:0006775	28	9.30E-01	1.00E+00	6.98E-01	1.00E+00	9.65E-01	1.00E+00	7.66E-01	1.00E+00	8.35E-01	1.00E+00	8.58E-01	1.00E+00	8.30E-01	1.00E+00	2.13E-01	1.00E+00	fat-soluble vitamin metabolism	P
GO:0006776	22	9.92E-01	1.00E+00	7.57E-01	1.00E+00	9.92E-01	1.00E+00	9.36E-01	1.00E+00	9.65E-01	1.00E+00	8.12E-01	1.00E+00	9.47E-01	1.00E+00	2.88E-01	1.00E+00	vitamin A metabolism	P
GO:0006778	26	6.73E-03	3.15E-01	1.78E-01	1.00E+00	2.50E-03	1.07E-01	6.77E-02	1.00E+00	3.26E-02	1.00E+00	3.61E-01	1.00E+00	2.24E-01	1.00E+00	4.63E-01	1.00E+00	porphyrin metabolism	P
GO:0006779	20	3.42E-02	1.00E+00	3.31E-01	1.00E+00	1.22E-02	6.53E-01	1.13E-01	1.00E+00	1.67E-01	1.00E+00	5.75E-01	1.00E+00	1.43E-01	1.00E+00	5.41E-01	1.00E+00	porphyrin biosynthesis	P
GO:0006783	13	6.26E-02	1.00E+00	2.77E-01	1.00E+00	1.04E-01	1.00E+00	5.40E-02	1.00E+00	8.75E-02	1.00E+00	3.99E-01	1.00E+00	9.06E-02	1.00E+00	4.04E-01	1.00E+00	heme biosynthesis	P
GO:0006790	85	4.96E-03	2.72E-01	2.06E-03	1.30E-01	6.09E-02	1.00E+00	1.93E-02	9.37E-01	2.95E-02	1.00E+00	1.88E-03	1.27E-01	1.18E-02	3.39E-01	1.51E-01	1.00E+00	sulfur metabolism	P
GO:0006793	1022	5.87E-07	2.76E-03	1.30E-17	0.00E+00	2.39E-07	2.00E-03	1.53E-12	0.00E+00	9.42E-04	1.20E-01	2.72E-10	6.20E-04	2.26E-03	8.40E-02	1.10E-11	0.00E+00	phosphorus metabolism	P
GO:0006796	1022	5.87E-07	2.76E-03	1.30E-17	0.00E+00	2.39E-07	2.00E-03	1.53E-12	0.00E+00	9.42E-04	1.20E-01	2.72E-10	6.20E-04	2.26E-03	8.40E-02	1.10E-11	0.00E+00	phosphate metabolism	P
GO:0006800	135	1.43E-04	1.43E-02	8.93E-05	1.50E-02	3.11E-03	1.35E-01	9.50E-04	9.40E-02	1.28E-02	6.92E-01	2.13E-04	2.33E-02	1.76E-04	8.00E-03	5.98E-02	1.00E+00	oxygen and reactive oxygen species metab	P
GO:0006801	19	3.34E-01	1.00E+00	1.61E-01	1.00E+00	3.10E-01	1.00E+00	8.37E-02	1.00E+00	6.12E-01	1.00E+00	6.77E-02	1.00E+00	9.03E-02	1.00E+00	9.65E-01	1.00E+00	superoxide metabolism	P
GO:0006805	13	1.28E-01	1.00E+00	6.65E-01	1.00E+00	4.75E-01	1.00E+00	5.76E-01	1.00E+00	2.90E-02	1.00E+00	7.10E-01	1.00E+00	1.99E-01	1.00E+00	4.39E-01	1.00E+00	xenobiotic metabolism	P
GO:0006807	572	3.15E-05	7.00E-03	6.93E-06	4.51E-03	2.39E-03	1.07E-01	5.01E-04	4.20E-02	1.47E-03	1.20E-01	1.50E-05	5.87E-03	1.32E-04	8.00E-03	6.94E-03	4.28E-01	nitrogen compound metabolism	P
GO:0006809	22	2.05E-01	1.00E+00	1.98E-02	1.00E+00	3.56E-01	1.00E+00	2.51E-01	1.00E+00	2.46E-01	1.00E+00	2.79E-02	1.00E+00	1.64E-01	1.00E+00	5.42E-02	1.00E+00	nitric oxide biosynthesis	P
GO:0006810	3038	1.79E-19	0.00E+00	2.16E-38	0.00E+00	6.59E-12	7.08E-04	1.86E-21	0.00E+00	1.10E-12	0.00E+00	1.23E-23	0.00E+00	3.28E-11	0.00E+00	5.47E-26	0.00E+00	transport	P
GO:0006811	968	5.71E-01	1.00E+00	1.53E-02	7.63E-01	9.63E-01	1.00E+00	3.75E-01	1.00E+00	8.43E-01	1.00E+00	2.27E-01	1.00E+00	4.31E-02	1.00E+00	5.03E-05	7.00E-03	ion transport	P
GO:0006812	697	1.47E-01	1.00E+00	2.80E-03	1.88E-01	4.99E-01	1.00E+00	1.05E-01	1.00E+00	4.48E-01	1.00E+00	1.87E-02	6.68E-01	3.59E-02	8.38E-01	9.05E-04	6.00E-02	cation transport	P
GO:0006813	288	4.48E-01	1.00E+00	1.85E-01	1.00E+00	8.24E-01	1.00E+00	5.05E-01	1.00E+00	7.88E-01	1.00E+00	1.53E-01	1.00E+00	5.31E-02	1.00E+00	4.66E-02	1.00E+00	potassium ion transport	P
GO:0006814	143	6.56E-01	1.00E+00	2.23E-01	1.00E+00	6.23E-01	1.00E+00	1.90E-01	1.00E+00	4.84E-01	1.00E+00	3.83E-01	1.00E+00	7.70E-01	1.00E+00	5.14E-01	1.00E+00	sodium ion transport	P
GO:0006816	165	4.27E-01	1.00E+00	1.62E-02	7.63E-01	9.09E-01	1.00E+00	3.09E-01	1.00E+00	7.35E-01	1.00E+00	2.24E-01	1.00E+00	1.21E-02	3.39E-01	1.17E-04	1.60E-02	calcium ion transport	P
GO:0006817	89	9.98E-01	1.00E+00	5.18E-01	1.00E+00	1.00E+00	1.00E+00	9.39E-01	1.00E+00	9.99E-01	1.00E+00	8.12E-01	1.00E+00	5.19E-01	1.00E+00	3.60E-02	1.00E+00	phosphate transport	P
GO:0006818	84	1.28E-01	1.00E+00	1.06E-01	1.00E+00	2.33E-01	1.00E+00	1.62E-01	1.00E+00	2.08E-01	1.00E+00	1.62E-01	1.00E+00	2.62E-01	1.00E+00	1.64E-01	1.00E+00	hydrogen transport	P
GO:0006820	216	1.00E+00	1.00E+00	6.08E-01	1.00E+00	1.00E+00	1.00E+00	8.98E-01	1.00E+00	9.98E-01	1.00E+00	9.79E-01	1.00E+00	9.09E-01	1.00E+00	1.91E-02	7.36E-01	anion transport	P
GO:0006821	74	9.98E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	9.59E-01	1.00E+00	9.93E-01	1.00E+00	9.88E-01	1.00E+00	9.38E-01	1.00E+00	chloride transport	P
GO:0006825	11	7.10E-02	1.00E+00	1.85E-01	1.00E+00	1.53E-01	1.00E+00	1.55E-01	1.00E+00	1.12E-01	1.00E+00	1.92E-01	1.00E+00	5.83E-02	1.00E+00	7.25E-01	1.00E+00	copper ion transport	P
GO:0006826	38	8.84E-01	1.00E+00	6.46E-01	1.00E+00	7.76E-01	1.00E+00	5.85E-01	1.00E+00	8.26E-01	1.00E+00	4.63E-01	1.00E+00	9.33E-01	1.00E+00	8.83E-01	1.00E+00	iron ion transport	P
GO:0006829	22	2.10E-02	1.00E+00	8.45E-03	4.69E-01	3.35E-02	1.00E+00	5.23E-02	1.00E+00	2.28E-01	1.00E+00	1.21E-01	1.00E+00	1.32E-01	1.00E+00	9.98E-03	4.76E-01	zinc ion transport	P
GO:0006833	11	4.91E-01	1.00E+00	1.57E-01	1.00E+00	2.94E-01	1.00E+00	2.81E-02	1.00E+00	4.79E-01	1.00E+00	3.93E-01	1.00E+00	8.32E-01	1.00E+00	5.17E-01	1.00E+00	water transport	P
GO:0006835	71	8.11E-01	1.00E+00	6.67E-01	1.00E+00	9.37E-01	1.00E+00	9.13E-01	1.00E+00	7.72E-01	1.00E+00	5.44E-01	1.00E+00	5.42E-01	1.00E+00	3.90E-01	1.00E+00	dicarboxylic acid transport	P
GO:0006836	66	8.85E-01	1.00E+00	5.13E-01	1.00E+00	8.05E-01	1.00E+00	8.68E-01	1.00E+00	8.80E-01	1.00E+00	1.94E-01	1.00E+00	7.57E-01	1.00E+00	4.79E-01	1.00E+00	neurotransmitter transport	P
GO:0006839	49	6.87E-03	3.15E-01	5.39E-04	4.74E-02	3.75E-02	1.00E+00	4.84E-02	1.00E+00	1.09E-02	6.92E-01	1.74E-02	6.68E-01	7.53E-02	1.00E+00	1.93E-03	7.90E-02	mitochondrial transport	P
GO:0006857	10	6.93E-01	1.00E+00	2.88E-01	1.00E+00	9.98E-01	1.00E+00	3.66E-01	1.00E+00	2.81E-01	1.00E+00	3.27E-01	1.00E+00	3.45E-01	1.00E+00	2.90E-01	1.00E+00	oligopeptide transport	P
GO:0006865	74	5.73E-02	1.00E+00	8.00E-04	8.10E-02	6.03E-02	1.00E+00	2.35E-02	9.37E-01	4.43E-02	1.00E+00	2.95E-03	1.44E-01	3.57E-01	1.00E+00	7.14E-04	6.00E-02	amino acid transport	P
GO:0006869	104	5.85E-03	3.09E-01	7.12E-03	3.12E-01	2.49E-02	1.00E+00	2.68E-02	1.00E+00	1.48E-02	6.92E-01	1.60E-01	1.00E+00	4.21E-02	1.00E+00	1.99E-02	7.36E-01	lipid transport	P
GO:0006873	163	4.23E-02	1.00E+00	1.26E-02	6.07E-01	4.33E-01	1.00E+00	5.54E-02	1.00E+00	2.47E-01	1.00E+00	4.18E-02	1.00E+00	5.86E-03	2.75E-01	3.32E-02	1.00E+00	cell ion homeostasis	P
GO:0006874	88	1.08E-01	1.00E+00	3.48E-02	1.00E+00	6.25E-01	1.00E+00	3.58E-01	1.00E+00	6.02E-01	1.00E+00	8.58E-02	1.00E+00	9.99E-04	3.62E-02	3.32E-03	1.27E-01	calcium ion homeostasis	P
GO:0006875	145	1.12E-01	1.00E+00	4.73E-02	1.00E+00	5.55E-01	1.00E+00	1.90E-01	1.00E+00	5.65E-01	1.00E+00	8.69E-02	1.00E+00	6.77E-03	2.75E-01	4.25E-02	1.00E+00	metal ion homeostasis	P
GO:0006879	35	9.36E-01	1.00E+00	8.09E-01	1.00E+00	8.52E-01	1.00E+00	6.01E-01	1.00E+00	8.51E-01	1.00E+00	6.99E-01	1.00E+00	8.44E-01	1.00E+00	8.11E-01	1.00E+00	iron ion homeostasis	P
GO:0006885	37	6.05E-02	1.00E+00	7.83E-02	1.00E+00	1.04E-01	1.00E+00	7.20E-02	1.00E+00	2.77E-02	1.00E+00	2.11E-01	1.00E+00	2.08E-01	1.00E+00	1.28E-01	1.00E+00	regulation of pH	P
GO:0006886	525	9.49E-17	0.00E+00	1.06E-23	0.00E+00	4.29E-12	7.08E-04	3.66E-21	0.00E+00	3.92E-14	0.00E+00	1.62E-14	6.20E-04	1.28E-05	3.63E-03	5.17E-09	0.00E+00	intracellular protein transport	P
GO:0006887	100	5.65E-03	3.09E-01	5.88E-03	3.08E-01	2.34E-02	1.00E+00	1.26E-01	1.00E+00	2.05E-01	1.00E+00	1.32E-02	6.68E-01	3.07E-03	8.78E-02	6.67E-03	4.28E-01	exocytosis	P
GO:0006888	27	3.11E-02	1.00E+00	1.71E-02	7.63E-01	4.24E-02	1.00E+00	9.61E-03	5.72E-01	1.00E-01	1.00E+00	2.72E-02	1.00E+00	3.99E-01	1.00E+00	2.35E-01	1.00E+00	ER to Golgi vesicle-mediated transport	P
GO:0006891	11	3.40E-02	1.00E+00	2.02E-02	1.00E+00	1.99E-02	1.00E+00	1.58E-02	6.47E-01	1.20E-01	1.00E+00	1.54E-01	1.00E+00	1.25E-01	1.00E+00	4.50E-02	1.00E+00	intra-Golgi vesicle-mediated transport	P
GO:0006892	15	9.81E-03	6.08E-01	8.83E-03	4.69E-01	1.68E-01	1.00E+00	2.08E-01	1.00E+00	2.02E-02	7.90E-01	2.13E-01	1.00E+00	8.66E-02	1.00E+00	1.48E-02	6.56E-01	post-Golgi vesicle-mediated transport	P
GO:0006897	200	3.64E-03	2.12E-01	9.15E-08	3.92E-03	1.34E-02	6.53E-01	3.60E-05	9.57E-03	3.37E-01	1.00E+00	1.78E-04	2.33E-02	1.07E-03	3.62E-02	1.09E-05	7.00E-03	endocytosis	P
GO:0006898	27	1.15E-01	1.00E+00	5.14E-03	2.79E-01	1.43E-01	1.00E+00	2.80E-02	1.00E+00	8.71E-01	1.00E+00	1.35E-01	1.00E+00	2.07E-02	6.36E-01	1.90E-03	7.90E-02	receptor mediated endocytosis	P
GO:0006904	18	8.00E-02	1.00E+00	2.43E-01	1.00E+00	2.11E-01	1.00E+00	4.23E-01	1.00E+00	8.58E-02	1.00E+00	1.88E-01	1.00E+00	2.12E-01	1.00E+00	3.31E-01	1.00E+00	vesicle docking during exocytosis	P
GO:0006909	50	4.91E-01	1.00E+00	9.04E-02	1.00E+00	4.12E-01	1.00E+00	3.43E-01	1.00E+00	8.80E-01	1.00E+00	9.96E-02	1.00E+00	3.62E-01	1.00E+00	8.19E-02	1.00E+00	phagocytosis	P
GO:0006910	12	8.45E-01	1.00E+00	4.24E-01	1.00E+00	5.47E-01	1.00E+00	8.46E-01	1.00E+00	9.91E-01	1.00E+00	5.96E-01	1.00E+00	8.29E-01	1.00E+00	1.42E-01	1.00E+00	phagocytosis, recognition	P
GO:0006911	13	1.00E+00	1.00E+00	5.80E-01	1.00E+00	9.23E-01	1.00E+00	7.81E-01	1.00E+00	9.88E-01	1.00E+00	5.13E-01	1.00E+00	1.00E+00	1.00E+00	3.83E-01	1.00E+00	phagocytosis, engulfment	P
GO:0006913	235	3.71E-10	2.57E-03	4.02E-17	0.00E+00	2.99E-08	9.80E-04	3.60E-12	0.00E+00	2.73E-08	9.59E-04	1.51E-10	6.20E-04	2.78E-03	8.40E-02	2.13E-09	0.00E+00	nucleocytoplasmic transport	P
GO:0006914	30	2.62E-02	1.00E+00	4.05E-03	1.88E-01	4.44E-02	1.00E+00	1.18E-02	6.47E-01	1.17E-02	6.92E-01	4.38E-02	1.00E+00	6.10E-01	1.00E+00	2.19E-02	9.99E-01	autophagy	P
GO:0006915	786	4.55E-12	2.57E-03	2.00E-14	0.00E+00	1.76E-08	9.80E-04	4.95E-11	0.00E+00	4.09E-07	9.59E-04	1.08E-09	6.20E-04	1.13E-06	8.23E-04	7.51E-07	2.00E-03	apoptosis	P
GO:0006916	109	6.27E-04	8.86E-02	1.80E-02	1.00E+00	1.31E-02	6.53E-01	3.48E-02	1.00E+00	1.03E-02	6.92E-01	6.58E-02	1.00E+00	1.07E-02	2.75E-01	3.09E-02	9.99E-01	anti-apoptosis	P
GO:0006917	189	1.17E-04	1.43E-02	1.79E-05	4.51E-03	1.79E-03	9.50E-02	1.73E-04	1.30E-02	4.51E-03	2.13E-01	7.76E-05	1.10E-02	1.25E-03	6.14E-02	1.03E-02	4.76E-01	induction of apoptosis	P
GO:0006919	37	4.61E-05	9.52E-03	1.20E-03	9.65E-02	1.15E-03	7.90E-02	1.87E-02	9.37E-01	1.18E-03	1.20E-01	3.58E-03	1.80E-01	7.42E-03	2.75E-01	1.09E-02	4.76E-01	caspase activation	P
GO:0006921	13	3.40E-03	2.12E-01	9.32E-03	4.69E-01	1.07E-02	6.53E-01	4.28E-03	2.88E-01	1.16E-02	6.92E-01	2.02E-02	7.56E-01	1.12E-02	3.39E-01	2.64E-01	1.00E+00	disassembly of cell structures during apopto	P
GO:0006928	448	2.40E-01	1.00E+00	4.87E-02	1.00E+00	6.96E-01	1.00E+00	3.26E-01	1.00E+00	3.83E-01	1.00E+00	4.06E-01	1.00E+00	6.99E-02	1.00E+00	3.17E-04	3.00E-02	cell motility	P
GO:0006935	173	7.39E-01	1.00E+00	2.29E-01	1.00E+00	9.99E-01	1.00E+00	8.64E-01	1.00E+00	8.76E-01	1.00E+00	1.15E-01	1.00E+00	4.95E-03	2.23E-01	2.02E-02	7.36E-01	chemotaxis	P
GO:0006936	76	6.54E-01	1.00E+00	1.10E-01	1.00E+00	7.94E-01	1.00E+00	5.56E-01	1.00E+00	7.17E-01	1.00E+00	2.28E-01	1.00E+00	5.55E-01	1.00E+00	1.09E-02	4.76E-01	muscle contraction	P
GO:0006937	30	6.69E-01	1.00E+00	1.58E-01	1.00E+00	6.74E-01	1.00E+00	6.59E-01	1.00E+00	9.83E-01	1.00E+00	4.08E-01	1.00E+00	1.74E-01	1.00E+00	8.63E-03	4.28E-01	regulation of muscle contraction	P
GO:0006939	24	8.68E-01	1.00E+00	5.70E-01	1.00E+00	9.42E-01	1.00E+00	9.95E-01	1.00E+00	9.50E-01	1.00E+00	7.52E-01	1.00E+00	2.23E-01	1.00E+00	5.05E-02	1.00E+00	smooth muscle contraction	P
GO:0006940	18	9.81E-01	1.00E+00	7.74E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.83E-01	1.00E+00	1.91E-01	1.00E+00	8.19E-02	1.00E+00	regulation of smooth muscle contraction	P
GO:0006941	28	5.80E-01	1.00E+00	4.28E-01	1.00E+00	5.70E-01	1.00E+00	5.33E-01	1.00E+00	6.80E-01	1.00E+00	3.30E-01	1.00E+00	8.10E-01	1.00E+00	3.86E-01	1.00E+00	striated muscle contraction	P
GO:0006944	23	1.68E-01	1.00E+00	2.32E-01	1.00E+00	2.00E-01	1.00E+00	1.04E-01	1.00E+00	6.82E-02	1.00E+00	3.12E-01	1.00E+00	5.89E-01	1.00E+00	6.58E-01	1.00E+00	membrane fusion	P

GO:0006950	1255	2.45E-15	0.00E+00	3.15E-15	0.00E+00	1.32E-11	7.08E-04	1.37E-13	0.00E+00	1.60E-07	9.59E-04	4.59E-08	9.03E-04	1.60E-09	0.00E+00	1.89E-08	0.00E+00	response to stress	P
GO:0006952	581	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	8.76E-01	1.00E+00	defense response	P
GO:0006953	29	9.81E-01	1.00E+00	9.94E-01	1.00E+00	9.39E-01	1.00E+00	9.13E-01	1.00E+00	8.63E-01	1.00E+00	9.97E-01	1.00E+00	9.70E-01	1.00E+00	8.32E-01	1.00E+00	acute-phase response	P
GO:0006954	300	9.61E-01	1.00E+00	9.28E-01	1.00E+00	9.77E-01	1.00E+00	8.72E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.68E-01	1.00E+00	1.69E-01	1.00E+00	inflammatory response	P
GO:0006955	559	4.91E-01	1.00E+00	4.24E-01	1.00E+00	7.10E-01	1.00E+00	6.85E-01	1.00E+00	9.54E-01	1.00E+00	4.53E-01	1.00E+00	9.01E-03	2.75E-01	1.48E-01	1.00E+00	immune response	P
GO:0006956	37	4.69E-01	1.00E+00	9.22E-01	1.00E+00	6.47E-01	1.00E+00	6.12E-01	1.00E+00	9.21E-01	1.00E+00	9.97E-01	1.00E+00	2.22E-01	1.00E+00	5.94E-01	1.00E+00	complement activation	P
GO:0006957	10	5.03E-01	1.00E+00	6.18E-01	1.00E+00	6.19E-01	1.00E+00	4.73E-01	1.00E+00	9.88E-01	1.00E+00	9.18E-01	1.00E+00	3.24E-01	1.00E+00	1.98E-01	1.00E+00	complement activation, alternative pathway	P
GO:0006958	29	5.11E-01	1.00E+00	8.93E-01	1.00E+00	6.54E-01	1.00E+00	6.13E-01	1.00E+00	8.74E-01	1.00E+00	9.97E-01	1.00E+00	2.69E-01	1.00E+00	5.08E-01	1.00E+00	complement activation, classical pathway	P
GO:0006959	57	5.95E-01	1.00E+00	8.60E-01	1.00E+00	5.12E-01	1.00E+00	6.65E-01	1.00E+00	9.83E-01	1.00E+00	9.69E-01	1.00E+00	2.35E-01	1.00E+00	5.46E-01	1.00E+00	humoral immune response	P
GO:0006968	13	5.17E-01	1.00E+00	3.38E-01	1.00E+00	7.89E-01	1.00E+00	9.76E-01	1.00E+00	7.21E-01	1.00E+00	3.66E-01	1.00E+00	3.03E-01	1.00E+00	1.20E-01	1.00E+00	cellular defense response	P
GO:0006970	16	2.88E-03	2.12E-01	8.03E-02	1.00E+00	1.23E-01	1.00E+00	5.16E-02	1.00E+00	1.63E-01	1.00E+00	1.63E-01	1.00E+00	2.40E-02	8.38E-01	3.82E-01	1.00E+00	response to osmotic stress	P
GO:0006974	308	2.23E-16	0.00E+00	2.89E-21	0.00E+00	4.92E-15	7.08E-04	9.23E-19	0.00E+00	8.70E-11	0.00E+00	2.51E-10	6.20E-04	3.05E-04	2.29E-02	6.52E-09	0.00E+00	response to DNA damage stimulus	P
GO:0006979	101	1.11E-04	1.43E-02	1.41E-04	1.50E-02	2.06E-03	9.50E-02	9.71E-04	9.40E-02	4.28E-03	2.13E-01	1.34E-03	9.00E-02	8.14E-04	3.44E-02	3.28E-02	1.00E+00	response to oxidative stress	P
GO:0006984	23	3.99E-03	2.12E-01	9.36E-04	8.70E-02	1.44E-02	6.53E-01	3.65E-04	4.20E-02	9.16E-03	6.92E-01	1.21E-02	5.03E-01	2.44E-02	8.38E-01	4.78E-02	1.00E+00	ER-nuclear signaling pathway	P
GO:0006986	49	6.92E-04	8.86E-02	1.23E-03	9.65E-02	1.71E-04	1.16E-02	2.58E-05	9.57E-03	7.73E-02	1.00E+00	9.63E-03	5.03E-01	7.45E-02	1.00E+00	5.13E-01	1.00E+00	response to unfolded protein	P
GO:0006996	1203	1.24E-29	0.00E+00	2.49E-36	0.00E+00	2.73E-28	0.00E+00	7.53E-32	0.00E+00	7.23E-15	0.00E+00	2.27E-20	0.00E+00	9.71E-13	0.00E+00	1.17E-16	0.00E+00	organelle organization and biogenesis	P
GO:0006997	15	1.12E-02	6.08E-01	9.42E-03	4.69E-01	2.03E-04	2.10E-02	2.88E-04	4.20E-02	2.14E-01	1.00E+00	6.21E-01	1.00E+00	8.01E-02	1.00E+00	6.77E-02	1.00E+00	nuclear organization and biogenesis	P
GO:0007001	401	1.54E-08	2.57E-03	1.97E-11	0.00E+00	1.29E-10	7.95E-04	2.36E-16	0.00E+00	5.48E-04	4.90E-02	2.88E-06	2.90E-03	1.66E-03	8.40E-02	8.86E-04	6.00E-02	chromosome organization and biogenesis (	P
GO:0007005	55	1.33E-03	8.86E-02	7.53E-05	1.50E-02	3.37E-03	2.03E-01	9.33E-04	9.40E-02	5.43E-02	1.00E+00	1.73E-03	1.27E-01	1.58E-02	4.88E-01	5.23E-03	2.01E-01	mitochondrion organization and biogenesis	P
GO:0007006	26	8.91E-03	6.08E-01	1.63E-03	9.65E-02	1.93E-02	1.00E+00	1.31E-02	6.47E-01	9.43E-02	1.00E+00	1.28E-02	6.68E-01	1.41E-02	4.78E-01	2.59E-02	9.99E-01	mitochondrial membrane organization and b	P
GO:0007007	10	3.14E-01	1.00E+00	2.37E-01	1.00E+00	4.57E-01	1.00E+00	1.94E-01	1.00E+00	2.83E-01	1.00E+00	8.51E-01	1.00E+00	2.37E-01	1.00E+00	2.44E-01	1.00E+00	inner mitochondrial membrane organization	P
GO:0007009	11	4.54E-01	1.00E+00	6.29E-01	1.00E+00	5.37E-01	1.00E+00	5.32E-01	1.00E+00	8.54E-01	1.00E+00	3.77E-01	1.00E+00	1.32E-01	1.00E+00	9.56E-01	1.00E+00	plasma membrane organization and biogen	P
GO:0007010	499	1.29E-11	2.57E-03	1.10E-15	0.00E+00	4.83E-09	9.80E-04	1.38E-08	8.93E-04	1.94E-05	5.37E-03	4.23E-10	6.20E-04	1.71E-08	0.00E+00	4.65E-11	0.00E+00	cytoskeleton organization and biogenesis	P
GO:0007015	55	8.01E-02	1.00E+00	3.27E-03	1.88E-01	2.04E-01	1.00E+00	2.18E-02	9.37E-01	4.59E-01	1.00E+00	7.58E-02	1.00E+00	4.76E-03	2.23E-01	3.60E-04	3.00E-02	actin filament organization	P
GO:0007017	219	2.11E-08	2.57E-03	2.44E-08	9.59E-04	8.69E-10	7.95E-04	3.21E-06	2.89E-03	1.79E-04	4.90E-02	1.79E-06	2.00E-03	9.23E-05	8.00E-03	2.29E-03	7.90E-02	microtubule-based process	P
GO:0007018	119	3.33E-05	7.00E-03	1.39E-04	1.50E-02	5.34E-06	2.91E-03	1.45E-03	9.40E-02	2.02E-03	1.20E-01	1.77E-03	1.27E-01	5.01E-03	2.23E-01	6.18E-03	4.28E-01	microtubule-based movement	P
GO:0007019	17	4.60E-03	2.72E-01	1.28E-02	6.07E-01	1.22E-02	6.53E-01	3.61E-02	1.00E+00	3.79E-02	1.00E+00	1.63E-02	6.68E-01	9.99E-03	2.75E-01	4.57E-02	1.00E+00	microtubule depolymerization	P
GO:0007026	16	4.91E-03	2.72E-01	2.70E-02	1.00E+00	1.37E-02	6.53E-01	6.15E-02	1.00E+00	1.86E-02	7.90E-01	3.35E-02	1.00E+00	1.61E-02	4.88E-01	6.48E-02	1.00E+00	negative regulation of microtubule depolym	P
GO:0007028	139	1.08E-10	2.57E-03	3.45E-05	7.00E-03	1.36E-09	9.80E-04	4.63E-05	1.07E-02	1.86E-08	9.59E-04	2.14E-03	1.27E-01	2.47E-03	8.40E-02	6.72E-02	1.00E+00	cytoplasm organization and biogenesis	P
GO:0007030	12	2.53E-02	1.00E+00	2.58E-03	1.80E-01	7.86E-02	1.00E+00	4.13E-02	1.00E+00	1.62E-01	1.00E+00	1.80E-02	6.68E-01	2.00E-01	1.00E+00	2.15E-03	7.90E-02	Golgi organization and biogenesis	P
GO:0007031	20	1.72E-03	2.12E-01	1.81E-02	1.00E+00	7.26E-02	1.00E+00	2.10E-02	9.37E-01	7.11E-03	6.92E-01	1.22E-01	1.00E+00	5.05E-03	2.23E-01	1.66E-02	6.56E-01	peroxisome organization and biogenesis	P
GO:0007033	31	1.73E-02	1.00E+00	1.41E-01	1.00E+00	8.73E-02	1.00E+00	2.68E-01	1.00E+00	9.22E-03	6.92E-01	3.60E-01	1.00E+00	2.14E-01	1.00E+00	6.52E-02	1.00E+00	vacuole organization and biogenesis	P
GO:0007034	22	2.68E-02	1.00E+00	4.75E-03	2.61E-01	2.55E-01	1.00E+00	2.29E-02	9.37E-01	3.19E-03	2.13E-01	1.30E-01	1.00E+00	4.15E-01	1.00E+00	1.39E-03	6.00E-02	vacuolar transport	P
GO:0007040	27	1.22E-02	6.08E-01	9.68E-02	1.00E+00	1.06E-01	1.00E+00	1.50E-01	1.00E+00	4.54E-03	2.13E-01	3.77E-01	1.00E+00	2.31E-01	1.00E+00	4.79E-02	1.00E+00	lysosome organization and biogenesis	P
GO:0007041	12	2.17E-01	1.00E+00	2.06E-01	1.00E+00	6.50E-01	1.00E+00	5.65E-01	1.00E+00	6.76E-02	1.00E+00	3.47E-01	1.00E+00	7.98E-01	1.00E+00	1.05E-01	1.00E+00	lysosomal transport	P
GO:0007046	70	1.60E-07	2.57E-03	1.18E-03	9.65E-02	2.02E-07	2.00E-03	8.29E-04	6.90E-02	7.93E-07	1.69E-03	1.57E-02	6.68E-01	8.51E-02	1.00E+00	2.27E-01	1.00E+00	ribosome biogenesis	P
GO:0007049	698	5.82E-23	0.00E+00	1.18E-31	0.00E+00	9.65E-23	0.00E+00	1.61E-30	0.00E+00	1.43E-12	0.00E+00	2.30E-18	0.00E+00	1.79E-08	0.00E+00	3.14E-09	0.00E+00	cell cycle	P
GO:0007050	63	8.48E-02	1.00E+00	9.02E-03	4.69E-01	6.31E-02	1.00E+00	3.95E-02	1.00E+00	1.96E-01	1.00E+00	5.73E-03	4.21E-01	2.58E-01	1.00E+00	8.95E-02	1.00E+00	cell cycle arrest	P
GO:0007051	18	4.97E-03	2.72E-01	8.17E-05	1.50E-02	1.04E-02	6.53E-01	1.59E-03	9.60E-02	1.02E-02	6.92E-01	4.25E-04	2.33E-02	2.09E-02	6.36E-01	5.57E-02	1.00E+00	spindle organization and biogenesis	P
GO:0007059	57	6.40E-04	8.86E-02	3.06E-06	3.92E-03	1.12E-05	2.91E-03	2.30E-07	2.89E-03	9.98E-02	1.00E+00	6.95E-04	4.48E-02	1.51E-01	1.00E+00	2.24E-03	7.90E-02	chromosome segregation	P
GO:0007067	192	8.88E-16	0.00E+00	1.20E-16	0.00E+00	5.65E-16	0.00E+00	3.63E-17	0.00E+00	1.66E-09	0.00E+00	2.44E-09	8.78E-04	3.75E-05	4.00E-03	6.47E-05	7.00E-03	mitosis	P
GO:0007076	16	4.21E-02	1.00E+00	7.97E-07	3.92E-03	1.29E-02	6.53E-01	1.95E-09	0.00E+00	2.68E-01	1.00E+00	2.05E-02	7.56E-01	1.14E-01	1.00E+00	1.52E-02	6.56E-01	mitotic chromosome condensation	P
GO:0007088	45	3.51E-05	7.00E-03	4.87E-05	7.00E-03	3.76E-04	4.00E-02	1.18E-05	2.89E-03	6.89E-04	1.20E-01	7.49E-04	4.48E-02	7.29E-04	3.44E-02	6.34E-02	1.00E+00	regulation of mitosis	P
GO:0007090	11	9.86E-02	1.00E+00	5.41E-02	1.00E+00	2.66E-02	1.00E+00	1.91E-01	1.00E+00	4.20E-01	1.00E+00	3.29E-02	1.00E+00	4.44E-01	1.00E+00	4.14E-01	1.00E+00	regulation of S phase of mitotic cell cycle	P
GO:0007093	13	2.68E-03	2.12E-01	1.43E-06	3.92E-03	9.42E-03	6.53E-01	4.99E-10	0.00E+00	1.53E-03	1.20E-01	2.36E-02	1.00E+00	3.32E-02	8.38E-01	5.64E-02	1.00E+00	mitotic checkpoint	P
GO:0007098	12	7.17E-03	3.15E-01	2.20E-05	7.00E-03	8.58E-03	6.53E-01	1.54E-04	1.30E-02	3.84E-02	1.00E+00	1.77E-03	1.27E-01	3.71E-01	1.00E+00	1.19E-01	1.00E+00	centrosome cycle	P
GO:0007126	84	2.46E-04	1.90E-02	1.13E-06	3.92E-03	2.90E-05	3.00E-03	2.88E-05	9.57E-03	4.83E-02	1.00E+00	8.08E-05	1.10E-02	2.95E-02	8.38E-01	4.24E-02	1.00E+00	meiosis	P
GO:0007127	29	3.77E-03	2.12E-01	8.95E-04	8.70E-02	4.67E-04	4.90E-02	1.86E-02	9.37E-01	3.15E-02	1.00E+00	5.40E-04	3.20E-02	1.13E-01	1.00E+00	2.02E-01	1.00E+00	meiosis I	P
GO:0007129	11	4.13E-02	1.00E+00	7.19E-04	5.90E-02	5.80E-02	1.00E+00	9.62E-02	1.00E+00	5.42E-02	1.00E+00	2.35E-06	2.00E-03	2.23E-01	1.00E+00	2.64E-02	9.99E-01	synapsis	P
GO:0007143	11	3.74E-02	1.00E+00	2.24E-01	1.00E+00	5.72E-02	1.00E+00	7.55E-01	1.00E+00	3.08E-01	1.00E+00	3.83E-01	1.00E+00	9.32E-02	1.00E+00	1.18E-01	1.00E+00	female meiosis	P
GO:0007154	4681	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell communication	P
GO:0007155	721	9.72E-01	1.00E+00	1.73E-01	1.00E+00	9.86E-01	1.00E+00	4.87E-01	1.00E+00	9.80E-01	1.00E+00	3.85E-01	1.00E+00	6.58E-01	1.00E+00	2.53E-02	9.99E-01	cell adhesion	P
GO:0007156	105	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	homophilic cell adhesion	P
GO:0007157	36	2.20E-01	1.00E+00	4.91E-02	1.00E+00	3.78E-01	1.00E+00	8.60E-02	1.00E+00	3.44E-01	1.00E+00	2.56E-02	1.00E+00	8.83E-02	1.00E+00	3.97E-01	1.00E+00	heterophilic cell adhesion	P
GO:0007159	18	1.62E-01	1.00E+00	1.63E-02	7.63E-01	2.80E-01	1.00E+00	1.78E-01	1.00E+00	1.85E-01	1.00E+00	3.69E-03	1.80E-01	1.28E-01	1.00E+00	8.84E-02	1.00E+00	leukocyte adhesion	P
GO:0007160	87	9.07E-02	1.00E+00	6.83E-02	1.00E+00	1.71E-01	1.00E+00	5.19E-01	1.00E+00	2.71E-01	1.00E+00	7.00E-02	1.00E+00	2.96E-02	8.38E-01	1.59E-02	6.56E-01	cell-matrix adhesion	P
GO:0007162	16	1.68E-01	1.00E+00	2.40E-01	1.00E+00	3.16E-01	1.00E+00	3.64E-01	1.00E+00	8.88E-02	1.00E+00	1.61E-01	1.00E+00	1.02E-01	1.00E+00	3.14E-01	1.00E+00	negative regulation of cell adhesion	P
GO:0007163	26	1.00E-01	1.00E+00	4.33E-03	1.88E-01	7.54E-02	1.00E+00	1.49E-02	6.47E-01	2.64E-01	1.00E+00	2.21E-02	1.00E+00	1.71E-01	1.00E+00	4.04E-02	1.00E+00	establishment and/or maintenance of cell p	P
GO:0007165	4360	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	signal transduction	P
GO:0007166	2996	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell surface receptor linked signal transduct	P
GO:0007167	306	1.73E-02	1.00E+00	3.65E-02	1.00E+00	2.81E-01	1.00E+00	3.97E-01	1.00E+00	5.17E-02	1.00E+00	5.27E-01	1.00E+00	4.83E-03	2.23E-01	5.56E-05	7.00E-03	enzyme linked receptor protein signaling pa	P
GO:0007169	195	1.17E-01	1.00E+00	1.02E-01	1.00E+00	4.97E-01	1.00E+00	3.92E-01	1.00E+00	1.82E-01	1.00E+00	5.52E-01	1.00E+00	4.86E-02	1.00E+00	2.25E-03	7.90E-02	transmembrane receptor protein tyrosine ki	P
GO:0007172	13	4.92E-01	1.00E+00	1.76E-01	1.00E+00	7.76E-01	1.00E+00	2.43E-01	1.00E+00	6.34E-01	1.00E+00	5.24E-01	1.00E+00	2.31E-01	1.00E+00	1.50E-01	1.00E+00	signal complex formation	P
GO:0007173	20	5.60E-01	1.00E+00	5.41E-01	1.00E+00	6.83E-01	1.00E+00	5.70E-01	1.00E+00	6.61E-01	1.00E+00	6.45E-01	1.00E+00	4.38E-01	1.00E+00	4.78E-01	1.00E+00	epidermal growth factor receptor signaling p	P
GO:0007178	107	3.74E-02	1.00E+00	1.24E-01	1.00E+00	1.97E-01	1.00E+00	4.65E-01	1.00E+00	6.09E-02	1.00E+00	4.48E-01	1.00E+00	5.34E-02	1.00E+00	7.15E-03	4.28E-01	transmembrane receptor protein serine/thre	P
GO:0007179	65	2.48E-02	1.00E+00	1.06E-01	1.00E+00	1.16E-01	1.00E+00	2.05E-01	1.00E+00	3.50E-02	1.00E+00	5.85E-01	1.00E+00	8.69E-02	1.00E+00	2.27E-02	9.99E-01	transforming growth factor beta receptor sig	P
GO:0007186	2337	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	G-protein coupled receptor protein signaling	P
GO:0007187	66	7.43E-01	1.00E+00	5.83E-01	1.00E+00	9.15E-01	1.00E+00	8.72E-01	1.00E+00	6.13E-01	1.00E+00	5.78E-01	1.00E+00	3.31E-01	1.00E+00	1.42E-01	1.00E+00	G-protein signaling, coupled to cyclic nucle	P
GO:0007188	62	7.47E-01	1.00E+00	6.16E-01	1.00E+00	9.12E-01	1.00E+00	8.64E-01	1.00E+00	6.35E-01	1.00E+00	6.09E-01	1.00E+00	3.28E-01	1.00E+00	1.61E-01	1.00E+00	G-protein signaling, coupled to cAMP nucle	P
GO:0007189	39	9.58E-01	1.00E+00	8.54E-01	1.00E+00	9.82E-01	1.00E+00	9.98E-01	1.00E+00	9.03E-01	1.00E+00	8.08E-01	1.00E+00	6.47E-01	1.00E+00	1.72E-01	1.00E+00	G-protein signaling, adenylate cyclase activ	P
GO:0007190	15	9.77E-01	1.00E+00	5.67E-01	1.00E+00	9.92E-01	1.00E+00	8.93E-01	1.00E+00	7.26E-01	1.00E+00	7.62E-01	1.00E+00	9.24E-01	1.00E+00	1.05E-01	1.00E+00	adenylate cyclase activation	P
GO:0007193	15	7.70E-02	1.00E+00	2.22E-01	1.00E+00	2.71E-01	1.00E+00	8.79E-02	1.00E+00	3.20E-01	1.00E+00	2.45E-01	1.00E+00	6.32E-02	1.00E+00	3.07E-01	1.00E+00	G-protein signaling, adenylate cyclase inhib	P
GO:0007200	45	4.30E-01	1.00E+00	6.32E-01	1.00E+00	7.88E-01	1.00E+00	8.35E-01	1.00E+00	5.59E-01	1.00E+00	8.75E-01	1.00E+00	1.06E-01	1.00E+00	1.13E-01	1.00E+00	G-protein signaling, coupled to IP3 second	P
GO:0007204	38	2.01E-01	1.00E+00	9.29E-02	1.00E+00	6.75E-01	1.00E+00	3.75E-01	1.00E+00	7.42E-01	1.00E+00	1.34E-01	1.00E+00	2.68E-03	8.40E-02	2.73E-02	9.99E-01	elevation of cytosolic calcium ion concentra	P
GO:0007205	21	1.62E-01	1.00E+00	4.70E-01	1.00E+00	2.54E-01	1.00E+00	4.59E-01	1.00E+00	4.42E-01	1.00E+00	8.12E-01	1.00E+00	6.69E-02	1.00E+00	2.77E-01	1.00E+00	protein kinase C activation	P

GO:0007212	16	9.87E-01	1.00E+00	7.07E-01	1.00E+00	9.39E-01	1.00E+00	9.15E-01	1.00E+00	9.02E-01	1.00E+00	3.97E-01	1.00E+00	9.15E-01	1.00E+00	3.62E-01	1.00E+00	dopamine receptor signaling pathway	P
GO:0007214	31	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.79E-01	1.00E+00	9.54E-01	1.00E+00	9.96E-01	1.00E+00	8.88E-01	1.00E+00	gamma-aminobutyric acid signaling pathwa	P
GO:0007215	13	4.49E-01	1.00E+00	5.54E-02	1.00E+00	2.88E-01	1.00E+00	2.26E-01	1.00E+00	6.72E-01	1.00E+00	1.49E-02	6.68E-01	6.33E-01	1.00E+00	4.28E-01	1.00E+00	glutamate signaling pathway	P
GO:0007218	99	3.83E-01	1.00E+00	2.22E-01	1.00E+00	6.27E-01	1.00E+00	4.00E-01	1.00E+00	3.06E-01	1.00E+00	4.98E-01	1.00E+00	2.62E-01	1.00E+00	2.82E-02	9.99E-01	neuropeptide signaling pathway	P
GO:0007219	57	5.17E-01	1.00E+00	2.74E-01	1.00E+00	7.23E-01	1.00E+00	1.19E-01	1.00E+00	7.18E-01	1.00E+00	4.36E-01	1.00E+00	2.58E-01	1.00E+00	6.61E-01	1.00E+00	Notch signaling pathway	P
GO:0007223	20	6.05E-02	1.00E+00	4.17E-01	1.00E+00	6.78E-01	1.00E+00	8.04E-01	1.00E+00	2.11E-03	1.20E-01	2.08E-01	1.00E+00	1.61E-01	1.00E+00	4.10E-01	1.00E+00	frizzled-2 signaling pathway	P
GO:0007224	29	6.19E-02	1.00E+00	9.03E-02	1.00E+00	3.04E-01	1.00E+00	4.71E-01	1.00E+00	2.50E-02	1.00E+00	3.41E-02	1.00E+00	1.31E-01	1.00E+00	2.20E-01	1.00E+00	smoothened signaling pathway	P
GO:0007229	96	6.23E-01	1.00E+00	3.04E-01	1.00E+00	7.59E-01	1.00E+00	5.67E-01	1.00E+00	4.95E-01	1.00E+00	5.72E-01	1.00E+00	5.35E-01	1.00E+00	8.27E-02	1.00E+00	integrin-mediated signaling pathway	P
GO:0007242	1232	1.30E-13	0.00E+00	3.22E-25	0.00E+00	4.89E-11	7.08E-04	2.57E-15	0.00E+00	7.15E-08	9.59E-04	2.47E-14	6.20E-04	6.32E-07	8.23E-04	8.75E-19	0.00E+00	intracellular signaling cascade	P
GO:0007243	358	1.17E-05	7.00E-03	1.05E-12	0.00E+00	3.55E-04	4.00E-02	1.40E-07	2.89E-03	1.38E-02	6.92E-01	1.42E-07	1.65E-03	4.36E-05	8.00E-03	1.82E-09	0.00E+00	protein kinase cascade	P
GO:0007249	104	7.33E-03	3.15E-01	4.96E-05	7.00E-03	6.97E-02	1.00E+00	1.24E-03	9.40E-02	2.44E-01	1.00E+00	1.16E-02	5.03E-01	1.15E-03	6.14E-02	1.98E-03	7.90E-02	I-kappaB kinase/NF-kappaB cascade	P
GO:0007254	50	3.53E-01	1.00E+00	4.75E-01	1.00E+00	5.75E-01	1.00E+00	6.29E-01	1.00E+00	3.34E-01	1.00E+00	6.40E-01	1.00E+00	3.49E-01	1.00E+00	2.08E-01	1.00E+00	JNK cascade	P
GO:0007257	12	2.03E-01	1.00E+00	7.40E-01	1.00E+00	5.34E-01	1.00E+00	9.59E-01	1.00E+00	2.39E-01	1.00E+00	7.21E-01	1.00E+00	4.05E-02	1.00E+00	3.64E-01	1.00E+00	activation of JNK activity	P
GO:0007259	42	2.67E-01	1.00E+00	6.78E-02	1.00E+00	2.13E-01	1.00E+00	1.61E-01	1.00E+00	6.15E-01	1.00E+00	8.97E-02	1.00E+00	9.36E-02	1.00E+00	1.50E-01	1.00E+00	JAK-STAT cascade	P
GO:0007260	19	9.83E-01	1.00E+00	2.32E-01	1.00E+00	9.83E-01	1.00E+00	6.31E-01	1.00E+00	1.00E+00	1.00E+00	3.29E-01	1.00E+00	3.31E-01	1.00E+00	8.63E-02	1.00E+00	tyrosine phosphorylation of STAT protein	P
GO:0007264	427	7.69E-06	3.62E-03	1.60E-10	0.00E+00	1.95E-04	2.10E-02	5.03E-07	2.89E-03	1.34E-04	2.70E-02	6.69E-08	1.65E-03	1.48E-02	4.78E-01	5.18E-06	2.91E-03	small GTPase mediated signal transduction	P
GO:0007265	35	2.69E-01	1.00E+00	1.01E-02	4.69E-01	2.38E-01	1.00E+00	1.96E-02	9.37E-01	6.81E-01	1.00E+00	3.14E-02	1.00E+00	3.65E-01	1.00E+00	4.56E-02	1.00E+00	Ras protein signal transduction	P
GO:0007266	97	9.97E-02	1.00E+00	3.34E-04	4.40E-02	1.45E-01	1.00E+00	1.56E-02	6.47E-01	7.18E-01	1.00E+00	2.36E-03	1.27E-01	4.78E-02	1.00E+00	5.95E-04	3.00E-02	Rho protein signal transduction	P
GO:0007267	406	5.16E-01	1.00E+00	2.83E-01	1.00E+00	9.64E-01	1.00E+00	8.42E-01	1.00E+00	5.91E-01	1.00E+00	1.45E-01	1.00E+00	2.24E-02	6.36E-01	1.15E-02	4.76E-01	cell-cell signaling	P
GO:0007268	241	9.24E-01	1.00E+00	6.94E-01	1.00E+00	9.98E-01	1.00E+00	9.83E-01	1.00E+00	8.89E-01	1.00E+00	1.84E-01	1.00E+00	2.56E-01	1.00E+00	2.64E-01	1.00E+00	synaptic transmission	P
GO:0007269	70	1.00E+00	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.21E-01	1.00E+00	9.85E-01	1.00E+00	6.82E-01	1.00E+00	neurotransmitter secretion	P
GO:0007270	51	9.97E-01	1.00E+00	8.81E-01	1.00E+00	9.98E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	4.85E-01	1.00E+00	6.12E-01	1.00E+00	7.01E-01	1.00E+00	nerve-nerve synaptic transmission	P
GO:0007271	12	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	6.76E-01	1.00E+00	2.83E-01	1.00E+00	synaptic transmission, cholinergic	P
GO:0007272	42	5.20E-01	1.00E+00	1.35E-01	1.00E+00	3.36E-01	1.00E+00	1.80E-01	1.00E+00	5.77E-01	1.00E+00	3.39E-01	1.00E+00	5.75E-01	1.00E+00	7.51E-02	1.00E+00	ensheathment of neurons	P
GO:0007274	14	1.77E-02	1.00E+00	2.41E-01	1.00E+00	6.72E-01	1.00E+00	3.13E-01	1.00E+00	2.20E-01	1.00E+00	1.21E-01	1.00E+00	2.23E-03	8.40E-02	4.30E-01	1.00E+00	neuromuscular synaptic transmission	P
GO:0007275	2714	2.32E-14	0.00E+00	9.10E-13	0.00E+00	1.03E-07	2.00E-03	8.16E-08	2.89E-03	6.26E-07	1.69E-03	7.61E-06	5.87E-03	5.84E-13	0.00E+00	2.23E-12	0.00E+00	development	P
GO:0007276	312	2.38E-04	1.90E-02	3.15E-03	1.88E-01	1.78E-04	1.16E-02	9.50E-03	5.72E-01	1.42E-02	6.92E-01	9.08E-03	5.03E-01	1.04E-02	2.75E-01	1.47E-01	1.00E+00	gametogenesis	P
GO:0007281	42	7.22E-02	1.00E+00	3.40E-02	1.00E+00	2.40E-02	1.00E+00	1.18E-01	1.00E+00	3.34E-01	1.00E+00	2.10E-02	7.56E-01	1.80E-01	1.00E+00	4.22E-01	1.00E+00	germ cell development	P
GO:0007283	233	4.70E-07	2.57E-03	1.41E-05	4.51E-03	4.04E-07	2.00E-03	8.35E-05	1.30E-02	9.49E-04	1.20E-01	1.63E-03	1.22E-01	1.44E-03	6.14E-02	6.90E-03	4.28E-01	spermatogenesis	P
GO:0007286	44	1.52E-02	1.00E+00	5.95E-03	3.08E-01	3.90E-03	2.20E-01	1.10E-02	5.72E-01	3.28E-01	1.00E+00	3.26E-02	1.00E+00	9.91E-03	2.75E-01	3.56E-02	1.00E+00	spermatid development	P
GO:0007292	43	1.98E-02	1.00E+00	4.19E-01	1.00E+00	7.09E-02	1.00E+00	4.10E-01	1.00E+00	1.14E-01	1.00E+00	3.92E-01	1.00E+00	2.96E-02	8.38E-01	7.96E-01	1.00E+00	female gamete generation	P
GO:0007338	48	2.32E-01	1.00E+00	1.51E-01	1.00E+00	3.07E-01	1.00E+00	1.56E-01	1.00E+00	4.76E-01	1.00E+00	2.78E-01	1.00E+00	8.15E-02	1.00E+00	1.24E-01	1.00E+00	fertilization (sensu Metazoa)	P
GO:0007339	21	6.78E-01	1.00E+00	2.07E-01	1.00E+00	7.66E-01	1.00E+00	1.27E-01	1.00E+00	8.67E-01	1.00E+00	3.17E-01	1.00E+00	3.65E-01	1.00E+00	3.42E-01	1.00E+00	binding of sperm to zona pellucida	P
GO:0007340	11	2.53E-01	1.00E+00	5.01E-01	1.00E+00	4.09E-01	1.00E+00	7.11E-01	1.00E+00	3.59E-01	1.00E+00	3.81E-01	1.00E+00	4.15E-02	1.00E+00	5.10E-01	1.00E+00	acrosome reaction	P
GO:0007346	38	1.11E-01	1.00E+00	1.46E-01	1.00E+00	5.10E-02	1.00E+00	6.35E-01	1.00E+00	3.36E-01	1.00E+00	2.76E-02	1.00E+00	2.51E-01	1.00E+00	4.27E-01	1.00E+00	regulation of progression through mitotic ce	P
GO:0007368	34	3.92E-01	1.00E+00	6.93E-01	1.00E+00	2.58E-01	1.00E+00	5.66E-01	1.00E+00	1.96E-01	1.00E+00	8.32E-01	1.00E+00	9.51E-01	1.00E+00	6.82E-01	1.00E+00	determination of left/right symmetry	P
GO:0007369	69	8.46E-03	6.08E-01	2.02E-03	1.30E-01	3.38E-03	2.03E-01	4.36E-03	2.88E-01	2.94E-02	1.00E+00	1.74E-02	6.68E-01	3.35E-01	1.00E+00	3.07E-02	9.99E-01	gastrulation	P
GO:0007379	10	9.67E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	9.69E-01	1.00E+00	9.99E-01	1.00E+00	9.62E-01	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	segment specification	P
GO:0007389	244	8.84E-01	1.00E+00	1.00E+00	1.00E+00	9.28E-01	1.00E+00	9.99E-01	1.00E+00	7.58E-01	1.00E+00	9.99E-01	1.00E+00	7.32E-01	1.00E+00	9.75E-01	1.00E+00	pattern specification	P
GO:0007398	142	4.41E-01	1.00E+00	5.87E-01	1.00E+00	7.16E-01	1.00E+00	7.17E-01	1.00E+00	6.78E-01	1.00E+00	4.99E-01	1.00E+00	7.92E-02	1.00E+00	3.41E-01	1.00E+00	ectoderm development	P
GO:0007399	753	8.03E-02	1.00E+00	2.14E-01	1.00E+00	6.25E-01	1.00E+00	7.06E-01	1.00E+00	3.00E-01	1.00E+00	5.04E-01	1.00E+00	9.56E-04	3.62E-02	7.67E-03	4.28E-01	nervous system development	P
GO:0007405	27	4.83E-02	1.00E+00	1.14E-01	1.00E+00	5.15E-01	1.00E+00	1.17E-01	1.00E+00	4.19E-02	1.00E+00	3.53E-01	1.00E+00	6.49E-03	2.75E-01	4.88E-02	1.00E+00	neuroblast proliferation	P
GO:0007409	179	6.25E-01	1.00E+00	7.58E-01	1.00E+00	9.04E-01	1.00E+00	9.37E-01	1.00E+00	4.33E-01	1.00E+00	7.64E-01	1.00E+00	3.50E-01	1.00E+00	2.22E-01	1.00E+00	axonogenesis	P
GO:0007411	93	9.65E-01	1.00E+00	9.41E-01	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	8.76E-01	1.00E+00	8.69E-01	1.00E+00	5.82E-01	1.00E+00	4.17E-01	1.00E+00	axon guidance	P
GO:0007416	21	9.78E-01	1.00E+00	7.42E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.99E-01	1.00E+00	9.60E-01	1.00E+00	5.27E-01	1.00E+00	8.04E-02	1.00E+00	synaptogenesis	P
GO:0007417	328	3.09E-01	1.00E+00	8.51E-01	1.00E+00	5.77E-01	1.00E+00	9.19E-01	1.00E+00	5.93E-01	1.00E+00	6.14E-01	1.00E+00	3.04E-02	8.38E-01	8.31E-01	1.00E+00	central nervous system development	P
GO:0007420	255	3.02E-01	1.00E+00	7.55E-01	1.00E+00	5.68E-01	1.00E+00	8.46E-01	1.00E+00	5.14E-01	1.00E+00	4.91E-01	1.00E+00	5.96E-02	1.00E+00	7.87E-01	1.00E+00	brain development	P
GO:0007422	29	7.52E-01	1.00E+00	8.72E-01	1.00E+00	8.22E-01	1.00E+00	6.69E-01	1.00E+00	7.06E-01	1.00E+00	7.88E-01	1.00E+00	5.03E-01	1.00E+00	9.93E-01	1.00E+00	peripheral nervous system development	P
GO:0007423	175	5.87E-01	1.00E+00	9.72E-01	1.00E+00	6.69E-01	1.00E+00	9.15E-01	1.00E+00	6.38E-01	1.00E+00	9.13E-01	1.00E+00	3.43E-01	1.00E+00	9.60E-01	1.00E+00	sensory organ development	P
GO:0007431	12	9.94E-01	1.00E+00	7.84E-01	1.00E+00	9.22E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	7.58E-01	1.00E+00	7.50E-01	1.00E+00	2.74E-01	1.00E+00	salivary gland development	P
GO:0007439	10	1.83E-01	1.00E+00	4.11E-02	1.00E+00	5.41E-01	1.00E+00	1.05E-01	1.00E+00	3.52E-01	1.00E+00	1.43E-01	1.00E+00	7.40E-02	1.00E+00	2.78E-03	1.27E-01	ectodermal gut development	P
GO:0007492	21	8.99E-01	1.00E+00	6.16E-01	1.00E+00	7.33E-01	1.00E+00	6.75E-01	1.00E+00	7.27E-01	1.00E+00	6.58E-01	1.00E+00	9.72E-01	1.00E+00	3.50E-01	1.00E+00	endoderm development	P
GO:0007498	57	1.98E-02	1.00E+00	7.98E-03	4.16E-01	3.79E-03	2.20E-01	5.91E-02	1.00E+00	2.35E-01	1.00E+00	1.78E-02	6.68E-01	9.63E-02	1.00E+00	6.14E-02	1.00E+00	mesoderm development	P
GO:0007507	166	4.79E-03	2.72E-01	1.99E-03	1.30E-01	7.48E-03	6.41E-01	4.67E-03	2.88E-01	1.00E-01	1.00E+00	9.17E-02	1.00E+00	8.17E-03	2.75E-01	2.82E-03	1.27E-01	heart development	P
GO:0007512	13	8.07E-01	1.00E+00	9.15E-01	1.00E+00	4.54E-01	1.00E+00	8.87E-01	1.00E+00	6.65E-01	1.00E+00	9.29E-01	1.00E+00	9.83E-01	1.00E+00	3.83E-01	1.00E+00	adult heart development	P
GO:0007517	211	2.25E-01	1.00E+00	9.46E-02	1.00E+00	7.75E-01	1.00E+00	1.34E-01	1.00E+00	7.77E-01	1.00E+00	4.53E-01	1.00E+00	1.74E-03	8.40E-02	2.66E-02	9.99E-01	muscle development	P
GO:0007519	152	2.81E-01	1.00E+00	7.15E-02	1.00E+00	6.56E-01	1.00E+00	5.14E-02	1.00E+00	6.92E-01	1.00E+00	4.19E-01	1.00E+00	2.76E-02	8.38E-01	5.55E-02	1.00E+00	striated muscle development	P
GO:0007528	23	4.54E-01	1.00E+00	9.39E-02	1.00E+00	8.31E-01	1.00E+00	1.95E-01	1.00E+00	3.32E-01	1.00E+00	2.89E-01	1.00E+00	1.99E-01	1.00E+00	4.51E-02	1.00E+00	neuromuscular junction development	P
GO:0007530	23	9.74E-01	1.00E+00	6.88E-01	1.00E+00	9.35E-01	1.00E+00	8.57E-01	1.00E+00	9.71E-01	1.00E+00	6.27E-01	1.00E+00	8.05E-01	1.00E+00	3.39E-01	1.00E+00	sex determination	P
GO:0007548	100	1.46E-01	1.00E+00	6.05E-01	1.00E+00	1.13E-01	1.00E+00	6.40E-01	1.00E+00	2.89E-01	1.00E+00	5.56E-01	1.00E+00	2.09E-01	1.00E+00	5.71E-01	1.00E+00	sex differentiation	P
GO:0007565	47	7.68E-01	1.00E+00	9.36E-01	1.00E+00	9.46E-01	1.00E+00	9.83E-01	1.00E+00	3.37E-01	1.00E+00	9.85E-01	1.00E+00	6.16E-01	1.00E+00	5.02E-01	1.00E+00	pregnancy	P
GO:0007566	15	4.72E-03	2.72E-01	5.31E-02	1.00E+00	1.52E-01	1.00E+00	2.08E-02	9.37E-01	3.76E-03	2.13E-01	3.46E-01	1.00E+00	3.40E-02	8.38E-01	7.37E-02	1.00E+00	embryo implantation	P
GO:0007568	53	2.24E-01	1.00E+00	3.68E-01	1.00E+00	3.18E-01	1.00E+00	2.52E-01	1.00E+00	4.38E-01	1.00E+00	2.16E-01	1.00E+00	1.92E-01	1.00E+00	9.40E-01	1.00E+00	aging	P
GO:0007569	28	2.99E-01	1.00E+00	3.02E-01	1.00E+00	4.43E-01	1.00E+00	2.56E-01	1.00E+00	6.22E-01	1.00E+00	3.56E-01	1.00E+00	2.92E-01	1.00E+00	6.62E-01	1.00E+00	cell aging	P
GO:0007582	12555	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.85E-35	0.00E+00	0.00E+00	0.00E+00	physiological process	P
GO:0007584	43	8.63E-05	1.43E-02	2.61E-04	4.40E-02	4.53E-06	2.91E-03	5.33E-05	1.07E-02	3.44E-02	1.00E+00	7.98E-04	4.48E-02	9.44E-02	1.00E+00	3.83E-01	1.00E+00	response to nutrient	P
GO:0007585	30	4.07E-01	1.00E+00	7.79E-01	1.00E+00	4.46E-01	1.00E+00	9.21E-01	1.00E+00	6.28E-01	1.00E+00	7.31E-01	1.00E+00	2.39E-01	1.00E+00	3.47E-01	1.00E+00	respiratory gaseous exchange	P
GO:0007586	34	1.91E-02	1.00E+00	2.30E-01	1.00E+00	9.51E-02	1.00E+00	7.11E-01	1.00E+00	4.37E-02	1.00E+00	1.89E-01	1.00E+00	1.03E-02	2.75E-01	7.42E-02	1.00E+00	digestion	P
GO:0007588	17	3.95E-01	1.00E+00	9.91E-01	1.00E+00	7.23E-01	1.00E+00	9.46E-01	1.00E+00	6.97E-01	1.00E+00	9.45E-01	1.00E+00	2.59E-01	1.00E+00	9.82E-01	1.00E+00	excretion	P
GO:0007595	25	9.53E-01	1.00E+00	8.12E-01	1.00E+00	8.60E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	7.77E-01	1.00E+00	4.92E-01	1.00E+00	3.63E-01	1.00E+00	lactation	P
GO:0007596	120	7.69E-01	1.00E+00	5.83E-01	1.00E+00	8.10E-01	1.00E+00	8.14E-01	1.00E+00	8.87E-01	1.00E+00	3.51E-01	1.00E+00	5.21E-01	1.00E+00	5.89E-01	1.00E+00	blood coagulation	P
GO:0007599	122	6.74E-01	1.00E+00	4.46E-01	1.00E+00	7.79E-01	1.00E+00	5.82E-01	1.00E+00	8.39E-01	1.00E+00	2.99E-01	1.00E+00	3.75E-01	1.00E+00	5.77E-01	1.00E+00	hemostasis	P
GO:0007600	400	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	sensory perception	P
GO:0007601	122	7.30E-01	1.00E+00	7.18E-01	1.00E+00	5.27E-01	1.00E+00	7.20E-01	1.00E+00	9.35E-01	1.00E+00	5.17E-01	1.00E+00	5.49E-01	1.00E+00	8.81E-01	1.00E+00	visual perception	P
GO:0007602	23	6.27E-01	1.00E+00	6.34E-01	1.00E+00	4.67E-01	1.00E+00	8.48E-01	1.00E+00	8.16E-01	1.00E+00	2.59E-01	1.00E+00	4.86E-01	1.00E+00	9.68E-01	1.00E+00	phototransduction	P

GO:0007605	76	2.55E-01	1.00E+00	4.61E-02	1.00E+00	7.06E-01	1.00E+00	8.61E-02	1.00E+00	5.30E-01	1.00E+00	1.67E-01	1.00E+00	6.84E-03	2.75E-01	1.14E-02	4.76E-01	sensory perception of sound	P
GO:0007606	175	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of chemical stimulus	P
GO:0007608	99	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sensory perception of smell	P
GO:0007610	428	6.79E-01	1.00E+00	2.68E-01	1.00E+00	9.99E-01	1.00E+00	9.63E-01	1.00E+00	8.43E-01	1.00E+00	1.38E-01	1.00E+00	1.79E-03	8.40E-02	5.85E-03	4.28E-01	behavior	P
GO:0007611	83	5.41E-01	1.00E+00	2.82E-01	1.00E+00	5.72E-01	1.00E+00	4.39E-01	1.00E+00	6.83E-01	1.00E+00	5.24E-01	1.00E+00	4.12E-01	1.00E+00	5.36E-02	1.00E+00	learning and/or memory	P
GO:0007612	54	8.30E-01	1.00E+00	7.53E-01	1.00E+00	9.14E-01	1.00E+00	8.78E-01	1.00E+00	8.22E-01	1.00E+00	7.11E-01	1.00E+00	5.26E-01	1.00E+00	1.95E-01	1.00E+00	learning	P
GO:0007613	25	3.41E-01	1.00E+00	1.87E-01	1.00E+00	7.10E-01	1.00E+00	2.58E-01	1.00E+00	4.97E-01	1.00E+00	2.74E-01	1.00E+00	1.30E-01	1.00E+00	3.13E-01	1.00E+00	memory	P
GO:0007617	15	9.75E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	6.33E-01	1.00E+00	8.83E-01	1.00E+00	9.93E-01	1.00E+00	8.45E-01	1.00E+00	mating behavior	P
GO:0007623	35	1.91E-01	1.00E+00	2.11E-01	1.00E+00	3.52E-01	1.00E+00	3.21E-01	1.00E+00	1.75E-01	1.00E+00	5.35E-01	1.00E+00	2.46E-01	1.00E+00	1.90E-01	1.00E+00	circadian rhythm	P
GO:0007626	284	7.74E-01	1.00E+00	4.18E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	9.39E-01	1.00E+00	2.82E-01	1.00E+00	2.03E-03	8.40E-02	1.50E-02	6.56E-01	locomotory behavior	P
GO:0007628	24	3.49E-01	1.00E+00	8.14E-01	1.00E+00	5.68E-01	1.00E+00	9.57E-01	1.00E+00	6.75E-01	1.00E+00	7.34E-01	1.00E+00	9.67E-02	1.00E+00	5.00E-01	1.00E+00	adult walking behavior	P
GO:0007631	47	2.95E-01	1.00E+00	7.84E-01	1.00E+00	7.90E-01	1.00E+00	9.80E-01	1.00E+00	2.87E-01	1.00E+00	5.79E-01	1.00E+00	2.72E-02	8.38E-01	4.76E-01	1.00E+00	feeding behavior	P
GO:0007632	27	9.79E-01	1.00E+00	5.51E-01	1.00E+00	9.72E-01	1.00E+00	6.36E-01	1.00E+00	1.00E+00	1.00E+00	7.53E-01	1.00E+00	1.90E-01	1.00E+00	1.30E-01	1.00E+00	visual behavior	P
GO:0008009	50	3.99E-01	1.00E+00	8.93E-01	1.00E+00	3.47E-01	1.00E+00	9.89E-01	1.00E+00	6.18E-01	1.00E+00	7.64E-01	1.00E+00	1.41E-01	1.00E+00	2.87E-01	1.00E+00	chemokine activity	F
GO:0008013	16	3.57E-04	3.10E-02	1.48E-03	9.65E-02	1.43E-04	1.16E-02	4.82E-03	2.88E-01	1.04E-02	6.92E-01	8.95E-03	5.03E-01	8.88E-03	2.75E-01	5.98E-02	1.00E+00	beta-catenin binding	F
GO:0008015	135	8.44E-01	1.00E+00	9.63E-01	1.00E+00	8.96E-01	1.00E+00	9.65E-01	1.00E+00	9.77E-01	1.00E+00	9.97E-01	1.00E+00	2.40E-01	1.00E+00	3.01E-01	1.00E+00	circulation	P
GO:0008016	45	8.09E-01	1.00E+00	8.65E-01	1.00E+00	9.68E-01	1.00E+00	9.32E-01	1.00E+00	8.73E-01	1.00E+00	9.61E-01	1.00E+00	3.25E-01	1.00E+00	1.48E-01	1.00E+00	regulation of heart contraction	P
GO:0008017	58	2.62E-05	7.00E-03	1.38E-04	1.50E-02	7.86E-04	4.90E-02	2.51E-03	1.39E-01	3.10E-04	4.90E-02	1.12E-03	9.00E-02	4.22E-03	2.23E-01	3.75E-03	1.27E-01	microtubule binding	F
GO:0008021	72	3.35E-01	1.00E+00	7.82E-02	1.00E+00	4.35E-01	1.00E+00	2.60E-01	1.00E+00	5.39E-01	1.00E+00	7.48E-02	1.00E+00	1.65E-01	1.00E+00	1.02E-01	1.00E+00	synaptic vesicle	C
GO:0008022	69	5.86E-07	2.76E-03	7.60E-05	1.50E-02	1.46E-05	3.00E-03	2.99E-04	4.20E-02	1.43E-03	1.20E-01	9.96E-04	9.00E-02	2.12E-04	1.20E-02	8.21E-03	4.28E-01	protein C-terminus binding	F
GO:0008026	102	4.51E-05	9.52E-03	1.10E-05	4.51E-03	5.15E-05	9.82E-03	7.48E-06	2.89E-03	3.42E-03	2.13E-01	3.29E-04	2.33E-02	1.86E-01	1.00E+00	4.98E-02	1.00E+00	ATP-dependent helicase activity	F
GO:0008028	17	5.34E-01	1.00E+00	1.68E-01	1.00E+00	2.39E-01	1.00E+00	1.68E-01	1.00E+00	6.35E-01	1.00E+00	5.10E-01	1.00E+00	9.34E-01	1.00E+00	1.40E-01	1.00E+00	monocarboxylic acid transporter activity	F
GO:0008033	59	6.02E-03	3.09E-01	1.19E-02	6.07E-01	2.49E-02	1.00E+00	2.44E-02	1.00E+00	8.57E-02	1.00E+00	9.04E-02	1.00E+00	8.17E-03	2.75E-01	8.05E-02	1.00E+00	tRNA processing	P
GO:0008034	23	1.41E-01	1.00E+00	1.77E-01	1.00E+00	1.96E-01	1.00E+00	2.03E-01	1.00E+00	2.03E-01	1.00E+00	8.72E-01	1.00E+00	2.08E-01	1.00E+00	4.71E-02	1.00E+00	lipoprotein binding	F
GO:0008037	18	9.79E-01	1.00E+00	5.75E-01	1.00E+00	9.99E-01	1.00E+00	8.56E-01	1.00E+00	5.66E-01	1.00E+00	4.42E-01	1.00E+00	7.73E-01	1.00E+00	4.56E-01	1.00E+00	cell recognition	P
GO:0008038	12	8.13E-01	1.00E+00	6.28E-01	1.00E+00	9.65E-01	1.00E+00	8.14E-01	1.00E+00	4.36E-01	1.00E+00	4.93E-01	1.00E+00	5.43E-01	1.00E+00	5.19E-01	1.00E+00	neuron recognition	P
GO:0008045	13	7.40E-01	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	9.88E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	2.01E-01	1.00E+00	9.12E-01	1.00E+00	motor axon guidance	P
GO:0008047	270	2.82E-04	1.90E-02	6.44E-09	8.90E-04	4.01E-03	2.20E-01	3.03E-06	2.89E-03	2.63E-02	1.00E+00	1.49E-08	8.78E-04	3.14E-03	8.78E-02	2.62E-03	8.32E-02	enzyme activator activity	F
GO:0008060	23	4.86E-02	1.00E+00	5.15E-03	2.79E-01	5.50E-02	1.00E+00	5.68E-02	1.00E+00	1.55E-01	1.00E+00	2.53E-03	1.27E-01	4.58E-02	1.00E+00	1.85E-01	1.00E+00	ARF GTPase activator activity	F
GO:0008064	53	6.15E-03	3.09E-01	5.45E-04	4.74E-02	7.83E-02	1.00E+00	1.25E-02	6.47E-01	1.00E-01	1.00E+00	2.06E-02	7.56E-01	7.54E-03	2.75E-01	2.35E-04	2.33E-02	regulation of actin polymerization and/or de	P
GO:0008066	74	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	glutamate receptor activity	F
GO:0008067	56	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	metabotropic glutamate, GABA-B-like recep	F
GO:0008076	143	4.32E-01	1.00E+00	2.22E-01	1.00E+00	4.81E-01	1.00E+00	6.53E-01	1.00E+00	8.66E-01	1.00E+00	1.59E-01	1.00E+00	1.01E-01	1.00E+00	3.62E-02	1.00E+00	voltage-gated potassium channel complex	C
GO:0008080	55	4.12E-03	2.14E-01	1.18E-03	9.65E-02	3.28E-03	2.03E-01	1.84E-03	1.24E-01	1.08E-02	6.92E-01	7.97E-03	4.21E-01	3.52E-01	1.00E+00	1.78E-02	6.56E-01	N-acetyltransferase activity	F
GO:0008081	75	1.71E-01	1.00E+00	6.13E-02	1.00E+00	2.41E-01	1.00E+00	3.58E-01	1.00E+00	9.94E-02	1.00E+00	3.30E-01	1.00E+00	5.15E-01	1.00E+00	1.96E-02	7.36E-01	phosphoric diester hydrolase activity	F
GO:0008083	166	8.48E-01	1.00E+00	4.91E-01	1.00E+00	7.82E-01	1.00E+00	6.11E-01	1.00E+00	9.77E-01	1.00E+00	8.55E-01	1.00E+00	6.85E-01	1.00E+00	1.29E-01	1.00E+00	growth factor activity	F
GO:0008088	11	2.02E-02	1.00E+00	5.88E-03	3.08E-01	2.41E-03	1.07E-01	2.15E-02	9.37E-01	1.76E-01	1.00E+00	1.38E-02	6.68E-01	8.73E-02	1.00E+00	1.12E-01	1.00E+00	axon cargo transport	P
GO:0008092	441	9.03E-12	2.57E-03	9.53E-19	0.00E+00	2.79E-05	3.00E-03	4.08E-09	8.93E-04	5.20E-06	1.69E-03	6.33E-10	6.20E-04	1.27E-11	0.00E+00	1.32E-15	0.00E+00	cytoskeletal protein binding	F
GO:0008094	33	5.09E-05	9.52E-03	6.27E-07	3.92E-03	7.66E-05	1.16E-02	1.11E-04	1.30E-02	1.78E-04	4.90E-02	4.44E-06	2.90E-03	4.09E-02	1.00E+00	1.31E-02	4.76E-01	DNA-dependent ATPase activity	F
GO:0008104	962	1.72E-25	0.00E+00	7.49E-36	0.00E+00	1.82E-18	0.00E+00	7.74E-29	0.00E+00	1.54E-22	0.00E+00	5.40E-24	0.00E+00	5.78E-08	0.00E+00	1.01E-12	0.00E+00	protein localization	P
GO:0008105	10	9.48E-01	1.00E+00	5.39E-02	1.00E+00	8.04E-01	1.00E+00	2.78E-02	1.00E+00	5.93E-01	1.00E+00	4.55E-01	1.00E+00	1.00E+00	1.00E+00	2.08E-01	1.00E+00	asymmetric protein localization	P
GO:0008121	13	5.88E-02	1.00E+00	1.81E-01	1.00E+00	3.40E-01	1.00E+00	1.97E-01	1.00E+00	1.24E-01	1.00E+00	2.69E-01	1.00E+00	2.50E-02	8.38E-01	2.37E-01	1.00E+00	ubiquinol-cytochrome-c reductase activity	F
GO:0008134	304	9.23E-17	0.00E+00	7.65E-21	0.00E+00	9.99E-15	7.08E-04	1.08E-15	0.00E+00	3.16E-08	9.59E-04	1.83E-11	6.20E-04	2.91E-07	8.23E-04	3.21E-10	0.00E+00	transcription factor binding	F
GO:0008135	139	3.34E-07	2.57E-03	9.75E-12	0.00E+00	3.28E-10	7.95E-04	1.41E-08	8.93E-04	5.26E-05	2.40E-02	4.08E-10	6.20E-04	4.72E-02	1.00E+00	1.81E-04	1.60E-02	translation factor activity, nucleic acid bindir	F
GO:0008137	41	1.14E-01	1.00E+00	4.33E-01	1.00E+00	1.97E-01	1.00E+00	6.70E-01	1.00E+00	1.34E-01	1.00E+00	2.10E-01	1.00E+00	3.27E-01	1.00E+00	5.35E-01	1.00E+00	NADH dehydrogenase (ubiquinone) activity	F
GO:0008138	47	1.27E-01	1.00E+00	2.20E-02	1.00E+00	1.31E-01	1.00E+00	9.79E-02	1.00E+00	4.54E-01	1.00E+00	2.93E-02	1.00E+00	5.34E-02	1.00E+00	6.58E-02	1.00E+00	protein tyrosine/serine/threonine phosphata	F
GO:0008144	15	1.73E-01	1.00E+00	2.77E-01	1.00E+00	6.66E-01	1.00E+00	1.96E-01	1.00E+00	1.37E-01	1.00E+00	9.97E-01	1.00E+00	7.66E-02	1.00E+00	5.20E-02	1.00E+00	drug binding	F
GO:0008146	55	1.00E+00	1.00E+00	8.68E-01	1.00E+00	1.00E+00	1.00E+00	7.92E-01	1.00E+00	9.88E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	7.63E-01	1.00E+00	sulfotransferase activity	F
GO:0008150	15727	5.35E-38	0.00E+00	0.00E+00	0.00E+00	1.25E-37	0.00E+00	0.00E+00	0.00E+00	9.76E-31	0.00E+00	0.00E+00	0.00E+00	3.62E-06	1.00E-03	1.30E-36	0.00E+00	biological_process	P
GO:0008152	8672	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.04E-25	0.00E+00	0.00E+00	0.00E+00	metabolism	P
GO:0008154	70	7.78E-03	6.08E-01	1.45E-04	1.50E-02	1.28E-01	1.00E+00	5.11E-03	2.88E-01	1.12E-01	1.00E+00	5.54E-02	1.00E+00	3.44E-03	2.23E-01	1.69E-05	7.00E-03	actin polymerization and/or depolymerizatio	P
GO:0008156	12	1.29E-03	8.86E-02	2.14E-04	2.40E-02	1.36E-02	6.53E-01	7.23E-03	4.92E-01	1.42E-02	6.92E-01	1.93E-04	2.33E-02	1.37E-01	1.00E+00	4.20E-01	1.00E+00	negative regulation of DNA replication	P
GO:0008168	198	2.99E-05	7.00E-03	5.86E-05	7.00E-03	1.85E-05	3.00E-03	3.43E-05	9.57E-03	6.99E-04	1.20E-01	1.37E-04	1.30E-02	5.62E-02	1.00E+00	1.72E-01	1.00E+00	methyltransferase activity	F
GO:0008170	60	6.28E-02	1.00E+00	2.16E-02	1.00E+00	1.24E-02	6.53E-01	7.25E-03	4.92E-01	1.77E-01	1.00E+00	2.04E-02	7.56E-01	5.53E-01	1.00E+00	5.13E-01	1.00E+00	N-methyltransferase activity	F
GO:0008172	11	5.42E-01	1.00E+00	7.08E-01	1.00E+00	2.34E-01	1.00E+00	8.20E-01	1.00E+00	7.74E-01	1.00E+00	7.05E-01	1.00E+00	6.31E-01	1.00E+00	6.91E-01	1.00E+00	S-methyltransferase activity	F
GO:0008173	20	1.30E-02	6.08E-01	3.43E-01	1.00E+00	1.83E-02	1.00E+00	3.89E-01	1.00E+00	4.13E-02	1.00E+00	2.91E-01	1.00E+00	4.87E-02	1.00E+00	9.03E-01	1.00E+00	RNA methyltransferase activity	F
GO:0008180	10	1.57E-02	1.00E+00	3.55E-02	1.00E+00	9.56E-03	6.53E-01	7.94E-02	1.00E+00	2.91E-02	1.00E+00	8.16E-02	1.00E+00	3.63E-01	1.00E+00	3.58E-02	1.00E+00	signalosome complex	C
GO:0008188	143	7.76E-01	1.00E+00	9.26E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	6.47E-01	1.00E+00	8.97E-01	1.00E+00	9.83E-02	1.00E+00	2.87E-01	1.00E+00	neuropeptide receptor activity	F
GO:0008194	99	3.93E-01	1.00E+00	4.61E-01	1.00E+00	2.62E-01	1.00E+00	7.15E-01	1.00E+00	2.39E-01	1.00E+00	2.83E-01	1.00E+00	7.17E-01	1.00E+00	3.53E-01	1.00E+00	UDP-glycosyltransferase activity	F
GO:0008199	23	1.00E+00	1.00E+00	9.14E-01	1.00E+00	9.72E-01	1.00E+00	9.11E-01	1.00E+00	9.99E-01	1.00E+00	6.24E-01	1.00E+00	9.85E-01	1.00E+00	9.22E-01	1.00E+00	ferric iron binding	F
GO:0008201	67	8.37E-01	1.00E+00	6.97E-01	1.00E+00	7.43E-01	1.00E+00	8.99E-01	1.00E+00	8.29E-01	1.00E+00	7.49E-01	1.00E+00	8.17E-01	1.00E+00	2.51E-01	1.00E+00	heparin binding	F
GO:0008202	176	5.19E-02	1.00E+00	2.95E-02	1.00E+00	2.55E-01	1.00E+00	1.25E-01	1.00E+00	6.14E-02	1.00E+00	1.00E-01	1.00E+00	3.70E-02	8.38E-01	6.97E-03	4.28E-01	steroid metabolism	P
GO:0008203	74	2.75E-03	2.12E-01	3.45E-03	1.88E-01	1.61E-02	1.00E+00	1.29E-02	6.47E-01	1.48E-02	6.92E-01	5.13E-02	1.00E+00	6.79E-03	2.75E-01	2.53E-03	7.90E-02	cholesterol metabolism	P
GO:0008206	14	3.63E-01	1.00E+00	4.50E-01	1.00E+00	4.98E-01	1.00E+00	6.18E-01	1.00E+00	3.37E-01	1.00E+00	4.88E-01	1.00E+00	3.12E-01	1.00E+00	3.98E-01	1.00E+00	bile acid metabolism	P
GO:0008207	20	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.13E-01	1.00E+00	9.97E-01	1.00E+00	8.94E-01	1.00E+00	9.98E-01	1.00E+00	C21-steroid hormone metabolism	P
GO:0008211	11	4.24E-01	1.00E+00	8.22E-01	1.00E+00	5.70E-01	1.00E+00	7.21E-01	1.00E+00	4.50E-01	1.00E+00	7.59E-01	1.00E+00	4.78E-01	1.00E+00	8.67E-01	1.00E+00	glucocorticoid metabolism	P
GO:0008213	36	3.25E-05	7.00E-03	9.32E-08	3.92E-03	7.06E-05	1.07E-02	6.69E-07	2.89E-03	2.22E-03	1.20E-01	3.81E-05	9.66E-03	1.28E-02	4.78E-01	7.06E-04	6.00E-02	protein amino acid alkylation	P
GO:0008216	10	2.55E-02	1.00E+00	8.38E-02	1.00E+00	6.59E-02	1.00E+00	6.78E-02	1.00E+00	3.80E-02	1.00E+00	2.51E-01	1.00E+00	8.72E-02	1.00E+00	8.63E-02	1.00E+00	spermidine metabolism	P
GO:0008217	63	7.96E-01	1.00E+00	9.97E-01	1.00E+00	8.15E-01	1.00E+00	9.97E-01	1.00E+00	9.60E-01	1.00E+00	9.97E-01	1.00E+00	2.49E-01	1.00E+00	8.21E-01	1.00E+00	blood pressure regulation	P
GO:0008219	821	1.04E-11	2.57E-03	1.12E-13	0.00E+00	7.95E-08	9.80E-04	2.18E-10	0.00E+00	4.57E-07	9.59E-04	5.37E-09	8.78E-04	9.55E-07	8.23E-04	5.28E-07	1.92E-03	cell death	
GO:0008227	147	4.72E-02	1.00E+00	3.04E-03	1.88E-01	9.99E-02	1.00E+00	8.84E-03	4.92E-01	1.13E-01	1.00E+00	2.31E-02	1.00E+00	4.08E-02	1.00E+00	2.60E-03	8.32E-02	amine receptor activity	F
GO:0008233	785	1.82E-01	1.00E+00	2.23E-02	1.00E+00	1.71E-01	1.00E+00	7.17E-02	1.00E+00	3.96E-01	1.00E+00	1.33E-01	1.00E+00	1.93E-01	1.00E+00	1.77E-03	7.90E-02	peptidase activity	F
GO:0008234	182	5.40E-02	1.00E+00	2.15E-03	1.71E-01	2.01E-02	1.00E+00	6.46E-04	4.20E-02	1.33E-01	1.00E+00	1.17E-01	1.00E+00	4.26E-01	1.00E+00	2.35E-03	7.90E-02	cysteine-type peptidase activity	F
GO:0008235	61	3.31E-01	1.00E+00	1.25E-01	1.00E+00	9.20E-02	1.00E+00	1.95E-01	1.00E+00	8.39E-01	1.00E+00	1.19E-01	1.00E+00	2.02E-01	1.00E+00	1.79E-01	1.00E+00	metalloexopeptidase activity	F
GO:0008236	258	6.94E-01	1.00E+00	4.10E-01	1.00E+00	8.31E-01	1.00E+00	5.71E-01	1.00E+00	7.60E-01	1.00E+00	4.37E-01	1.00E+00	4.39E-01	1.00E+00	8.80E-02	1.00E+00	serine-type peptidase activity	F

GO:0008237	224	4.68E-01	1.00E+00	5.96E-01	1.00E+00	4.82E-01	1.00E+00	7.02E-01	1.00E+00	8.34E-01	1.00E+00	5.55E-01	1.00E+00	8.70E-02	1.00E+00	3.14E-01	1.00E+00	metallopeptidase activity	F
GO:0008238	106	2.42E-01	1.00E+00	2.08E-01	1.00E+00	1.48E-02	6.53E-01	3.64E-01	1.00E+00	8.14E-01	1.00E+00	1.51E-01	1.00E+00	2.88E-01	1.00E+00	2.62E-01	1.00E+00	exopeptidase activity	F
GO:0008239	12	2.15E-01	1.00E+00	2.55E-01	1.00E+00	2.10E-01	1.00E+00	1.91E-01	1.00E+00	5.28E-01	1.00E+00	2.43E-01	1.00E+00	1.12E-01	1.00E+00	4.24E-01	1.00E+00	dipeptidyl-peptidase activity	F
GO:0008252	10	9.89E-03	6.08E-01	2.41E-02	1.00E+00	2.78E-02	1.00E+00	6.62E-02	1.00E+00	3.33E-02	1.00E+00	8.67E-03	5.03E-01	3.97E-01	1.00E+00	3.23E-01	1.00E+00	nucleotidase activity	F
GO:0008270	2212	2.39E-25	0.00E+00	4.53E-38	0.00E+00	1.47E-29	0.00E+00	3.68E-39	0.00E+00	2.97E-17	0.00E+00	3.64E-28	0.00E+00	2.85E-04	2.29E-02	1.27E-07	9.38E-04	zinc ion binding	F
GO:0008271	11	8.11E-01	1.00E+00	9.81E-01	1.00E+00	9.63E-01	1.00E+00	8.98E-01	1.00E+00	6.31E-01	1.00E+00	9.95E-01	1.00E+00	7.50E-01	1.00E+00	7.98E-01	1.00E+00	sulfate porter activity	F
GO:0008272	16	8.73E-01	1.00E+00	9.67E-01	1.00E+00	9.64E-01	1.00E+00	8.99E-01	1.00E+00	8.22E-01	1.00E+00	9.47E-01	1.00E+00	5.57E-01	1.00E+00	7.83E-01	1.00E+00	sulfate transport	P
GO:0008276	45	7.11E-05	1.41E-02	3.79E-08	9.59E-04	2.31E-05	3.00E-03	1.44E-06	2.89E-03	2.46E-03	1.20E-01	2.07E-06	2.00E-03	8.55E-02	1.00E+00	1.09E-03	6.00E-02	protein methyltransferase activity	F
GO:0008277	21	4.73E-02	1.00E+00	6.88E-03	3.12E-01	1.16E-01	1.00E+00	9.21E-03	5.72E-01	4.22E-02	1.00E+00	4.95E-02	1.00E+00	2.42E-01	1.00E+00	3.36E-03	1.27E-01	regulation of G-protein coupled receptor prc	P
GO:0008283	661	1.79E-06	3.00E-03	4.66E-06	4.51E-03	1.74E-03	9.50E-02	6.20E-04	4.20E-02	2.08E-03	1.20E-01	4.91E-04	2.33E-02	1.66E-07	0.00E+00	1.13E-04	1.60E-02	cell proliferation	P
GO:0008284	260	1.55E-01	1.00E+00	9.83E-02	1.00E+00	4.82E-01	1.00E+00	3.07E-01	1.00E+00	3.50E-01	1.00E+00	3.16E-01	1.00E+00	1.56E-02	4.88E-01	2.18E-02	9.99E-01	positive regulation of cell proliferation	P
GO:0008285	201	1.16E-02	6.08E-01	1.80E-02	1.00E+00	8.31E-02	1.00E+00	2.22E-02	9.37E-01	1.24E-01	1.00E+00	1.04E-01	1.00E+00	4.41E-03	2.23E-01	4.56E-02	1.00E+00	negative regulation of cell proliferation	P
GO:0008286	34	8.06E-02	1.00E+00	5.99E-02	1.00E+00	2.31E-01	1.00E+00	1.55E-01	1.00E+00	3.78E-01	1.00E+00	1.05E-01	1.00E+00	3.16E-02	8.38E-01	2.14E-01	1.00E+00	insulin receptor signaling pathway	P
GO:0008287	40	5.40E-02	1.00E+00	1.65E-02	7.63E-01	3.66E-02	1.00E+00	7.50E-02	1.00E+00	1.32E-01	1.00E+00	2.41E-02	1.00E+00	2.17E-01	1.00E+00	6.98E-02	1.00E+00	protein serine/threonine phosphatase comp	C
GO:0008289	330	1.66E-03	2.12E-01	1.09E-06	3.92E-03	6.93E-02	1.00E+00	2.82E-04	4.20E-02	8.20E-03	6.92E-01	8.04E-04	4.48E-02	8.44E-04	3.44E-02	1.20E-05	7.00E-03	lipid binding	F
GO:0008299	17	2.11E-01	1.00E+00	1.44E-01	1.00E+00	7.06E-02	1.00E+00	2.02E-01	1.00E+00	3.80E-01	1.00E+00	4.39E-01	1.00E+00	2.72E-01	1.00E+00	2.08E-03	7.90E-02	isoprenoid biosynthesis	P
GO:0008305	34	3.04E-01	1.00E+00	4.26E-02	1.00E+00	4.36E-01	1.00E+00	3.08E-01	1.00E+00	3.77E-01	1.00E+00	9.22E-02	1.00E+00	2.66E-01	1.00E+00	3.62E-02	1.00E+00	integrin complex	C
GO:0008306	14	3.91E-01	1.00E+00	7.45E-01	1.00E+00	9.26E-01	1.00E+00	8.51E-01	1.00E+00	3.04E-01	1.00E+00	7.35E-01	1.00E+00	1.34E-01	1.00E+00	1.54E-01	1.00E+00	associative learning	P
GO:0008307	11	6.73E-01	1.00E+00	4.18E-01	1.00E+00	5.21E-01	1.00E+00	5.94E-01	1.00E+00	8.04E-01	1.00E+00	6.04E-01	1.00E+00	6.12E-01	1.00E+00	1.50E-01	1.00E+00	structural constituent of muscle	F
GO:0008312	13	2.83E-03	2.12E-01	5.05E-02	1.00E+00	1.03E-01	1.00E+00	7.34E-02	1.00E+00	7.60E-03	6.92E-01	1.00E-01	1.00E+00	2.34E-02	8.38E-01	1.01E-01	1.00E+00	7S RNA binding	F
GO:0008318	13	3.80E-01	1.00E+00	3.40E-01	1.00E+00	6.09E-01	1.00E+00	4.60E-01	1.00E+00	1.67E-01	1.00E+00	2.60E-01	1.00E+00	8.78E-01	1.00E+00	5.00E-01	1.00E+00	protein prenyltransferase activity	F
GO:0008324	748	4.34E-02	1.00E+00	1.57E-04	1.50E-02	3.29E-01	1.00E+00	3.11E-02	1.00E+00	3.07E-01	1.00E+00	1.43E-03	9.30E-02	5.63E-03	2.23E-01	8.20E-05	1.60E-02	cation transporter activity	F
GO:0008344	52	3.37E-01	1.00E+00	3.47E-01	1.00E+00	6.03E-01	1.00E+00	5.37E-01	1.00E+00	5.42E-01	1.00E+00	3.15E-01	1.00E+00	1.48E-01	1.00E+00	2.21E-01	1.00E+00	adult locomotory behavior	P
GO:0008360	51	5.52E-03	3.09E-01	3.02E-02	1.00E+00	3.44E-02	1.00E+00	2.38E-01	1.00E+00	3.26E-02	1.00E+00	1.60E-02	6.68E-01	2.05E-02	6.36E-01	5.53E-02	1.00E+00	regulation of cell shape	P
GO:0008361	165	7.35E-03	3.15E-01	3.46E-03	1.88E-01	6.96E-02	1.00E+00	2.46E-02	1.00E+00	4.66E-02	1.00E+00	1.97E-02	7.56E-01	6.47E-02	1.00E+00	3.89E-03	1.34E-01	regulation of cell size	P
GO:0008366	42	5.20E-01	1.00E+00	1.35E-01	1.00E+00	3.36E-01	1.00E+00	1.80E-01	1.00E+00	5.77E-01	1.00E+00	3.39E-01	1.00E+00	5.75E-01	1.00E+00	7.51E-02	1.00E+00	axon ensheathment	P
GO:0008373	21	3.74E-01	1.00E+00	6.04E-01	1.00E+00	5.47E-01	1.00E+00	9.47E-01	1.00E+00	5.69E-01	1.00E+00	4.08E-01	1.00E+00	1.53E-02	4.88E-01	1.81E-01	1.00E+00	sialyltransferase activity	F
GO:0008374	36	6.21E-02	1.00E+00	3.20E-02	1.00E+00	1.64E-02	1.00E+00	1.20E-02	6.47E-01	9.85E-02	1.00E+00	4.35E-02	1.00E+00	4.40E-01	1.00E+00	1.71E-01	1.00E+00	O-acyltransferase activity	F
GO:0008375	32	2.66E-02	1.00E+00	3.67E-02	1.00E+00	1.36E-02	6.53E-01	8.62E-02	1.00E+00	5.05E-02	1.00E+00	6.69E-02	1.00E+00	2.42E-01	1.00E+00	7.23E-02	1.00E+00	acetylglucosaminyltransferase activity	F
GO:0008376	27	9.73E-01	1.00E+00	8.00E-01	1.00E+00	9.85E-01	1.00E+00	9.68E-01	1.00E+00	9.69E-01	1.00E+00	7.10E-01	1.00E+00	6.39E-01	1.00E+00	2.73E-01	1.00E+00	acetylgalactosaminyltransferase activity	F
GO:0008378	36	3.41E-01	1.00E+00	6.30E-01	1.00E+00	4.78E-01	1.00E+00	5.90E-01	1.00E+00	1.35E-01	1.00E+00	2.39E-01	1.00E+00	7.96E-01	1.00E+00	9.44E-01	1.00E+00	galactosyltransferase activity	F
GO:0008380	194	1.51E-17	0.00E+00	4.36E-16	0.00E+00	1.92E-15	0.00E+00	9.63E-16	0.00E+00	4.11E-11	0.00E+00	2.62E-08	9.03E-04	6.35E-06	1.00E-03	6.43E-05	7.00E-03	RNA splicing	P
GO:0008395	10	9.98E-01	1.00E+00	8.13E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	8.61E-01	1.00E+00	2.85E-01	1.00E+00	8.33E-01	1.00E+00	9.42E-01	1.00E+00	steroid hydroxylase activity	F
GO:0008406	69	7.52E-02	1.00E+00	6.79E-01	1.00E+00	6.92E-02	1.00E+00	8.04E-01	1.00E+00	1.79E-01	1.00E+00	3.94E-01	1.00E+00	1.74E-01	1.00E+00	7.83E-01	1.00E+00	gonad development	P
GO:0008408	22	3.24E-02	1.00E+00	1.98E-02	1.00E+00	2.17E-02	1.00E+00	3.01E-02	1.00E+00	8.38E-02	1.00E+00	3.37E-02	1.00E+00	5.00E-01	1.00E+00	6.03E-02	1.00E+00	3'-5' exonuclease activity	F
GO:0008415	191	4.14E-06	3.02E-03	9.55E-07	3.92E-03	4.06E-05	9.82E-03	3.61E-05	9.57E-03	6.74E-05	2.40E-02	2.34E-05	5.87E-03	2.02E-02	6.36E-01	9.40E-03	4.28E-01	acyltransferase activity	F
GO:0008417	12	5.28E-01	1.00E+00	4.04E-01	1.00E+00	6.23E-01	1.00E+00	1.85E-01	1.00E+00	8.36E-01	1.00E+00	5.72E-01	1.00E+00	2.41E-01	1.00E+00	6.99E-01	1.00E+00	fucosyltransferase activity	F
GO:0008430	32	1.96E-02	1.00E+00	2.04E-04	2.40E-02	1.60E-02	1.00E+00	2.49E-03	1.39E-01	8.64E-02	1.00E+00	1.30E-03	9.00E-02	9.85E-02	1.00E+00	1.07E-02	4.76E-01	selenium binding	F
GO:0008443	11	3.40E-01	1.00E+00	3.65E-01	1.00E+00	1.89E-01	1.00E+00	3.79E-01	1.00E+00	3.51E-01	1.00E+00	2.89E-01	1.00E+00	8.42E-01	1.00E+00	6.27E-01	1.00E+00	phosphofructokinase activity	F
GO:0008483	26	8.14E-02	1.00E+00	2.19E-02	1.00E+00	1.61E-01	1.00E+00	1.02E-01	1.00E+00	1.08E-01	1.00E+00	1.58E-02	6.68E-01	3.59E-01	1.00E+00	4.74E-02	1.00E+00	transaminase activity	F
GO:0008484	14	6.87E-01	1.00E+00	2.87E-01	1.00E+00	8.90E-01	1.00E+00	3.94E-01	1.00E+00	2.93E-01	1.00E+00	4.62E-01	1.00E+00	7.71E-01	1.00E+00	2.23E-01	1.00E+00	sulfuric ester hydrolase activity	F
GO:0008493	26	7.35E-01	1.00E+00	3.12E-01	1.00E+00	9.59E-01	1.00E+00	7.76E-01	1.00E+00	6.24E-01	1.00E+00	2.94E-01	1.00E+00	6.60E-01	1.00E+00	1.47E-01	1.00E+00	tetracycline transporter activity	F
GO:0008509	181	9.55E-01	1.00E+00	4.30E-01	1.00E+00	9.85E-01	1.00E+00	7.30E-01	1.00E+00	8.83E-01	1.00E+00	7.41E-01	1.00E+00	8.83E-01	1.00E+00	8.41E-02	1.00E+00	anion transporter activity	F
GO:0008514	11	1.00E+00	1.00E+00	7.04E-01	1.00E+00	9.71E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	9.96E-01	1.00E+00	1.59E-01	1.00E+00	organic anion transporter activity	F
GO:0008527	14	8.99E-01	1.00E+00	1.00E+00	1.00E+00	7.86E-01	1.00E+00	9.95E-01	1.00E+00	6.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	taste receptor activity	F
GO:0008528	719	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide receptor activity, G-protein coupled	F
GO:0008533	15	9.23E-01	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	9.99E-01	1.00E+00	9.54E-01	1.00E+00	9.42E-01	1.00E+00	4.83E-01	1.00E+00	1.00E+00	1.00E+00	astacin activity	F
GO:0008542	26	9.82E-01	1.00E+00	5.69E-01	1.00E+00	9.77E-01	1.00E+00	6.51E-01	1.00E+00	1.00E+00	1.00E+00	7.13E-01	1.00E+00	2.20E-01	1.00E+00	1.18E-01	1.00E+00	visual learning	P
GO:0008543	16	5.07E-01	1.00E+00	7.12E-01	1.00E+00	6.88E-01	1.00E+00	4.90E-01	1.00E+00	3.27E-01	1.00E+00	9.02E-01	1.00E+00	4.62E-01	1.00E+00	3.93E-01	1.00E+00	fibroblast growth factor receptor signaling p	P
GO:0008544	135	4.92E-01	1.00E+00	7.34E-01	1.00E+00	8.26E-01	1.00E+00	8.23E-01	1.00E+00	6.81E-01	1.00E+00	6.59E-01	1.00E+00	7.01E-02	1.00E+00	4.36E-01	1.00E+00	epidermis development	P
GO:0008553	23	1.07E-03	8.86E-02	1.19E-02	6.07E-01	8.44E-03	6.53E-01	5.92E-02	1.00E+00	4.62E-02	1.00E+00	2.91E-02	1.00E+00	8.39E-03	2.75E-01	3.29E-02	1.00E+00	hydrogen-exporting ATPase activity, phosph	F
GO:0008565	132	7.72E-09	2.57E-03	3.66E-11	0.00E+00	5.41E-07	2.00E-03	1.21E-11	0.00E+00	1.08E-05	2.00E-03	6.56E-07	2.00E-03	1.69E-04	8.00E-03	1.49E-04	1.60E-02	protein transporter activity	F
GO:0008584	27	3.15E-01	1.00E+00	7.70E-01	1.00E+00	2.07E-01	1.00E+00	6.93E-01	1.00E+00	6.73E-01	1.00E+00	6.55E-01	1.00E+00	2.07E-01	1.00E+00	7.64E-01	1.00E+00	male gonad development	P
GO:0008585	46	2.73E-02	1.00E+00	4.42E-01	1.00E+00	8.67E-02	1.00E+00	5.49E-01	1.00E+00	3.51E-02	1.00E+00	2.47E-01	1.00E+00	1.65E-01	1.00E+00	7.34E-01	1.00E+00	female gonad development	P
GO:0008589	14	1.96E-01	1.00E+00	3.15E-01	1.00E+00	4.72E-01	1.00E+00	6.34E-01	1.00E+00	1.99E-01	1.00E+00	1.84E-01	1.00E+00	1.48E-01	1.00E+00	5.30E-01	1.00E+00	regulation of smoothened signaling pathwa	P
GO:0008601	20	1.76E-01	1.00E+00	1.85E-01	1.00E+00	1.20E-01	1.00E+00	6.86E-01	1.00E+00	2.68E-01	1.00E+00	1.43E-01	1.00E+00	2.85E-01	1.00E+00	1.18E-01	1.00E+00	protein phosphatase type 2A regulator activ	F
GO:0008603	26	7.00E-01	1.00E+00	5.65E-01	1.00E+00	8.77E-01	1.00E+00	7.11E-01	1.00E+00	9.04E-01	1.00E+00	9.24E-01	1.00E+00	8.91E-02	1.00E+00	1.16E-01	1.00E+00	cAMP-dependent protein kinase regulator a	F
GO:0008610	302	2.71E-04	1.90E-02	8.19E-06	4.51E-03	4.02E-04	4.00E-02	6.13E-04	4.20E-02	1.93E-03	1.20E-01	9.56E-04	9.00E-02	3.27E-02	8.38E-01	1.72E-04	1.60E-02	lipid biosynthesis	P
GO:0008624	23	1.68E-02	1.00E+00	4.86E-03	2.61E-01	2.35E-01	1.00E+00	6.66E-03	3.33E-01	2.29E-02	1.00E+00	1.61E-02	6.68E-01	2.06E-02	6.36E-01	8.39E-02	1.00E+00	induction of apoptosis by extracellular signa	P
GO:0008629	34	9.62E-04	8.86E-02	3.60E-04	4.40E-02	1.05E-03	7.90E-02	2.06E-03	1.39E-01	1.41E-02	6.92E-01	3.94E-03	1.84E-01	3.32E-02	8.38E-01	1.36E-02	4.76E-01	induction of apoptosis by intracellular signal	P
GO:0008630	21	8.43E-02	1.00E+00	1.63E-03	9.65E-02	6.72E-02	1.00E+00	1.07E-02	5.72E-01	1.23E-01	1.00E+00	2.27E-02	1.00E+00	3.42E-01	1.00E+00	1.03E-02	4.76E-01	DNA damage response, signal transduction	P
GO:0008632	78	2.08E-08	2.57E-03	2.16E-06	3.92E-03	7.95E-06	2.91E-03	2.42E-05	9.57E-03	1.14E-05	2.00E-03	7.52E-05	1.10E-02	1.53E-04	8.00E-03	3.61E-03	1.27E-01	apoptotic program	P
GO:0008637	25	2.94E-06	3.02E-03	3.35E-04	4.40E-02	2.46E-05	3.00E-03	2.32E-04	1.30E-02	3.70E-04	4.90E-02	1.11E-03	9.00E-02	1.15E-03	6.14E-02	7.40E-02	1.00E+00	apoptotic mitochondrial changes	P
GO:0008643	77	3.63E-02	1.00E+00	1.11E-02	4.69E-01	1.07E-01	1.00E+00	9.60E-02	1.00E+00	3.97E-02	1.00E+00	1.84E-02	6.68E-01	1.05E-01	1.00E+00	5.77E-02	1.00E+00	carbohydrate transport	P
GO:0008645	42	7.54E-02	1.00E+00	6.90E-02	1.00E+00	1.42E-01	1.00E+00	2.89E-01	1.00E+00	1.28E-01	1.00E+00	5.30E-02	1.00E+00	5.97E-02	1.00E+00	2.02E-01	1.00E+00	hexose transport	P
GO:0008652	90	3.87E-02	1.00E+00	1.70E-03	9.65E-02	6.52E-02	1.00E+00	9.30E-02	1.00E+00	1.53E-01	1.00E+00	2.14E-04	2.33E-02	5.86E-02	1.00E+00	4.91E-02	1.00E+00	amino acid biosynthesis	P
GO:0008654	77	1.32E-02	6.08E-01	4.51E-04	4.74E-02	2.24E-03	1.03E-01	4.89E-04	4.20E-02	9.75E-02	1.00E+00	9.13E-02	1.00E+00	3.98E-01	1.00E+00	1.14E-01	1.00E+00	phospholipid biosynthesis	P
GO:0008667	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	2,3-dihydro-2,3-dihydroxybenzoate dehydrc	F
GO:0008757	83	8.93E-07	2.76E-03	1.05E-05	4.51E-03	5.40E-07	2.00E-03	5.38E-05	1.07E-02	3.00E-04	4.90E-02	3.37E-04	2.33E-02	4.88E-03	2.23E-01	1.36E-02	4.76E-01	S-adenosylmethionine-dependent methyltra	F
GO:0008943	30	9.82E-01	1.00E+00	8.65E-01	1.00E+00	8.79E-01	1.00E+00	9.74E-01	1.00E+00	9.99E-01	1.00E+00	4.98E-01	1.00E+00	8.81E-01	1.00E+00	7.42E-01	1.00E+00	glyceraldehyde-3-phosphate dehydrogenas	F
GO:0009055	368	7.18E-01	1.00E+00	8.78E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	5.14E-01	1.00E+00	6.76E-01	1.00E+00	5.74E-01	1.00E+00	4.59E-01	1.00E+00	electron carrier activity	F
GO:0009056	677	1.55E-16	0.00E+00	4.82E-22	0.00E+00	6.84E-13	7.08E-04	3.12E-15	0.00E+00	3.11E-13	0.00E+00	1.52E-15	0.00E+00	2.31E-04	1.20E-02	5.26E-10	0.00E+00	catabolism	P
GO:0009057	379	1.58E-14	0.00E+00	1.01E-15	0.00E+00	5.11E-14	7.08E-04	5.28E-13	0.00E+00	9.26E-10	0.00E+00	3.80E-11	6.20E-04	1.61E-03	8.40E-02	2.59E-06	2.00E-03	macromolecule catabolism	P
GO:0009058	1720	1.56E-22	0.00E+00	1.93E-23	0.00E+00	6.42E-19	0.00E+00	2.36E-15	0.00E+00	3.97E-16	0.00E+00	1.25E-15	0.00E+00	9.69E-09	0.00E+00	1.35E-12	0.00E+00	biosynthesis	P
GO:0009059	1053	6.70E-17	0.00E+00	2.76E-15	0.00E+00	3.70E-14	7.08E-04	5.82E-11	0.00E+00	5.73E-12	0.00E+00	2.46E-11	6.20E-04	5.99E-07	8.23E-04	2.33E-07	9.38E-04	macromolecule biosynthesis	P

GO:0009060	29	4.13E-02	1.00E+00	7.80E-02	1.00E+00	9.45E-02	1.00E+00	1.56E-01	1.00E+00	1.15E-01	1.00E+00	1.32E-01	1.00E+00	2.34E-01	1.00E+00	9.63E-02	1.00E+00	aerobic respiration	P
GO:0009063	56	1.61E-01	1.00E+00	8.96E-03	4.69E-01	4.58E-01	1.00E+00	3.85E-02	1.00E+00	1.32E-01	1.00E+00	4.45E-02	1.00E+00	2.37E-01	1.00E+00	2.33E-02	9.99E-01	amino acid catabolism	P
GO:0009064	42	7.84E-02	1.00E+00	1.20E-02	6.07E-01	1.08E-01	1.00E+00	8.20E-02	1.00E+00	1.01E-01	1.00E+00	3.33E-02	1.00E+00	1.94E-01	1.00E+00	3.07E-02	9.99E-01	glutamine family amino acid metabolism	P
GO:0009065	10	1.30E-01	1.00E+00	2.76E-01	1.00E+00	1.97E-01	1.00E+00	1.64E-01	1.00E+00	1.08E-01	1.00E+00	4.92E-01	1.00E+00	4.23E-01	1.00E+00	3.09E-01	1.00E+00	glutamine family amino acid catabolism	P
GO:0009066	24	4.20E-01	1.00E+00	5.61E-01	1.00E+00	1.45E-01	1.00E+00	4.78E-01	1.00E+00	7.41E-01	1.00E+00	2.23E-01	1.00E+00	3.65E-01	1.00E+00	9.79E-01	1.00E+00	aspartate family amino acid metabolism	P
GO:0009067	14	1.64E-01	1.00E+00	3.67E-01	1.00E+00	1.27E-01	1.00E+00	3.11E-01	1.00E+00	3.52E-01	1.00E+00	5.49E-02	1.00E+00	1.53E-01	1.00E+00	9.94E-01	1.00E+00	aspartate family amino acid biosynthesis	P
GO:0009069	23	1.65E-01	1.00E+00	1.03E-03	9.65E-02	1.43E-01	1.00E+00	1.78E-03	1.24E-01	2.73E-01	1.00E+00	3.74E-03	1.80E-01	2.70E-01	1.00E+00	7.60E-02	1.00E+00	serine family amino acid metabolism	P
GO:0009071	10	5.24E-01	1.00E+00	1.83E-04	1.80E-02	5.89E-01	1.00E+00	2.69E-04	4.20E-02	5.49E-01	1.00E+00	7.13E-03	4.21E-01	5.43E-01	1.00E+00	3.33E-04	3.00E-02	serine family amino acid catabolism	P
GO:0009072	75	4.67E-01	1.00E+00	9.45E-02	1.00E+00	6.06E-01	1.00E+00	6.34E-01	1.00E+00	5.32E-01	1.00E+00	5.83E-02	1.00E+00	4.01E-01	1.00E+00	2.92E-02	9.99E-01	aromatic amino acid family metabolism	P
GO:0009073	48	4.63E-01	1.00E+00	6.43E-02	1.00E+00	4.11E-01	1.00E+00	3.13E-01	1.00E+00	5.06E-01	1.00E+00	1.55E-02	6.68E-01	5.76E-01	1.00E+00	1.37E-01	1.00E+00	aromatic amino acid family biosynthesis	P
GO:0009074	12	6.41E-01	1.00E+00	7.36E-01	1.00E+00	9.32E-01	1.00E+00	9.94E-01	1.00E+00	7.45E-01	1.00E+00	8.57E-01	1.00E+00	3.75E-01	1.00E+00	4.35E-01	1.00E+00	aromatic amino acid family catabolism	P
GO:0009075	11	6.48E-01	1.00E+00	5.73E-01	1.00E+00	8.78E-01	1.00E+00	7.22E-01	1.00E+00	4.94E-01	1.00E+00	6.43E-01	1.00E+00	3.26E-01	1.00E+00	2.53E-01	1.00E+00	histidine family amino acid metabolism	P
GO:0009077	11	6.48E-01	1.00E+00	5.73E-01	1.00E+00	8.78E-01	1.00E+00	7.22E-01	1.00E+00	4.94E-01	1.00E+00	6.43E-01	1.00E+00	3.26E-01	1.00E+00	2.53E-01	1.00E+00	histidine family amino acid catabolism	P
GO:0009081	12	5.96E-04	8.86E-02	2.06E-02	1.00E+00	1.06E-02	6.53E-01	5.71E-03	2.88E-01	5.04E-03	3.75E-01	5.63E-02	1.00E+00	5.40E-02	1.00E+00	1.61E-01	1.00E+00	branched chain family amino acid metaboli	P
GO:0009084	17	1.18E-02	6.08E-01	9.86E-03	4.69E-01	6.42E-02	1.00E+00	3.38E-01	1.00E+00	3.70E-02	1.00E+00	2.40E-02	1.00E+00	2.03E-02	6.36E-01	6.70E-03	4.28E-01	glutamine family amino acid biosynthesis	P
GO:0009100	115	3.03E-02	1.00E+00	4.83E-02	1.00E+00	5.84E-02	1.00E+00	1.03E-01	1.00E+00	2.47E-01	1.00E+00	1.48E-01	1.00E+00	7.69E-03	2.75E-01	1.22E-02	4.76E-01	glycoprotein metabolism	P
GO:0009101	98	7.66E-02	1.00E+00	3.39E-02	1.00E+00	1.77E-01	1.00E+00	1.52E-01	1.00E+00	4.65E-01	1.00E+00	9.12E-02	1.00E+00	7.05E-03	2.75E-01	7.52E-03	4.28E-01	glycoprotein biosynthesis	P
GO:0009108	98	5.51E-03	3.09E-01	9.94E-02	1.00E+00	2.15E-02	1.00E+00	2.13E-01	1.00E+00	2.94E-03	2.13E-01	1.82E-01	1.00E+00	1.73E-01	1.00E+00	2.97E-01	1.00E+00	coenzyme biosynthesis	P
GO:0009109	29	1.32E-02	6.08E-01	3.08E-02	1.00E+00	7.01E-02	1.00E+00	6.97E-02	1.00E+00	2.79E-02	1.00E+00	4.53E-02	1.00E+00	1.55E-01	1.00E+00	1.21E-01	1.00E+00	coenzyme catabolism	P
GO:0009110	25	1.81E-02	1.00E+00	1.69E-01	1.00E+00	5.47E-02	1.00E+00	2.81E-01	1.00E+00	2.90E-02	1.00E+00	4.43E-01	1.00E+00	3.75E-01	1.00E+00	1.28E-01	1.00E+00	vitamin biosynthesis	P
GO:0009112	18	1.59E-02	1.00E+00	1.51E-01	1.00E+00	3.31E-03	2.03E-01	2.23E-01	1.00E+00	1.01E-02	6.92E-01	2.59E-01	1.00E+00	6.31E-01	1.00E+00	2.28E-01	1.00E+00	nucleobase metabolism	P
GO:0009116	28	9.66E-02	1.00E+00	7.22E-02	1.00E+00	1.11E-01	1.00E+00	4.09E-02	1.00E+00	8.87E-02	1.00E+00	1.27E-01	1.00E+00	2.68E-01	1.00E+00	2.34E-01	1.00E+00	nucleoside metabolism	P
GO:0009117	212	1.34E-04	1.43E-02	9.49E-05	1.50E-02	1.08E-02	6.53E-01	7.63E-04	6.90E-02	1.04E-04	2.70E-02	6.97E-04	4.48E-02	2.36E-02	8.38E-01	1.79E-02	6.56E-01	nucleotide metabolism	P
GO:0009119	10	9.86E-02	1.00E+00	4.10E-02	1.00E+00	1.19E-01	1.00E+00	1.52E-02	6.47E-01	7.75E-02	1.00E+00	3.31E-01	1.00E+00	2.67E-01	1.00E+00	6.37E-02	1.00E+00	ribonucleoside metabolism	P
GO:0009123	21	3.46E-01	1.00E+00	1.07E-02	4.69E-01	2.15E-01	1.00E+00	4.49E-03	2.88E-01	3.89E-01	1.00E+00	4.99E-02	1.00E+00	7.23E-01	1.00E+00	1.42E-01	1.00E+00	nucleoside monophosphate metabolism	P
GO:0009124	20	5.45E-01	1.00E+00	1.84E-02	1.00E+00	4.35E-01	1.00E+00	9.88E-03	5.72E-01	5.09E-01	1.00E+00	5.33E-02	1.00E+00	7.48E-01	1.00E+00	1.72E-01	1.00E+00	nucleoside monophosphate biosynthesis	P
GO:0009126	15	3.11E-01	1.00E+00	3.07E-02	1.00E+00	1.55E-01	1.00E+00	1.25E-02	6.47E-01	4.10E-01	1.00E+00	1.26E-01	1.00E+00	8.17E-01	1.00E+00	2.60E-01	1.00E+00	purine nucleoside monophosphate metabol	P
GO:0009127	14	5.26E-01	1.00E+00	5.70E-02	1.00E+00	3.42E-01	1.00E+00	2.87E-02	1.00E+00	5.46E-01	1.00E+00	1.35E-01	1.00E+00	8.44E-01	1.00E+00	3.29E-01	1.00E+00	purine nucleoside monophosphate biosynth	P
GO:0009132	14	1.20E-01	1.00E+00	2.19E-02	1.00E+00	1.98E-01	1.00E+00	3.32E-02	1.00E+00	7.81E-02	1.00E+00	9.81E-02	1.00E+00	2.50E-01	1.00E+00	2.63E-01	1.00E+00	nucleoside diphosphate metabolism	P
GO:0009141	80	1.69E-02	1.00E+00	1.26E-02	6.07E-01	4.01E-02	1.00E+00	4.56E-02	1.00E+00	4.00E-03	2.13E-01	2.11E-02	7.56E-01	5.67E-01	1.00E+00	7.59E-02	1.00E+00	nucleoside triphosphate metabolism	P
GO:0009142	61	4.20E-02	1.00E+00	9.86E-02	1.00E+00	5.29E-02	1.00E+00	8.03E-02	1.00E+00	1.04E-02	6.92E-01	1.72E-01	1.00E+00	8.15E-01	1.00E+00	3.11E-01	1.00E+00	nucleoside triphosphate biosynthesis	P
GO:0009144	70	9.30E-03	6.08E-01	9.09E-03	4.69E-01	2.46E-02	1.00E+00	4.72E-02	1.00E+00	2.33E-03	1.20E-01	1.43E-02	6.68E-01	5.25E-01	1.00E+00	5.44E-02	1.00E+00	purine nucleoside triphosphate metabolism	P
GO:0009145	57	3.80E-02	1.00E+00	8.63E-02	1.00E+00	5.32E-02	1.00E+00	9.53E-02	1.00E+00	6.57E-03	6.92E-01	1.27E-01	1.00E+00	8.92E-01	1.00E+00	3.41E-01	1.00E+00	purine nucleoside triphosphate biosynthesis	P
GO:0009147	18	1.32E-01	1.00E+00	3.23E-02	1.00E+00	1.62E-01	1.00E+00	5.24E-02	1.00E+00	8.55E-02	1.00E+00	3.69E-02	1.00E+00	4.18E-01	1.00E+00	2.09E-01	1.00E+00	pyrimidine nucleoside triphosphate metabol	P
GO:0009150	85	1.59E-02	1.00E+00	3.55E-03	1.88E-01	1.71E-02	1.00E+00	3.15E-03	1.61E-01	5.06E-03	3.75E-01	1.30E-02	6.68E-01	8.44E-01	1.00E+00	1.44E-01	1.00E+00	purine ribonucleotide metabolism	P
GO:0009152	73	5.41E-02	1.00E+00	2.94E-02	1.00E+00	5.58E-02	1.00E+00	2.19E-02	9.37E-01	1.55E-02	6.92E-01	7.56E-02	1.00E+00	9.58E-01	1.00E+00	2.78E-01	1.00E+00	purine ribonucleotide biosynthesis	P
GO:0009156	18	4.59E-01	1.00E+00	2.49E-02	1.00E+00	4.40E-01	1.00E+00	1.04E-02	5.72E-01	4.86E-01	1.00E+00	7.90E-02	1.00E+00	5.51E-01	1.00E+00	2.04E-01	1.00E+00	ribonucleoside monophosphate biosynthesi	P
GO:0009161	19	2.74E-01	1.00E+00	1.46E-02	6.07E-01	2.15E-01	1.00E+00	4.61E-03	2.88E-01	3.65E-01	1.00E+00	7.44E-02	1.00E+00	5.20E-01	1.00E+00	1.69E-01	1.00E+00	ribonucleoside monophosphate metabolism	P
GO:0009165	144	4.68E-03	2.72E-01	6.12E-03	3.08E-01	7.59E-02	1.00E+00	9.50E-03	5.72E-01	2.55E-03	1.29E-01	7.16E-02	1.00E+00	7.58E-02	1.00E+00	2.37E-02	9.99E-01	nucleotide biosynthesis	P
GO:0009166	27	1.82E-01	1.00E+00	2.27E-02	1.00E+00	3.71E-01	1.00E+00	2.88E-02	1.00E+00	8.15E-02	1.00E+00	9.22E-02	1.00E+00	4.27E-01	1.00E+00	2.43E-01	1.00E+00	nucleotide catabolism	P
GO:0009167	15	3.11E-01	1.00E+00	3.07E-02	1.00E+00	1.55E-01	1.00E+00	1.25E-02	6.47E-01	4.10E-01	1.00E+00	1.26E-01	1.00E+00	8.17E-01	1.00E+00	2.60E-01	1.00E+00	purine ribonucleoside monophosphate meta	P
GO:0009168	14	5.26E-01	1.00E+00	5.70E-02	1.00E+00	3.42E-01	1.00E+00	2.87E-02	1.00E+00	5.46E-01	1.00E+00	1.35E-01	1.00E+00	8.44E-01	1.00E+00	3.29E-01	1.00E+00	purine ribonucleoside monophosphate biosy	P
GO:0009187	47	5.47E-01	1.00E+00	3.23E-01	1.00E+00	9.76E-01	1.00E+00	7.71E-01	1.00E+00	3.98E-01	1.00E+00	4.87E-01	1.00E+00	1.55E-01	1.00E+00	6.24E-02	1.00E+00	cyclic nucleotide metabolism	P
GO:0009190	35	2.59E-01	1.00E+00	3.01E-01	1.00E+00	8.62E-01	1.00E+00	5.37E-01	1.00E+00	1.93E-01	1.00E+00	6.81E-01	1.00E+00	6.43E-02	1.00E+00	6.32E-02	1.00E+00	cyclic nucleotide biosynthesis	P
GO:0009199	68	1.82E-02	1.00E+00	2.55E-02	1.00E+00	2.74E-02	1.00E+00	2.96E-02	1.00E+00	3.67E-03	2.13E-01	4.95E-02	1.00E+00	7.78E-01	1.00E+00	1.64E-01	1.00E+00	ribonucleoside triphosphate metabolism	P
GO:0009200	11	2.28E-01	1.00E+00	1.09E-01	1.00E+00	6.05E-01	1.00E+00	4.74E-01	1.00E+00	2.72E-01	1.00E+00	1.60E-01	1.00E+00	6.72E-02	1.00E+00	1.00E-01	1.00E+00	deoxyribonucleoside triphosphate metaboli	P
GO:0009201	58	4.03E-02	1.00E+00	7.83E-02	1.00E+00	5.45E-02	1.00E+00	7.12E-02	1.00E+00	7.24E-03	6.92E-01	1.51E-01	1.00E+00	8.90E-01	1.00E+00	2.97E-01	1.00E+00	ribonucleoside triphosphate biosynthesis	P
GO:0009205	66	1.88E-02	1.00E+00	3.03E-02	1.00E+00	2.84E-02	1.00E+00	5.10E-02	1.00E+00	4.11E-03	2.13E-01	3.19E-02	1.00E+00	7.65E-01	1.00E+00	1.93E-01	1.00E+00	purine ribonucleoside triphosphate metabol	P
GO:0009206	57	3.80E-02	1.00E+00	8.63E-02	1.00E+00	5.32E-02	1.00E+00	9.53E-02	1.00E+00	6.57E-03	6.92E-01	1.27E-01	1.00E+00	8.92E-01	1.00E+00	3.41E-01	1.00E+00	purine ribonucleoside triphosphate biosynth	P
GO:0009208	13	6.96E-02	1.00E+00	1.59E-03	9.65E-02	1.08E-01	1.00E+00	1.55E-02	6.47E-01	2.36E-02	1.00E+00	1.14E-02	5.03E-01	5.54E-01	1.00E+00	5.21E-02	1.00E+00	pyrimidine ribonucleoside triphosphate meta	P
GO:0009209	13	6.96E-02	1.00E+00	1.59E-03	9.65E-02	1.08E-01	1.00E+00	1.55E-02	6.47E-01	2.36E-02	1.00E+00	1.14E-02	5.03E-01	5.54E-01	1.00E+00	5.21E-02	1.00E+00	pyrimidine ribonucleoside triphosphate bios	P
GO:0009218	15	3.32E-02	1.00E+00	1.01E-03	9.65E-02	7.21E-02	1.00E+00	7.61E-03	4.92E-01	8.88E-03	6.92E-01	7.13E-03	4.21E-01	2.48E-01	1.00E+00	6.25E-02	1.00E+00	pyrimidine ribonucleotide metabolism	P
GO:0009220	15	3.32E-02	1.00E+00	1.01E-03	9.65E-02	7.21E-02	1.00E+00	7.61E-03	4.92E-01	8.88E-03	6.92E-01	7.13E-03	4.21E-01	2.48E-01	1.00E+00	6.25E-02	1.00E+00	pyrimidine ribonucleotide biosynthesis	P
GO:0009225	15	5.16E-01	1.00E+00	2.32E-01	1.00E+00	5.16E-01	1.00E+00	1.53E-01	1.00E+00	2.70E-01	1.00E+00	2.35E-01	1.00E+00	7.46E-01	1.00E+00	7.15E-01	1.00E+00	nucleotide-sugar metabolism	P
GO:0009237	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	siderophore metabolism	P
GO:0009238	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	enterobactin metabolism	P
GO:0009239	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	enterobactin biosynthesis	P
GO:0009250	26	8.63E-01	1.00E+00	7.74E-02	1.00E+00	9.38E-01	1.00E+00	4.84E-01	1.00E+00	6.26E-01	1.00E+00	2.72E-02	1.00E+00	8.11E-01	1.00E+00	7.57E-02	1.00E+00	glucan biosynthesis	P
GO:0009259	93	1.23E-02	6.08E-01	1.19E-03	9.65E-02	1.83E-02	1.00E+00	6.80E-04	4.20E-02	4.03E-03	2.13E-01	1.19E-02	5.03E-01	6.79E-01	1.00E+00	8.68E-02	1.00E+00	ribonucleotide metabolism	P
GO:0009260	79	4.51E-02	1.00E+00	9.93E-03	4.69E-01	5.95E-02	1.00E+00	6.01E-03	2.88E-01	1.36E-02	6.92E-01	5.56E-02	1.00E+00	8.59E-01	1.00E+00	1.43E-01	1.00E+00	ribonucleotide biosynthesis	P
GO:0009262	16	1.86E-01	1.00E+00	6.65E-02	1.00E+00	3.91E-01	1.00E+00	1.63E-01	1.00E+00	2.17E-01	1.00E+00	5.24E-02	1.00E+00	1.38E-01	1.00E+00	2.73E-01	1.00E+00	deoxyribonucleotide metabolism	P
GO:0009266	229	4.65E-02	1.00E+00	5.15E-02	1.00E+00	3.23E-02	1.00E+00	7.00E-02	1.00E+00	2.72E-01	1.00E+00	9.39E-02	1.00E+00	3.35E-02	8.38E-01	1.66E-01	1.00E+00	response to temperature stimulus	P
GO:0009267	12	3.16E-01	1.00E+00	5.11E-01	1.00E+00	5.68E-01	1.00E+00	4.56E-01	1.00E+00	2.76E-01	1.00E+00	4.95E-01	1.00E+00	2.46E-01	1.00E+00	5.98E-01	1.00E+00	cellular response to starvation	P
GO:0009288	40	5.40E-01	1.00E+00	1.72E-01	1.00E+00	4.61E-01	1.00E+00	3.10E-01	1.00E+00	5.02E-01	1.00E+00	6.10E-01	1.00E+00	5.12E-01	1.00E+00	3.49E-02	1.00E+00	flagellum (sensu Bacteria)	C
GO:0009296	14	6.47E-02	1.00E+00	3.10E-04	4.40E-02	4.67E-02	1.00E+00	3.49E-02	1.00E+00	2.70E-01	1.00E+00	8.06E-04	4.48E-02	1.35E-01	1.00E+00	4.54E-02	1.00E+00	flagellum biogenesis	P
GO:0009306	56	1.85E-01	1.00E+00	1.05E-01	1.00E+00	2.27E-01	1.00E+00	2.48E-01	1.00E+00	2.00E-01	1.00E+00	7.69E-02	1.00E+00	3.41E-01	1.00E+00	2.74E-01	1.00E+00	protein secretion	P
GO:0009308	534	2.26E-04	1.72E-02	3.01E-05	7.00E-03	7.44E-03	6.41E-01	6.49E-04	4.20E-02	3.69E-03	2.13E-01	4.62E-05	9.66E-03	7.28E-04	3.44E-02	1.72E-02	6.56E-01	amine metabolism	P
GO:0009309	121	7.89E-02	1.00E+00	4.07E-03	1.88E-01	1.62E-01	1.00E+00	9.39E-02	1.00E+00	2.51E-01	1.00E+00	1.30E-03	9.00E-02	4.48E-02	1.00E+00	4.14E-02	1.00E+00	amine biosynthesis	P
GO:0009310	66	2.15E-01	1.00E+00	7.35E-03	3.12E-01	4.47E-01	1.00E+00	3.47E-02	1.00E+00	1.59E-01	1.00E+00	3.46E-02	1.00E+00	3.51E-01	1.00E+00	3.94E-02	1.00E+00	amine catabolism	P
GO:0009311	11	9.21E-02	1.00E+00	3.14E-02	1.00E+00	1.08E-01	1.00E+00	1.38E-01	1.00E+00	3.97E-01	1.00E+00	9.53E-03	5.03E-01	5.15E-03	2.23E-01	3.62E-02	1.00E+00	oligosaccharide metabolism	P
GO:0009314	124	1.42E-03	8.86E-02	9.05E-04	8.70E-02	2.15E-03	9.50E-02	5.99E-03	2.88E-01	4.67E-02	1.00E+00	7.99E-02	1.00E+00	2.36E-03	8.40E-02	6.10E-04	3.00E-02	response to radiation	P
GO:0009331	12	1.00E-01	1.00E+00	9.27E-02	1.00E+00	1.72E-01	1.00E+00	1.46E-01	1.00E+00	3.71E-01	1.00E+00	1.55E-01	1.00E+00	5.60E-02	1.00E+00	1.85E-01	1.00E+00	glycerol-3-phosphate dehydrogenase comp	C
GO:0009395	15	2.75E-02	1.00E+00	1.48E-01	1.00E+00	7.57E-02	1.00E+00	2.38E-01	1.00E+00	1.53E-02	6.92E-01	1.47E-01	1.00E+00	1.82E-01	1.00E+00	5.50E-01	1.00E+00	phospholipid catabolism	P
GO:0009396	10	1.74E-01	1.00E+00	1.64E-01	1.00E+00	4.94E-01	1.00E+00	2.63E-01	1.00E+00	2.62E-01	1.00E+00	1.43E-01	1.00E+00	7.61E-02	1.00E+00	2.92E-01	1.00E+00	folic acid and derivative biosynthesis	P
GO:0009405	32	6.03E-01	1.00E+00	4.68E-01	1.00E+00	4.14E-01	1.00E+00	3.71E-01	1.00E+00	9.41E-01	1.00E+00	9.36E-01	1.00E+00	4.69E-01	1.00E+00	2.71E-01	1.00E+00	pathogenesis	P

GO:0009408	18	5.19E-02	1.00E+00	3.08E-02	1.00E+00	8.88E-03	6.53E-01	1.96E-01	1.00E+00	6.42E-01	1.00E+00	7.54E-03	4.21E-01	5.81E-02	1.00E+00	5.44E-01	1.00E+00	response to heat	P
GO:0009409	205	1.00E-01	1.00E+00	1.32E-01	1.00E+00	7.61E-02	1.00E+00	9.02E-02	1.00E+00	3.03E-01	1.00E+00	3.21E-01	1.00E+00	8.88E-02	1.00E+00	2.00E-01	1.00E+00	response to cold	P
GO:0009410	16	7.08E-02	1.00E+00	5.80E-01	1.00E+00	2.31E-01	1.00E+00	3.36E-01	1.00E+00	5.17E-02	1.00E+00	7.38E-01	1.00E+00	9.90E-02	1.00E+00	4.77E-01	1.00E+00	response to xenobiotic stimulus	P
GO:0009411	40	1.21E-04	1.43E-02	3.16E-05	7.00E-03	3.27E-04	4.00E-02	1.78E-03	1.24E-01	6.16E-03	3.75E-01	4.81E-03	2.66E-01	1.37E-03	6.14E-02	2.91E-05	7.00E-03	response to UV	P
GO:0009416	97	1.45E-02	8.50E-01	4.88E-03	2.61E-01	2.96E-02	1.00E+00	3.47E-02	1.00E+00	2.93E-01	1.00E+00	5.61E-02	1.00E+00	2.65E-03	8.40E-02	3.37E-03	1.27E-01	response to light stimulus	P
GO:0009434	25	7.59E-01	1.00E+00	4.77E-01	1.00E+00	7.49E-01	1.00E+00	6.04E-01	1.00E+00	8.66E-01	1.00E+00	4.17E-01	1.00E+00	6.49E-01	1.00E+00	5.59E-01	1.00E+00	flagellum (sensu Eukaryota)	C
GO:0009451	31	7.34E-03	3.15E-01	8.26E-02	1.00E+00	2.72E-02	1.00E+00	1.75E-01	1.00E+00	2.76E-02	1.00E+00	4.02E-01	1.00E+00	2.23E-02	6.36E-01	5.69E-02	1.00E+00	RNA modification	P
GO:0009566	61	3.92E-02	1.00E+00	1.60E-02	7.63E-01	4.95E-02	1.00E+00	3.40E-02	1.00E+00	2.18E-01	1.00E+00	5.58E-02	1.00E+00	3.00E-02	8.38E-01	4.47E-02	1.00E+00	fertilization	P
GO:0009581	58	6.93E-01	1.00E+00	9.11E-01	1.00E+00	6.75E-01	1.00E+00	9.64E-01	1.00E+00	9.43E-01	1.00E+00	5.16E-01	1.00E+00	3.82E-01	1.00E+00	9.87E-01	1.00E+00	detection of external stimulus	P
GO:0009582	48	7.33E-01	1.00E+00	9.38E-01	1.00E+00	7.00E-01	1.00E+00	9.22E-01	1.00E+00	9.22E-01	1.00E+00	5.82E-01	1.00E+00	5.13E-01	1.00E+00	1.00E+00	1.00E+00	detection of abiotic stimulus	P
GO:0009583	28	7.34E-01	1.00E+00	6.61E-01	1.00E+00	6.77E-01	1.00E+00	8.86E-01	1.00E+00	9.09E-01	1.00E+00	2.19E-01	1.00E+00	4.93E-01	1.00E+00	9.88E-01	1.00E+00	detection of light stimulus	P
GO:0009593	29	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	9.27E-01	1.00E+00	detection of chemical stimulus	P
GO:0009595	11	5.24E-01	1.00E+00	5.13E-01	1.00E+00	5.25E-01	1.00E+00	9.42E-01	1.00E+00	8.02E-01	1.00E+00	4.45E-01	1.00E+00	3.30E-01	1.00E+00	3.27E-01	1.00E+00	detection of biotic stimulus	P
GO:0009605	736	5.40E-01	1.00E+00	1.89E-01	1.00E+00	9.08E-01	1.00E+00	6.82E-01	1.00E+00	9.70E-01	1.00E+00	2.75E-01	1.00E+00	4.42E-03	2.23E-01	1.13E-02	4.76E-01	response to external stimulus	P
GO:0009607	255	7.00E-01	1.00E+00	7.63E-01	1.00E+00	6.61E-01	1.00E+00	8.00E-01	1.00E+00	8.87E-01	1.00E+00	4.12E-01	1.00E+00	2.61E-01	1.00E+00	9.07E-01	1.00E+00	response to biotic stimulus	P
GO:0009611	467	9.02E-01	1.00E+00	7.39E-01	1.00E+00	9.78E-01	1.00E+00	7.75E-01	1.00E+00	9.93E-01	1.00E+00	9.28E-01	1.00E+00	1.41E-01	1.00E+00	8.99E-02	1.00E+00	response to wounding	P
GO:0009612	31	7.75E-02	1.00E+00	1.69E-01	1.00E+00	1.05E-01	1.00E+00	1.46E-01	1.00E+00	2.34E-01	1.00E+00	7.05E-02	1.00E+00	6.56E-02	1.00E+00	4.87E-01	1.00E+00	response to mechanical stimulus	P
GO:0009615	81	9.70E-01	1.00E+00	8.59E-01	1.00E+00	9.85E-01	1.00E+00	9.00E-01	1.00E+00	9.89E-01	1.00E+00	7.75E-01	1.00E+00	4.98E-01	1.00E+00	8.15E-01	1.00E+00	response to virus	P
GO:0009617	101	9.86E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	9.63E-01	1.00E+00	4.56E-01	1.00E+00	8.15E-01	1.00E+00	response to bacterium	P
GO:0009620	14	7.16E-01	1.00E+00	5.08E-01	1.00E+00	7.66E-01	1.00E+00	7.47E-01	1.00E+00	7.11E-01	1.00E+00	4.60E-01	1.00E+00	6.15E-01	1.00E+00	3.32E-01	1.00E+00	response to fungus	P
GO:0009628	407	4.49E-05	9.52E-03	1.25E-04	1.50E-02	1.24E-04	1.16E-02	4.12E-04	4.20E-02	2.05E-02	7.90E-01	4.29E-03	2.66E-01	3.07E-05	4.00E-03	4.11E-03	2.01E-01	response to abiotic stimulus	P
GO:0009636	31	5.42E-02	1.00E+00	3.79E-02	1.00E+00	9.48E-02	1.00E+00	2.66E-02	1.00E+00	2.18E-01	1.00E+00	1.05E-01	1.00E+00	6.20E-02	1.00E+00	3.91E-01	1.00E+00	response to toxin	P
GO:0009653	1355	1.97E-04	1.72E-02	5.86E-04	5.90E-02	1.90E-02	1.00E+00	3.72E-02	1.00E+00	7.12E-03	6.92E-01	2.24E-02	1.00E+00	2.24E-04	1.20E-02	1.01E-05	7.00E-03	morphogenesis	P
GO:0009698	48	4.63E-01	1.00E+00	6.43E-02	1.00E+00	4.11E-01	1.00E+00	3.13E-01	1.00E+00	5.06E-01	1.00E+00	1.55E-02	6.68E-01	5.76E-01	1.00E+00	1.37E-01	1.00E+00	phenylpropanoid metabolism	P
GO:0009712	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	catechol metabolism	P
GO:0009719	423	4.05E-13	0.00E+00	7.40E-17	0.00E+00	3.97E-11	7.08E-04	2.61E-14	0.00E+00	1.30E-08	0.00E+00	1.29E-09	6.20E-04	7.76E-05	8.00E-03	1.21E-07	9.38E-04	response to endogenous stimulus	P
GO:0009725	99	3.26E-01	1.00E+00	2.52E-01	1.00E+00	3.64E-01	1.00E+00	5.12E-01	1.00E+00	6.58E-01	1.00E+00	7.15E-02	1.00E+00	9.73E-02	1.00E+00	5.41E-01	1.00E+00	response to hormone stimulus	P
GO:0009743	26	4.06E-02	1.00E+00	4.82E-03	2.61E-01	1.50E-01	1.00E+00	5.41E-02	1.00E+00	6.11E-02	1.00E+00	3.37E-02	1.00E+00	2.10E-02	6.36E-01	3.28E-03	1.27E-01	response to carbohydrate stimulus	P
GO:0009746	21	6.72E-02	1.00E+00	4.21E-03	1.88E-01	1.39E-01	1.00E+00	5.93E-02	1.00E+00	1.03E-01	1.00E+00	8.57E-02	1.00E+00	4.33E-02	1.00E+00	1.01E-04	1.60E-02	response to hexose stimulus	P
GO:0009749	21	6.72E-02	1.00E+00	4.21E-03	1.88E-01	1.39E-01	1.00E+00	5.93E-02	1.00E+00	1.03E-01	1.00E+00	8.57E-02	1.00E+00	4.33E-02	1.00E+00	1.01E-04	1.60E-02	response to glucose stimulus	P
GO:0009755	11	1.87E-02	1.00E+00	1.24E-02	6.07E-01	2.17E-03	9.50E-02	5.78E-02	1.00E+00	4.44E-02	1.00E+00	3.91E-02	1.00E+00	3.93E-01	1.00E+00	1.43E-02	4.76E-01	hormone-mediated signaling	P
GO:0009790	541	3.50E-03	2.12E-01	1.46E-02	6.07E-01	1.27E-02	6.53E-01	5.04E-02	1.00E+00	1.54E-02	6.92E-01	9.20E-02	1.00E+00	5.64E-02	1.00E+00	2.08E-02	9.99E-01	embryonic development	P
GO:0009791	91	4.14E-02	1.00E+00	5.34E-01	1.00E+00	1.98E-01	1.00E+00	4.89E-01	1.00E+00	4.01E-02	1.00E+00	4.48E-01	1.00E+00	4.07E-02	1.00E+00	6.08E-01	1.00E+00	post-embryonic development	P
GO:0009792	314	1.78E-04	1.72E-02	1.36E-03	9.65E-02	1.08E-04	1.16E-02	6.77E-04	4.20E-02	1.78E-03	1.20E-01	2.39E-02	1.00E+00	1.29E-01	1.00E+00	8.80E-02	1.00E+00	embryonic development (sensu Metazoa)	P
GO:0009798	19	1.34E-01	1.00E+00	2.68E-01	1.00E+00	1.67E-01	1.00E+00	2.38E-01	1.00E+00	5.15E-01	1.00E+00	3.73E-01	1.00E+00	9.03E-02	1.00E+00	1.80E-01	1.00E+00	axis specification	P
GO:0009799	35	3.58E-01	1.00E+00	7.13E-01	1.00E+00	2.86E-01	1.00E+00	5.70E-01	1.00E+00	1.42E-01	1.00E+00	8.74E-01	1.00E+00	9.32E-01	1.00E+00	6.44E-01	1.00E+00	determination of symmetry	P
GO:0009855	35	3.58E-01	1.00E+00	7.13E-01	1.00E+00	2.86E-01	1.00E+00	5.70E-01	1.00E+00	1.42E-01	1.00E+00	8.74E-01	1.00E+00	9.32E-01	1.00E+00	6.44E-01	1.00E+00	determination of bilateral symmetry	P
GO:0009880	49	3.79E-01	1.00E+00	8.15E-01	1.00E+00	5.69E-01	1.00E+00	9.52E-01	1.00E+00	7.08E-01	1.00E+00	7.75E-01	1.00E+00	7.58E-02	1.00E+00	3.82E-01	1.00E+00	embryonic pattern specification	P
GO:0009881	11	5.26E-01	1.00E+00	4.93E-01	1.00E+00	6.37E-01	1.00E+00	8.47E-01	1.00E+00	4.56E-01	1.00E+00	9.82E-02	1.00E+00	2.06E-01	1.00E+00	9.06E-01	1.00E+00	photoreceptor activity	F
GO:0009887	763	7.65E-02	1.00E+00	5.24E-01	1.00E+00	4.12E-01	1.00E+00	7.00E-01	1.00E+00	1.93E-01	1.00E+00	8.57E-01	1.00E+00	1.19E-02	3.39E-01	4.79E-02	1.00E+00	organ morphogenesis	P
GO:0009888	403	1.23E-02	6.08E-01	2.09E-01	1.00E+00	2.19E-01	1.00E+00	3.02E-01	1.00E+00	3.27E-02	1.00E+00	4.34E-01	1.00E+00	9.50E-03	2.75E-01	6.08E-02	1.00E+00	tissue development	P
GO:0009889	206	2.93E-04	1.90E-02	3.32E-07	3.92E-03	1.09E-02	6.53E-01	1.54E-03	9.60E-02	1.67E-02	6.92E-01	8.86E-05	1.10E-02	1.83E-04	8.00E-03	9.49E-06	7.00E-03	regulation of biosynthesis	P
GO:0009890	47	1.34E-04	1.43E-02	4.18E-05	7.00E-03	5.34E-04	4.90E-02	1.22E-02	6.47E-01	1.19E-02	6.92E-01	1.33E-03	9.00E-02	1.04E-03	3.62E-02	3.25E-03	1.27E-01	negative regulation of biosynthesis	P
GO:0009891	87	1.80E-01	1.00E+00	6.44E-03	3.12E-01	7.78E-01	1.00E+00	2.12E-01	1.00E+00	4.25E-01	1.00E+00	1.42E-01	1.00E+00	5.24E-03	2.23E-01	6.13E-05	7.00E-03	positive regulation of biosynthesis	P
GO:0009892	476	3.67E-15	0.00E+00	1.02E-15	0.00E+00	9.40E-14	7.08E-04	2.13E-12	0.00E+00	2.84E-07	9.59E-04	1.99E-09	8.78E-04	2.57E-09	0.00E+00	4.39E-09	0.00E+00	negative regulation of metabolism	P
GO:0009893	598	4.19E-06	3.02E-03	3.80E-09	8.90E-04	1.73E-05	3.00E-03	2.28E-05	9.57E-03	3.53E-02	1.00E+00	7.68E-06	5.87E-03	1.40E-05	3.63E-03	7.55E-09	0.00E+00	positive regulation of metabolism	P
GO:0009894	32	2.64E-02	1.00E+00	3.33E-04	4.40E-02	7.75E-02	1.00E+00	4.55E-04	4.20E-02	1.07E-01	1.00E+00	4.84E-02	1.00E+00	2.05E-01	1.00E+00	5.56E-03	4.28E-01	regulation of catabolism	P
GO:0009896	10	2.10E-01	1.00E+00	1.52E-01	1.00E+00	8.48E-01	1.00E+00	1.23E-01	1.00E+00	2.42E-01	1.00E+00	2.86E-01	1.00E+00	2.16E-01	1.00E+00	2.58E-01	1.00E+00	positive regulation of catabolism	P
GO:0009897	151	9.34E-01	1.00E+00	3.31E-01	1.00E+00	9.01E-01	1.00E+00	5.83E-01	1.00E+00	9.72E-01	1.00E+00	4.02E-01	1.00E+00	6.25E-01	1.00E+00	1.23E-01	1.00E+00	external side of plasma membrane	C
GO:0009913	60	8.89E-01	1.00E+00	8.59E-01	1.00E+00	9.40E-01	1.00E+00	8.97E-01	1.00E+00	8.16E-01	1.00E+00	6.91E-01	1.00E+00	7.83E-01	1.00E+00	8.41E-01	1.00E+00	epidermal cell differentiation	P
GO:0009925	30	8.62E-01	1.00E+00	8.50E-01	1.00E+00	5.21E-01	1.00E+00	7.25E-01	1.00E+00	9.84E-01	1.00E+00	5.63E-01	1.00E+00	3.77E-01	1.00E+00	9.91E-01	1.00E+00	basal plasma membrane	C
GO:0009948	12	6.68E-02	1.00E+00	1.50E-01	1.00E+00	1.20E-01	1.00E+00	7.16E-02	1.00E+00	3.01E-01	1.00E+00	4.11E-01	1.00E+00	4.88E-02	1.00E+00	2.51E-01	1.00E+00	anterior/posterior axis specification	P
GO:0009952	139	9.96E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	9.69E-01	1.00E+00	9.51E-01	1.00E+00	9.76E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	anterior/posterior pattern formation	P
GO:0009953	48	2.48E-01	1.00E+00	8.99E-01	1.00E+00	4.69E-01	1.00E+00	9.85E-01	1.00E+00	1.64E-01	1.00E+00	8.98E-01	1.00E+00	3.21E-01	1.00E+00	3.57E-01	1.00E+00	dorsal/ventral pattern formation	P
GO:0009954	24	9.29E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.44E-01	1.00E+00	1.00E+00	1.00E+00	3.41E-01	1.00E+00	9.89E-01	1.00E+00	proximal/distal pattern formation	P
GO:0009966	519	8.91E-03	6.08E-01	4.28E-07	3.92E-03	1.97E-01	1.00E+00	5.50E-03	2.88E-01	1.86E-01	1.00E+00	4.15E-04	2.33E-02	2.54E-04	1.20E-02	7.72E-09	0.00E+00	regulation of signal transduction	P
GO:0009967	161	3.02E-02	1.00E+00	1.14E-04	1.50E-02	1.63E-01	1.00E+00	1.10E-02	5.72E-01	4.33E-01	1.00E+00	2.20E-02	1.00E+00	8.35E-04	3.44E-02	7.12E-05	7.00E-03	positive regulation of signal transduction	P
GO:0009968	130	1.92E-02	1.00E+00	7.46E-03	3.12E-01	2.10E-01	1.00E+00	3.76E-01	1.00E+00	1.02E-01	1.00E+00	1.66E-02	6.68E-01	9.37E-03	2.75E-01	2.39E-04	2.33E-02	negative regulation of signal transduction	P
GO:0009975	25	3.90E-01	1.00E+00	2.85E-01	1.00E+00	6.06E-01	1.00E+00	5.06E-01	1.00E+00	2.22E-01	1.00E+00	3.60E-01	1.00E+00	5.49E-01	1.00E+00	1.77E-01	1.00E+00	cyclase activity	F
GO:0009982	35	2.01E-01	1.00E+00	1.01E-01	1.00E+00	2.88E-01	1.00E+00	2.43E-01	1.00E+00	4.90E-01	1.00E+00	2.94E-01	1.00E+00	1.10E-01	1.00E+00	7.28E-02	1.00E+00	pseudouridine synthase activity	F
GO:0009986	282	7.65E-01	1.00E+00	2.72E-02	1.00E+00	8.42E-01	1.00E+00	1.52E-01	1.00E+00	8.97E-01	1.00E+00	3.63E-02	1.00E+00	4.11E-01	1.00E+00	1.48E-02	6.56E-01	cell surface	C
GO:0009987	14223	2.55E-29	0.00E+00	0.00E+00	0.00E+00	9.03E-31	0.00E+00	0.00E+00	0.00E+00	9.01E-22	0.00E+00	1.40E-45	0.00E+00	6.72E-05	8.00E-03	8.85E-29	0.00E+00	cellular process	P
GO:0009991	78	2.71E-03	2.12E-01	5.18E-03	2.79E-01	6.96E-04	4.90E-02	3.85E-03	2.88E-01	4.79E-02	1.00E+00	9.26E-03	5.03E-01	1.30E-01	1.00E+00	2.05E-01	1.00E+00	response to extracellular stimulus	P
GO:0009994	14	2.15E-02	1.00E+00	2.41E-01	1.00E+00	6.21E-02	1.00E+00	3.82E-01	1.00E+00	1.16E-01	1.00E+00	1.43E-01	1.00E+00	1.40E-01	1.00E+00	7.45E-01	1.00E+00	oocyte differentiation	P
GO:0010001	45	5.83E-01	1.00E+00	8.22E-01	1.00E+00	3.62E-01	1.00E+00	5.79E-01	1.00E+00	7.67E-01	1.00E+00	7.42E-01	1.00E+00	5.10E-01	1.00E+00	9.03E-01	1.00E+00	glial cell differentiation	P
GO:0010008	93	5.75E-05	1.20E-02	1.81E-07	3.92E-03	1.34E-02	6.53E-01	1.57E-04	1.30E-02	1.79E-03	1.20E-01	6.35E-05	9.66E-03	1.43E-03	6.14E-02	1.08E-03	6.00E-02	endosome membrane	C
GO:0010033	83	1.25E-01	1.00E+00	1.15E-01	1.00E+00	6.25E-01	1.00E+00	1.93E-01	1.00E+00	1.14E-01	1.00E+00	1.42E-01	1.00E+00	2.04E-02	6.36E-01	7.69E-02	1.00E+00	response to organic substance	P
GO:0010035	54	5.73E-02	1.00E+00	6.69E-02	1.00E+00	1.26E-01	1.00E+00	4.39E-02	1.00E+00	4.61E-01	1.00E+00	1.75E-01	1.00E+00	1.38E-02	4.78E-01	5.41E-01	1.00E+00	response to inorganic substance	P
GO:0010038	48	6.13E-02	1.00E+00	1.00E-01	1.00E+00	1.82E-01	1.00E+00	5.47E-02	1.00E+00	3.53E-01	1.00E+00	2.13E-01	1.00E+00	1.84E-02	6.36E-01	5.66E-01	1.00E+00	response to metal ion	P
GO:0010092	14	7.19E-01	1.00E+00	8.45E-01	1.00E+00	8.85E-01	1.00E+00	5.04E-01	1.00E+00	5.26E-01	1.00E+00	9.71E-01	1.00E+00	6.36E-01	1.00E+00	8.13E-01	1.00E+00	specification of organ identity	P
GO:0010165	15	2.26E-02	1.00E+00	5.66E-02	1.00E+00	2.84E-03	1.35E-01	1.15E-01	1.00E+00	1.49E-01	1.00E+00	1.71E-01	1.00E+00	6.67E-02	1.00E+00	2.00E-01	1.00E+00	response to X-ray	P
GO:0010181	12	1.95E-01	1.00E+00	5.65E-01	1.00E+00	1.01E-01	1.00E+00	8.70E-01	1.00E+00	6.33E-01	1.00E+00	7.21E-01	1.00E+00	2.53E-01	1.00E+00	2.62E-01	1.00E+00	FMN binding	F
GO:0010212	13	2.60E-01	1.00E+00	5.46E-02	1.00E+00	2.67E-01	1.00E+00	7.40E-02	1.00E+00	1.05E-01	1.00E+00	3.39E-01	1.00E+00	8.08E-01	1.00E+00	4.27E-02	1.00E+00	response to ionizing radiation	P
GO:0012501	795	4.61E-12	2.57E-03	2.56E-14	0.00E+00	1.59E-08	9.80E-04	4.30E-11	0.00E+00	5.67E-07	1.00E-03	2.07E-09	8.78E-04	7.56E-07	8.23E-04	5.00E-07	1.92E-03	programmed cell death	P
GO:0012502	189	1.17E-04	1.43E-02	1.79E-05	4.51E-03	1.79E-03	9.50E-02	1.73E-04	1.30E-02	4.51E-03	2.13E-01	7.76E-05	1.10E-02	1.25E-03	6.14E-02	1.03E-02	4.76E-01	induction of programmed cell death	P

GO:0012505	1009	1.70E-12	0.00E+00	2.41E-20	0.00E+00	1.66E-09	9.80E-04	8.51E-15	0.00E+00	2.39E-09	0.00E+00	8.89E-13	6.20E-04	2.09E-05	4.00E-03	7.60E-10	0.00E+00	endomembrane system	C
GO:0012506	117	1.90E-03	2.12E-01	2.38E-05	7.00E-03	5.74E-03	4.69E-01	2.04E-04	1.30E-02	2.27E-02	1.00E+00	2.73E-04	2.33E-02	2.36E-02	8.38E-01	6.26E-03	4.28E-01	vesicle membrane	C
GO:0012510	11	2.04E-01	1.00E+00	1.11E-01	1.00E+00	2.17E-01	1.00E+00	3.44E-01	1.00E+00	5.34E-01	1.00E+00	9.38E-02	1.00E+00	1.14E-01	1.00E+00	1.51E-01	1.00E+00	trans-Golgi network transport vesicle membr	C
GO:0014003	11	4.84E-01	1.00E+00	5.46E-01	1.00E+00	1.60E-01	1.00E+00	5.43E-01	1.00E+00	7.84E-01	1.00E+00	4.64E-01	1.00E+00	4.33E-01	1.00E+00	6.19E-01	1.00E+00	oligodendrocyte development	P
GO:0014013	12	9.22E-01	1.00E+00	9.62E-01	1.00E+00	9.43E-01	1.00E+00	9.54E-01	1.00E+00	6.48E-01	1.00E+00	8.82E-01	1.00E+00	9.37E-01	1.00E+00	9.40E-01	1.00E+00	regulation of gliogenesis	P
GO:0014020	35	3.10E-01	1.00E+00	5.28E-02	1.00E+00	3.10E-01	1.00E+00	6.88E-02	1.00E+00	1.77E-01	1.00E+00	8.74E-02	1.00E+00	4.91E-01	1.00E+00	1.34E-01	1.00E+00	primary neural tube formation	P
GO:0014031	42	8.96E-01	1.00E+00	9.45E-01	1.00E+00	6.87E-01	1.00E+00	8.75E-01	1.00E+00	9.78E-01	1.00E+00	8.92E-01	1.00E+00	5.60E-01	1.00E+00	9.50E-01	1.00E+00	mesenchymal cell development	P
GO:0014032	31	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.87E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	9.97E-01	1.00E+00	neural crest cell development	P
GO:0014033	31	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.87E-01	1.00E+00	9.27E-01	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	9.97E-01	1.00E+00	neural crest cell differentiation	P
GO:0014037	10	4.25E-01	1.00E+00	3.94E-01	1.00E+00	5.42E-01	1.00E+00	2.30E-01	1.00E+00	3.61E-01	1.00E+00	2.86E-01	1.00E+00	4.23E-01	1.00E+00	8.96E-01	1.00E+00	Schwann cell differentiation	P
GO:0014069	22	9.38E-01	1.00E+00	6.47E-01	1.00E+00	9.88E-01	1.00E+00	7.87E-01	1.00E+00	9.91E-01	1.00E+00	8.44E-01	1.00E+00	2.37E-01	1.00E+00	2.60E-01	1.00E+00	postsynaptic density	C
GO:0015002	30	1.65E-01	1.00E+00	2.39E-01	1.00E+00	8.87E-02	1.00E+00	5.95E-02	1.00E+00	2.03E-01	1.00E+00	2.69E-01	1.00E+00	5.78E-01	1.00E+00	6.57E-01	1.00E+00	heme-copper terminal oxidase activity	F
GO:0015020	16	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	1.00E+00	1.00E+00	glucuronosyltransferase activity	F
GO:0015031	828	2.38E-25	0.00E+00	3.70E-37	0.00E+00	1.98E-19	0.00E+00	2.19E-30	0.00E+00	4.37E-22	0.00E+00	2.00E-24	0.00E+00	2.63E-07	0.00E+00	1.15E-13	0.00E+00	protein transport	P
GO:0015035	11	8.57E-01	1.00E+00	4.86E-01	1.00E+00	9.52E-01	1.00E+00	4.23E-01	1.00E+00	3.50E-01	1.00E+00	3.03E-01	1.00E+00	9.88E-01	1.00E+00	4.57E-01	1.00E+00	protein disulfide oxidoreductase activity	F
GO:0015036	17	4.52E-01	1.00E+00	1.59E-01	1.00E+00	5.98E-01	1.00E+00	1.78E-01	1.00E+00	1.31E-01	1.00E+00	3.90E-02	1.00E+00	7.54E-01	1.00E+00	4.58E-01	1.00E+00	disulfide oxidoreductase activity	F
GO:0015057	39	7.86E-01	1.00E+00	3.54E-01	1.00E+00	9.63E-01	1.00E+00	6.38E-01	1.00E+00	5.26E-01	1.00E+00	4.47E-01	1.00E+00	5.60E-01	1.00E+00	3.30E-01	1.00E+00	thrombin receptor activity	F
GO:0015075	897	1.72E-01	1.00E+00	1.73E-03	9.65E-02	6.72E-01	1.00E+00	1.12E-01	1.00E+00	5.02E-01	1.00E+00	2.46E-02	1.00E+00	2.02E-02	6.36E-01	1.01E-04	1.60E-02	ion transporter activity	F
GO:0015077	140	8.08E-04	8.86E-02	6.22E-03	3.08E-01	7.44E-03	6.41E-01	1.61E-02	6.47E-01	1.92E-03	1.20E-01	1.62E-02	6.68E-01	3.04E-02	8.38E-01	4.29E-02	1.00E+00	monovalent inorganic cation transporter act	F
GO:0015078	135	5.97E-04	8.86E-02	6.61E-03	3.12E-01	4.42E-03	3.08E-01	2.11E-02	9.37E-01	1.57E-03	1.20E-01	1.30E-02	6.68E-01	2.79E-02	8.38E-01	4.94E-02	1.00E+00	hydrogen ion transporter activity	F
GO:0015082	39	1.66E-01	1.00E+00	2.43E-02	1.00E+00	1.23E-01	1.00E+00	3.09E-02	1.00E+00	3.92E-01	1.00E+00	8.19E-02	1.00E+00	6.12E-01	1.00E+00	4.06E-01	1.00E+00	di-, tri-valent inorganic cation transporter ac	F
GO:0015103	39	4.21E-01	1.00E+00	2.53E-01	1.00E+00	5.35E-01	1.00E+00	1.27E-01	1.00E+00	3.24E-01	1.00E+00	6.89E-01	1.00E+00	6.55E-01	1.00E+00	2.76E-01	1.00E+00	inorganic anion transporter activity	F
GO:0015106	22	4.04E-01	1.00E+00	1.76E-01	1.00E+00	8.52E-01	1.00E+00	8.78E-02	1.00E+00	1.79E-01	1.00E+00	7.47E-01	1.00E+00	3.50E-01	1.00E+00	9.76E-02	1.00E+00	bicarbonate transporter activity	F
GO:0015108	23	3.72E-01	1.00E+00	1.41E-01	1.00E+00	8.31E-01	1.00E+00	6.88E-02	1.00E+00	1.67E-01	1.00E+00	6.79E-01	1.00E+00	3.56E-01	1.00E+00	8.46E-02	1.00E+00	chloride transporter activity	F
GO:0015116	11	8.11E-01	1.00E+00	9.81E-01	1.00E+00	9.63E-01	1.00E+00	8.98E-01	1.00E+00	6.31E-01	1.00E+00	9.95E-01	1.00E+00	7.50E-01	1.00E+00	7.98E-01	1.00E+00	sulfate transporter activity	F
GO:0015144	47	6.74E-02	1.00E+00	2.10E-02	1.00E+00	1.82E-01	1.00E+00	9.09E-02	1.00E+00	5.10E-02	1.00E+00	3.01E-02	1.00E+00	2.04E-01	1.00E+00	8.38E-02	1.00E+00	carbohydrate transporter activity	F
GO:0015145	14	6.76E-02	1.00E+00	2.24E-02	1.00E+00	1.97E-01	1.00E+00	2.05E-01	1.00E+00	1.05E-01	1.00E+00	8.51E-03	5.03E-01	3.39E-02	8.38E-01	9.22E-02	1.00E+00	monosaccharide transporter activity	F
GO:0015149	13	1.18E-01	1.00E+00	3.76E-02	1.00E+00	3.37E-01	1.00E+00	3.22E-01	1.00E+00	1.51E-01	1.00E+00	1.23E-02	5.03E-01	4.86E-02	1.00E+00	1.09E-01	1.00E+00	hexose transporter activity	F
GO:0015171	56	3.20E-01	1.00E+00	1.19E-02	6.07E-01	2.63E-01	1.00E+00	6.61E-02	1.00E+00	3.02E-01	1.00E+00	1.61E-02	6.68E-01	5.27E-01	1.00E+00	8.14E-02	1.00E+00	amino acid transporter activity	F
GO:0015172	10	4.76E-01	1.00E+00	2.15E-01	1.00E+00	3.92E-01	1.00E+00	1.70E-01	1.00E+00	4.82E-01	1.00E+00	4.94E-01	1.00E+00	5.29E-01	1.00E+00	3.47E-01	1.00E+00	acidic amino acid transporter activity	F
GO:0015175	12	3.38E-01	1.00E+00	4.78E-02	1.00E+00	4.98E-01	1.00E+00	3.84E-01	1.00E+00	7.71E-01	1.00E+00	2.01E-02	7.56E-01	6.20E-02	1.00E+00	3.81E-02	1.00E+00	neutral amino acid transporter activity	F
GO:0015179	31	4.24E-01	1.00E+00	3.48E-01	1.00E+00	4.70E-01	1.00E+00	5.07E-01	1.00E+00	3.03E-01	1.00E+00	7.00E-01	1.00E+00	4.13E-01	1.00E+00	2.07E-01	1.00E+00	L-amino acid transporter activity	F
GO:0015197	15	6.04E-01	1.00E+00	1.25E-01	1.00E+00	8.33E-01	1.00E+00	4.14E-01	1.00E+00	4.66E-01	1.00E+00	9.87E-02	1.00E+00	3.22E-01	1.00E+00	1.31E-01	1.00E+00	peptide transporter activity	F
GO:0015198	10	6.93E-01	1.00E+00	2.88E-01	1.00E+00	9.98E-01	1.00E+00	3.66E-01	1.00E+00	2.81E-01	1.00E+00	3.27E-01	1.00E+00	3.45E-01	1.00E+00	2.90E-01	1.00E+00	oligopeptide transporter activity	F
GO:0015203	20	7.01E-01	1.00E+00	6.68E-01	1.00E+00	8.75E-01	1.00E+00	6.93E-01	1.00E+00	6.35E-01	1.00E+00	3.98E-01	1.00E+00	4.57E-01	1.00E+00	8.17E-01	1.00E+00	polyamine transporter activity	F
GO:0015232	20	8.14E-01	1.00E+00	3.15E-01	1.00E+00	6.49E-01	1.00E+00	3.17E-01	1.00E+00	8.42E-01	1.00E+00	2.04E-01	1.00E+00	9.12E-01	1.00E+00	8.44E-01	1.00E+00	heme transporter activity	F
GO:0015238	34	9.24E-01	1.00E+00	4.87E-01	1.00E+00	9.97E-01	1.00E+00	9.11E-01	1.00E+00	8.55E-01	1.00E+00	4.45E-01	1.00E+00	7.52E-01	1.00E+00	2.19E-01	1.00E+00	drug transporter activity	F
GO:0015247	16	9.81E-01	1.00E+00	6.80E-01	1.00E+00	8.54E-01	1.00E+00	5.51E-01	1.00E+00	1.00E+00	1.00E+00	5.68E-01	1.00E+00	8.80E-01	1.00E+00	8.71E-01	1.00E+00	aminophospholipid transporter activity	F
GO:0015248	10	4.40E-01	1.00E+00	9.05E-01	1.00E+00	6.69E-01	1.00E+00	8.67E-01	1.00E+00	1.54E-01	1.00E+00	9.42E-01	1.00E+00	6.94E-01	1.00E+00	6.67E-01	1.00E+00	sterol transporter activity	F
GO:0015250	10	3.80E-01	1.00E+00	1.09E-01	1.00E+00	2.78E-01	1.00E+00	1.36E-02	6.47E-01	3.54E-01	1.00E+00	2.93E-01	1.00E+00	7.26E-01	1.00E+00	4.80E-01	1.00E+00	water channel activity	F
GO:0015267	461	6.22E-01	1.00E+00	2.38E-01	1.00E+00	9.45E-01	1.00E+00	6.83E-01	1.00E+00	9.18E-01	1.00E+00	5.67E-01	1.00E+00	1.98E-02	6.36E-01	4.38E-03	2.01E-01	channel or pore class transporter activity	F
GO:0015268	461	6.22E-01	1.00E+00	2.38E-01	1.00E+00	9.45E-01	1.00E+00	6.83E-01	1.00E+00	9.18E-01	1.00E+00	5.67E-01	1.00E+00	1.98E-02	6.36E-01	4.38E-03	2.01E-01	alpha-type channel activity	F
GO:0015269	12	6.98E-01	1.00E+00	9.38E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	4.15E-01	1.00E+00	2.32E-01	1.00E+00	2.73E-01	1.00E+00	calcium-activated potassium channel activit	F
GO:0015276	104	9.12E-01	1.00E+00	9.28E-01	1.00E+00	9.92E-01	1.00E+00	8.85E-01	1.00E+00	8.50E-01	1.00E+00	9.28E-01	1.00E+00	3.88E-01	1.00E+00	6.53E-01	1.00E+00	ligand-gated ion channel activity	F
GO:0015290	304	5.46E-01	1.00E+00	4.25E-02	1.00E+00	5.95E-01	1.00E+00	1.89E-01	1.00E+00	3.05E-01	1.00E+00	1.30E-01	1.00E+00	8.33E-01	1.00E+00	4.07E-02	1.00E+00	electrochemical potential-driven transporter	F
GO:0015291	304	5.46E-01	1.00E+00	4.25E-02	1.00E+00	5.95E-01	1.00E+00	1.89E-01	1.00E+00	3.05E-01	1.00E+00	1.30E-01	1.00E+00	8.33E-01	1.00E+00	4.07E-02	1.00E+00	porter activity	F
GO:0015293	186	8.48E-01	1.00E+00	2.79E-01	1.00E+00	7.27E-01	1.00E+00	4.32E-01	1.00E+00	7.34E-01	1.00E+00	3.00E-01	1.00E+00	9.34E-01	1.00E+00	3.74E-01	1.00E+00	symporter activity	F
GO:0015294	125	8.86E-01	1.00E+00	3.47E-01	1.00E+00	8.62E-01	1.00E+00	6.83E-01	1.00E+00	9.24E-01	1.00E+00	2.52E-01	1.00E+00	6.88E-01	1.00E+00	2.66E-01	1.00E+00	solute:cation symporter activity	F
GO:0015296	75	6.36E-01	1.00E+00	3.50E-01	1.00E+00	7.25E-01	1.00E+00	6.51E-01	1.00E+00	7.19E-01	1.00E+00	2.76E-01	1.00E+00	4.97E-01	1.00E+00	3.14E-01	1.00E+00	anion:cation symporter activity	F
GO:0015297	86	3.47E-01	1.00E+00	8.58E-02	1.00E+00	4.82E-01	1.00E+00	2.15E-01	1.00E+00	1.70E-01	1.00E+00	3.14E-01	1.00E+00	5.76E-01	1.00E+00	2.11E-02	9.99E-01	antiporter activity	F
GO:0015298	39	7.27E-01	1.00E+00	1.93E-01	1.00E+00	8.29E-01	1.00E+00	4.05E-01	1.00E+00	6.05E-01	1.00E+00	3.14E-01	1.00E+00	7.62E-01	1.00E+00	1.16E-01	1.00E+00	solute:cation antiporter activity	F
GO:0015299	39	7.27E-01	1.00E+00	1.93E-01	1.00E+00	8.29E-01	1.00E+00	4.05E-01	1.00E+00	6.05E-01	1.00E+00	3.14E-01	1.00E+00	7.62E-01	1.00E+00	1.16E-01	1.00E+00	solute:hydrogen antiporter activity	F
GO:0015300	41	6.15E-01	1.00E+00	1.39E-01	1.00E+00	8.02E-01	1.00E+00	3.27E-01	1.00E+00	3.42E-01	1.00E+00	1.99E-01	1.00E+00	7.96E-01	1.00E+00	1.03E-01	1.00E+00	solute:solute antiporter activity	F
GO:0015301	22	4.04E-01	1.00E+00	1.76E-01	1.00E+00	8.52E-01	1.00E+00	8.78E-02	1.00E+00	1.79E-01	1.00E+00	7.47E-01	1.00E+00	3.50E-01	1.00E+00	9.76E-02	1.00E+00	anion:anion antiporter activity	F
GO:0015307	26	7.35E-01	1.00E+00	3.12E-01	1.00E+00	9.59E-01	1.00E+00	7.76E-01	1.00E+00	6.24E-01	1.00E+00	2.94E-01	1.00E+00	6.60E-01	1.00E+00	1.47E-01	1.00E+00	drug:hydrogen antiporter activity	F
GO:0015370	122	9.40E-01	1.00E+00	4.58E-01	1.00E+00	9.11E-01	1.00E+00	7.77E-01	1.00E+00	9.55E-01	1.00E+00	3.21E-01	1.00E+00	8.14E-01	1.00E+00	3.71E-01	1.00E+00	solute:sodium symporter activity	F
GO:0015380	21	3.18E-01	1.00E+00	1.45E-01	1.00E+00	7.82E-01	1.00E+00	7.49E-02	1.00E+00	1.34E-01	1.00E+00	6.63E-01	1.00E+00	2.58E-01	1.00E+00	9.71E-02	1.00E+00	anion exchanger activity	F
GO:0015385	19	1.93E-01	1.00E+00	2.71E-01	1.00E+00	1.77E-01	1.00E+00	3.23E-01	1.00E+00	9.20E-02	1.00E+00	4.93E-01	1.00E+00	4.57E-01	1.00E+00	1.06E-01	1.00E+00	sodium:hydrogen antiporter activity	F
GO:0015399	128	1.22E-01	1.00E+00	5.23E-02	1.00E+00	1.22E-01	1.00E+00	8.29E-02	1.00E+00	1.80E-01	1.00E+00	4.66E-02	1.00E+00	4.88E-01	1.00E+00	2.88E-01	1.00E+00	primary active transporter activity	F
GO:0015405	128	1.22E-01	1.00E+00	5.23E-02	1.00E+00	1.22E-01	1.00E+00	8.29E-02	1.00E+00	1.80E-01	1.00E+00	4.66E-02	1.00E+00	4.88E-01	1.00E+00	2.88E-01	1.00E+00	P-P-bond-hydrolysis-driven transporter acti	F
GO:0015450	29	5.54E-01	1.00E+00	5.95E-01	1.00E+00	4.15E-01	1.00E+00	3.76E-01	1.00E+00	4.80E-01	1.00E+00	4.49E-01	1.00E+00	7.02E-01	1.00E+00	8.16E-01	1.00E+00	protein translocase activity	F
GO:0015457	27	7.12E-01	1.00E+00	1.72E-01	1.00E+00	9.10E-01	1.00E+00	4.07E-01	1.00E+00	9.41E-01	1.00E+00	1.87E-01	1.00E+00	7.94E-02	1.00E+00	4.42E-02	1.00E+00	auxiliary transport protein activity	F
GO:0015464	26	9.65E-01	1.00E+00	9.98E-01	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.66E-01	1.00E+00	7.01E-01	1.00E+00	7.35E-01	1.00E+00	acetylcholine receptor activity	F
GO:0015485	12	2.95E-01	1.00E+00	5.00E-01	1.00E+00	1.34E-01	1.00E+00	5.32E-01	1.00E+00	1.47E-01	1.00E+00	3.67E-01	1.00E+00	9.02E-01	1.00E+00	7.42E-01	1.00E+00	cholesterol binding	F
GO:0015491	26	2.94E-01	1.00E+00	4.20E-01	1.00E+00	1.93E-01	1.00E+00	6.44E-01	1.00E+00	2.62E-01	1.00E+00	6.65E-01	1.00E+00	4.22E-01	1.00E+00	3.20E-02	1.00E+00	cation:cation antiporter activity	F
GO:0015520	26	7.35E-01	1.00E+00	3.12E-01	1.00E+00	9.59E-01	1.00E+00	7.76E-01	1.00E+00	6.24E-01	1.00E+00	2.94E-01	1.00E+00	6.60E-01	1.00E+00	1.47E-01	1.00E+00	tetracycline:hydrogen antiporter activity	F
GO:0015629	288	1.97E-06	3.00E-03	2.64E-08	9.59E-04	5.20E-04	4.90E-02	9.03E-05	1.30E-02	2.25E-05	5.37E-03	6.94E-04	4.48E-02	2.82E-04	2.29E-02	2.71E-08	0.00E+00	actin cytoskeleton	C
GO:0015630	416	7.82E-14	0.00E+00	1.06E-13	0.00E+00	2.05E-14	7.08E-04	6.29E-13	0.00E+00	6.16E-08	9.59E-04	2.26E-08	9.03E-04	7.48E-06	1.00E-03	1.08E-04	1.60E-02	microtubule cytoskeleton	C
GO:0015631	75	7.85E-06	3.62E-03	6.90E-06	4.51E-03	1.40E-04	1.16E-02	4.85E-04	4.20E-02	7.91E-04	1.20E-01	3.69E-04	2.33E-02	2.79E-03	8.40E-02	1.65E-04	1.60E-02	tubulin binding	F
GO:0015645	15	1.46E-01	1.00E+00	6.48E-02	1.00E+00	3.22E-01	1.00E+00	7.54E-02	1.00E+00	3.55E-01	1.00E+00	2.97E-01	1.00E+00	1.10E-02	3.39E-01	1.19E-01	1.00E+00	fatty-acid ligase activity	F
GO:0015662	70	1.96E-01	1.00E+00	5.50E-02	1.00E+00	3.41E-01	1.00E+00	8.80E-02	1.00E+00	4.76E-01	1.00E+00	4.51E-02	1.00E+00	1.34E-01	1.00E+00	2.74E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0015669	16	8.37E-01	1.00E+00	2.27E-01	1.00E+00	3.06E-01	1.00E+00	1.21E-01	1.00E+00	1.00E+00	1.00E+00	1.43E-01	1.00E+00	6.55E-01	1.00E+00	8.23E-01	1.00E+00	gas transport	P
GO:0015671	14	8.33E-01	1.00E+00	2.00E-01	1.00E+00	3.39E-01	1.00E+00	1.18E-01	1.00E+00	9.99E-01	1.00E+00	1.25E-01	1.00E+00	6.65E-01	1.00E+00	7.71E-01	1.00E+00	oxygen transport	P
GO:0015672	465	2.71E-01	1.00E+00	5.34E-02	1.00E+00	6.09E-01	1.00E+00	2.01E-01	1.00E+00	4.08E-01	1.00E+00	7.44E-02	1.00E+00	1.80E-01	1.00E+00	5.97E-02	1.00E+00	monovalent inorganic cation transport	P
GO:0015674	237	2.70E-01	1.00E+00	4.66E-03	2.61E-01	7.27E-01	1.00E+00	1.34E-01	1.00E+00	6.31E-01	1.00E+00	7.67E-02	1.00E+00	2.39E-02	8.38E-01	4.39E-04	3.00E-02	di-, tri-valent inorganic cation transport	P

GO:0015698	178	1.00E+00	1.00E+00	9.51E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	9.07E-01	1.00E+00	2.08E-01	1.00E+00	inorganic anion transport	P
GO:0015711	15	7.02E-01	1.00E+00	2.83E-01	1.00E+00	3.68E-01	1.00E+00	7.33E-01	1.00E+00	9.45E-01	1.00E+00	7.94E-01	1.00E+00	7.66E-01	1.00E+00	2.28E-02	9.99E-01	organic anion transport	P
GO:0015749	42	7.54E-02	1.00E+00	6.90E-02	1.00E+00	1.42E-01	1.00E+00	2.89E-01	1.00E+00	1.28E-01	1.00E+00	5.30E-02	1.00E+00	5.97E-02	1.00E+00	2.02E-01	1.00E+00	monosaccharide transport	P
GO:0015758	41	7.67E-02	1.00E+00	6.21E-02	1.00E+00	1.50E-01	1.00E+00	2.85E-01	1.00E+00	1.37E-01	1.00E+00	5.17E-02	1.00E+00	4.96E-02	1.00E+00	1.65E-01	1.00E+00	glucose transport	P
GO:0015800	16	6.21E-03	3.09E-01	1.35E-03	9.65E-02	1.61E-02	1.00E+00	9.82E-04	9.40E-02	9.52E-03	6.92E-01	2.30E-02	1.00E+00	1.34E-01	1.00E+00	2.57E-02	9.99E-01	acidic amino acid transport	P
GO:0015804	11	6.29E-01	1.00E+00	1.15E-01	1.00E+00	6.70E-01	1.00E+00	5.23E-01	1.00E+00	9.03E-01	1.00E+00	4.60E-02	1.00E+00	1.40E-01	1.00E+00	9.02E-02	1.00E+00	neutral amino acid transport	P
GO:0015807	15	5.58E-02	1.00E+00	1.50E-01	1.00E+00	1.36E-01	1.00E+00	6.01E-01	1.00E+00	1.67E-01	1.00E+00	4.99E-01	1.00E+00	1.19E-01	1.00E+00	3.13E-02	9.99E-01	L-amino acid transport	P
GO:0015813	16	6.21E-03	3.09E-01	1.35E-03	9.65E-02	1.61E-02	1.00E+00	9.82E-04	9.40E-02	9.52E-03	6.92E-01	2.30E-02	1.00E+00	1.34E-01	1.00E+00	2.57E-02	9.99E-01	glutamate transport	P
GO:0015833	64	3.08E-01	1.00E+00	7.39E-02	1.00E+00	6.14E-01	1.00E+00	4.48E-01	1.00E+00	5.07E-01	1.00E+00	1.37E-01	1.00E+00	3.28E-02	8.38E-01	6.48E-03	4.28E-01	peptide transport	P
GO:0015837	91	1.53E-01	1.00E+00	1.26E-02	6.07E-01	8.51E-02	1.00E+00	1.79E-01	1.00E+00	1.45E-01	1.00E+00	1.25E-02	5.03E-01	4.97E-01	1.00E+00	9.52E-03	4.28E-01	amine transport	P
GO:0015849	150	2.27E-01	1.00E+00	4.83E-02	1.00E+00	3.03E-01	1.00E+00	3.47E-01	1.00E+00	1.36E-01	1.00E+00	4.80E-02	1.00E+00	3.98E-01	1.00E+00	2.71E-02	9.99E-01	organic acid transport	P
GO:0015886	20	8.14E-01	1.00E+00	3.15E-01	1.00E+00	6.49E-01	1.00E+00	3.17E-01	1.00E+00	8.42E-01	1.00E+00	2.04E-01	1.00E+00	9.12E-01	1.00E+00	8.44E-01	1.00E+00	heme transport	P
GO:0015893	33	9.24E-01	1.00E+00	4.77E-01	1.00E+00	9.98E-01	1.00E+00	9.11E-01	1.00E+00	8.55E-01	1.00E+00	4.56E-01	1.00E+00	7.53E-01	1.00E+00	2.19E-01	1.00E+00	drug transport	P
GO:0015904	26	7.35E-01	1.00E+00	3.12E-01	1.00E+00	9.59E-01	1.00E+00	7.76E-01	1.00E+00	6.24E-01	1.00E+00	2.94E-01	1.00E+00	6.60E-01	1.00E+00	1.47E-01	1.00E+00	tetracycline transport	P
GO:0015914	20	8.19E-01	1.00E+00	8.34E-01	1.00E+00	9.72E-01	1.00E+00	8.71E-01	1.00E+00	9.87E-01	1.00E+00	6.04E-01	1.00E+00	3.11E-01	1.00E+00	7.62E-01	1.00E+00	phospholipid transport	P
GO:0015918	16	3.27E-01	1.00E+00	6.32E-01	1.00E+00	3.48E-01	1.00E+00	6.25E-01	1.00E+00	7.11E-01	1.00E+00	6.89E-01	1.00E+00	7.80E-02	1.00E+00	4.26E-01	1.00E+00	sterol transport	P
GO:0015923	16	9.86E-02	1.00E+00	2.30E-02	1.00E+00	1.70E-01	1.00E+00	2.80E-01	1.00E+00	7.30E-02	1.00E+00	3.96E-02	1.00E+00	3.83E-01	1.00E+00	1.39E-02	4.76E-01	mannosidase activity	F
GO:0015924	10	1.89E-01	1.00E+00	2.27E-02	1.00E+00	1.18E-01	1.00E+00	4.71E-01	1.00E+00	2.13E-01	1.00E+00	6.63E-02	1.00E+00	4.43E-01	1.00E+00	7.30E-03	4.28E-01	mannosyl-oligosaccharide mannosidase ac	F
GO:0015929	15	3.21E-01	1.00E+00	4.80E-01	1.00E+00	3.67E-01	1.00E+00	4.16E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	2.50E-01	1.00E+00	7.09E-01	1.00E+00	hexosaminidase activity	F
GO:0015931	70	2.32E-06	3.00E-03	2.63E-09	8.90E-04	1.05E-04	1.16E-02	3.07E-09	0.00E+00	1.07E-05	2.00E-03	8.19E-05	1.10E-02	2.79E-01	1.00E+00	6.01E-04	3.00E-02	nucleobase, nucleoside, nucleotide and nuc	P
GO:0015932	14	3.40E-01	1.00E+00	5.25E-01	1.00E+00	6.89E-01	1.00E+00	5.81E-01	1.00E+00	2.92E-01	1.00E+00	5.05E-01	1.00E+00	2.77E-01	1.00E+00	2.79E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	F
GO:0015934	43	7.27E-02	1.00E+00	1.11E-01	1.00E+00	7.72E-02	1.00E+00	5.39E-02	1.00E+00	4.30E-02	1.00E+00	1.55E-01	1.00E+00	6.11E-01	1.00E+00	5.27E-01	1.00E+00	large ribosomal subunit	C
GO:0015935	42	6.81E-04	8.86E-02	1.03E-02	4.69E-01	6.61E-04	4.90E-02	1.08E-01	1.00E+00	3.68E-03	2.13E-01	4.53E-03	2.66E-01	3.05E-01	1.00E+00	7.26E-02	1.00E+00	small ribosomal subunit	C
GO:0015936	12	1.51E-02	1.00E+00	3.17E-02	1.00E+00	2.60E-02	1.00E+00	2.80E-02	1.00E+00	2.82E-02	1.00E+00	3.74E-01	1.00E+00	1.65E-01	1.00E+00	1.70E-02	6.56E-01	coenzyme A metabolism	P
GO:0015980	184	1.61E-03	2.12E-01	1.53E-05	4.51E-03	1.46E-03	7.90E-02	2.67E-02	1.00E+00	3.22E-02	1.00E+00	6.19E-06	5.87E-03	1.42E-01	1.00E+00	3.23E-03	1.27E-01	energy derivation by oxidation of organic co	P
GO:0015985	37	4.53E-01	1.00E+00	6.11E-01	1.00E+00	4.14E-01	1.00E+00	6.12E-01	1.00E+00	2.79E-01	1.00E+00	5.61E-01	1.00E+00	9.62E-01	1.00E+00	6.61E-01	1.00E+00	energy coupled proton transport, down elec	P
GO:0015986	37	4.53E-01	1.00E+00	6.11E-01	1.00E+00	4.14E-01	1.00E+00	6.12E-01	1.00E+00	2.79E-01	1.00E+00	5.61E-01	1.00E+00	9.62E-01	1.00E+00	6.61E-01	1.00E+00	ATP synthesis coupled proton transport	P
GO:0015988	10	3.69E-01	1.00E+00	3.97E-01	1.00E+00	7.09E-01	1.00E+00	6.28E-01	1.00E+00	3.84E-01	1.00E+00	2.03E-01	1.00E+00	2.73E-01	1.00E+00	6.19E-01	1.00E+00	energy coupled proton transport, against el	P
GO:0015992	80	1.25E-01	1.00E+00	7.79E-02	1.00E+00	2.42E-01	1.00E+00	1.36E-01	1.00E+00	1.58E-01	1.00E+00	1.12E-01	1.00E+00	3.13E-01	1.00E+00	1.93E-01	1.00E+00	proton transport	P
GO:0016010	14	8.04E-01	1.00E+00	9.35E-01	1.00E+00	9.38E-01	1.00E+00	8.52E-01	1.00E+00	6.35E-01	1.00E+00	9.78E-01	1.00E+00	3.14E-01	1.00E+00	7.60E-01	1.00E+00	dystrophin-associated glycoprotein complex	C
GO:0016020	7990	1.00E+00	1.00E+00	7.06E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.28E-01	1.00E+00	9.99E-01	1.00E+00	6.09E-04	3.00E-02	membrane	C
GO:0016021	6123	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	integral to membrane	C
GO:0016023	349	2.86E-10	2.57E-03	7.71E-17	0.00E+00	3.24E-07	2.00E-03	2.84E-12	0.00E+00	2.79E-06	1.69E-03	5.03E-10	6.20E-04	4.54E-07	8.23E-04	1.04E-09	0.00E+00	cytoplasmic membrane-bound vesicle	C
GO:0016032	33	3.91E-01	1.00E+00	7.88E-02	1.00E+00	7.72E-01	1.00E+00	2.82E-01	1.00E+00	6.12E-01	1.00E+00	2.52E-01	1.00E+00	8.59E-02	1.00E+00	1.30E-01	1.00E+00	viral life cycle	P
GO:0016042	116	7.85E-04	8.86E-02	6.82E-05	7.00E-03	3.96E-02	1.00E+00	2.23E-02	9.37E-01	2.12E-04	4.90E-02	3.15E-04	2.33E-02	1.69E-02	4.88E-01	1.58E-03	6.00E-02	lipid catabolism	P
GO:0016043	2251	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.40E-35	0.00E+00	0.00E+00	0.00E+00	9.86E-32	0.00E+00	1.56E-33	0.00E+00	1.88E-16	0.00E+00	1.91E-25	0.00E+00	cell organization and biogenesis	P
GO:0016044	88	6.58E-03	3.15E-01	1.22E-02	6.07E-01	3.75E-02	1.00E+00	3.09E-03	1.61E-01	3.22E-02	1.00E+00	1.50E-01	1.00E+00	1.29E-02	4.78E-01	1.94E-01	1.00E+00	membrane organization and biogenesis	P
GO:0016049	151	4.46E-03	2.14E-01	2.03E-03	1.30E-01	5.09E-02	1.00E+00	2.09E-02	9.37E-01	2.63E-02	1.00E+00	1.08E-02	5.03E-01	5.28E-02	1.00E+00	2.48E-03	7.90E-02	cell growth	P
GO:0016051	121	1.28E-01	1.00E+00	4.61E-04	4.74E-02	6.74E-01	1.00E+00	9.88E-03	5.72E-01	7.81E-02	1.00E+00	2.63E-03	1.44E-01	1.14E-01	1.00E+00	9.90E-03	4.76E-01	carbohydrate biosynthesis	P
GO:0016052	99	2.41E-03	2.12E-01	2.27E-03	1.71E-01	1.12E-03	7.90E-02	1.95E-01	1.00E+00	4.15E-03	2.13E-01	3.37E-05	9.52E-03	2.47E-01	1.00E+00	9.56E-02	1.00E+00	carbohydrate catabolism	P
GO:0016053	94	4.11E-02	1.00E+00	3.39E-03	1.88E-01	1.03E-01	1.00E+00	1.12E-01	1.00E+00	4.32E-02	1.00E+00	1.47E-02	6.68E-01	7.03E-02	1.00E+00	2.43E-03	7.90E-02	organic acid biosynthesis	P
GO:0016055	126	1.09E-03	8.86E-02	4.63E-04	4.74E-02	7.80E-03	6.41E-01	1.98E-03	1.39E-01	2.40E-03	1.20E-01	1.96E-02	7.56E-01	2.81E-02	8.38E-01	1.75E-03	7.90E-02	Wnt receptor signaling pathway	P
GO:0016064	126	6.69E-01	1.00E+00	8.09E-01	1.00E+00	7.26E-01	1.00E+00	2.38E-01	1.00E+00	9.74E-01	1.00E+00	9.89E-01	1.00E+00	2.33E-01	1.00E+00	7.46E-01	1.00E+00	immunoglobulin mediated immune respons	P
GO:0016068	56	9.97E-01	1.00E+00	9.88E-01	1.00E+00	9.70E-01	1.00E+00	8.47E-01	1.00E+00	9.99E-01	1.00E+00	9.91E-01	1.00E+00	8.85E-01	1.00E+00	9.82E-01	1.00E+00	type I hypersensitivity	P
GO:0016070	549	2.12E-32	0.00E+00	8.30E-30	0.00E+00	9.65E-30	0.00E+00	9.89E-28	0.00E+00	1.07E-20	0.00E+00	1.74E-17	0.00E+00	1.91E-09	0.00E+00	2.09E-08	0.00E+00	RNA metabolism	P
GO:0016071	286	7.26E-23	0.00E+00	4.27E-21	0.00E+00	4.23E-20	0.00E+00	1.24E-19	0.00E+00	8.91E-15	0.00E+00	1.65E-11	6.20E-04	3.55E-08	0.00E+00	9.19E-07	2.00E-03	mRNA metabolism	P
GO:0016072	72	2.35E-07	2.57E-03	8.90E-04	8.70E-02	1.34E-07	2.00E-03	4.36E-04	4.20E-02	1.71E-06	1.69E-03	1.88E-02	6.68E-01	7.10E-02	1.00E+00	2.59E-01	1.00E+00	rRNA metabolism	P
GO:0016073	12	2.29E-02	1.00E+00	9.52E-03	4.69E-01	2.02E-02	1.00E+00	2.09E-02	9.37E-01	1.41E-01	1.00E+00	6.30E-02	1.00E+00	6.29E-02	1.00E+00	2.59E-02	9.99E-01	snRNA metabolism	P
GO:0016079	15	1.51E-01	1.00E+00	8.48E-02	1.00E+00	7.78E-02	1.00E+00	2.06E-01	1.00E+00	3.65E-01	1.00E+00	8.35E-02	1.00E+00	3.01E-01	1.00E+00	1.61E-01	1.00E+00	synaptic vesicle exocytosis	P
GO:0016089	48	4.63E-01	1.00E+00	6.43E-02	1.00E+00	4.11E-01	1.00E+00	3.13E-01	1.00E+00	5.06E-01	1.00E+00	1.55E-02	6.68E-01	5.76E-01	1.00E+00	1.37E-01	1.00E+00	aromatic amino acid family biosynthesis, sh	P
GO:0016125	81	2.14E-03	2.12E-01	5.36E-03	3.08E-01	1.73E-02	1.00E+00	2.28E-02	9.37E-01	1.24E-02	6.92E-01	6.85E-02	1.00E+00	5.29E-03	2.23E-01	2.09E-03	7.90E-02	sterol metabolism	P
GO:0016126	34	4.36E-02	1.00E+00	1.77E-01	1.00E+00	3.58E-02	1.00E+00	2.12E-01	1.00E+00	1.18E-01	1.00E+00	1.27E-01	1.00E+00	1.48E-01	1.00E+00	3.89E-01	1.00E+00	sterol biosynthesis	P
GO:0016180	12	2.29E-02	1.00E+00	9.52E-03	4.69E-01	2.02E-02	1.00E+00	2.09E-02	9.37E-01	1.41E-01	1.00E+00	6.30E-02	1.00E+00	6.29E-02	1.00E+00	2.59E-02	9.99E-01	snRNA processing	P
GO:0016192	507	6.42E-12	2.57E-03	1.15E-20	0.00E+00	7.53E-08	9.80E-04	2.50E-13	0.00E+00	5.02E-06	1.69E-03	5.61E-14	6.20E-04	7.73E-08	0.00E+00	4.85E-11	0.00E+00	vesicle-mediated transport	P
GO:0016197	34	2.83E-02	1.00E+00	2.43E-04	2.40E-02	1.55E-01	1.00E+00	9.92E-03	5.72E-01	2.64E-02	1.00E+00	4.84E-04	2.33E-02	2.59E-01	1.00E+00	3.49E-03	1.27E-01	endosome transport	P
GO:0016202	15	2.08E-01	1.00E+00	1.41E-01	1.00E+00	2.03E-01	1.00E+00	1.07E-01	1.00E+00	2.00E-01	1.00E+00	1.44E-01	1.00E+00	5.02E-01	1.00E+00	4.05E-01	1.00E+00	regulation of striated muscle development	P
GO:0016208	24	4.68E-01	1.00E+00	6.21E-01	1.00E+00	6.98E-01	1.00E+00	6.16E-01	1.00E+00	8.03E-01	1.00E+00	6.80E-01	1.00E+00	7.66E-02	1.00E+00	5.86E-01	1.00E+00	AMP binding	F
GO:0016209	61	5.77E-03	3.09E-01	2.71E-02	1.00E+00	2.11E-02	1.00E+00	3.48E-02	1.00E+00	5.14E-02	1.00E+00	5.75E-02	1.00E+00	1.62E-02	4.88E-01	1.80E-01	1.00E+00	antioxidant activity	F
GO:0016229	36	8.05E-01	1.00E+00	6.59E-01	1.00E+00	9.98E-01	1.00E+00	6.46E-01	1.00E+00	5.80E-01	1.00E+00	5.43E-01	1.00E+00	3.52E-01	1.00E+00	3.78E-01	1.00E+00	steroid dehydrogenase activity	F
GO:0016234	10	1.19E-01	1.00E+00	8.22E-02	1.00E+00	1.08E-01	1.00E+00	1.38E-01	1.00E+00	1.19E-01	1.00E+00	1.37E-01	1.00E+00	4.91E-01	1.00E+00	2.99E-01	1.00E+00	inclusion body	C
GO:0016236	18	2.51E-02	1.00E+00	1.74E-02	7.63E-01	2.17E-02	1.00E+00	4.14E-02	1.00E+00	1.51E-02	6.92E-01	7.76E-02	1.00E+00	7.00E-01	1.00E+00	2.29E-02	9.99E-01	macroautophagy	P
GO:0016247	26	7.08E-01	1.00E+00	2.12E-01	1.00E+00	9.10E-01	1.00E+00	4.43E-01	1.00E+00	9.38E-01	1.00E+00	2.39E-01	1.00E+00	8.59E-02	1.00E+00	5.83E-02	1.00E+00	channel regulator activity	F
GO:0016251	20	5.85E-03	3.09E-01	3.36E-02	1.00E+00	8.84E-04	4.90E-02	1.82E-02	9.37E-01	4.35E-02	1.00E+00	1.31E-01	1.00E+00	1.47E-01	1.00E+00	3.17E-01	1.00E+00	general RNA polymerase II transcription fac	F
GO:0016265	827	6.08E-12	2.57E-03	7.46E-14	0.00E+00	6.95E-08	9.80E-04	1.69E-10	0.00E+00	3.13E-07	9.59E-04	3.67E-09	8.78E-04	5.82E-07	8.23E-04	5.28E-07	1.92E-03	death	P
GO:0016272	10	4.92E-02	1.00E+00	4.72E-02	1.00E+00	7.61E-04	4.90E-02	8.56E-02	1.00E+00	5.03E-01	1.00E+00	1.28E-01	1.00E+00	3.69E-01	1.00E+00	2.37E-01	1.00E+00	prefoldin complex	C
GO:0016278	24	1.25E-04	1.43E-02	4.96E-08	9.59E-04	3.42E-05	9.82E-03	3.87E-06	2.89E-03	3.71E-03	2.13E-01	1.03E-04	1.10E-02	9.39E-02	1.00E+00	6.99E-05	7.00E-03	lysine N-methyltransferase activity	F
GO:0016279	24	1.25E-04	1.43E-02	4.96E-08	9.59E-04	3.42E-05	9.82E-03	3.87E-06	2.89E-03	3.71E-03	2.13E-01	1.03E-04	1.10E-02	9.39E-02	1.00E+00	6.99E-05	7.00E-03	protein-lysine N-methyltransferase activity	F
GO:0016284	12	6.85E-01	1.00E+00	3.04E-01	1.00E+00	3.38E-01	1.00E+00	4.29E-01	1.00E+00	7.26E-01	1.00E+00	3.24E-01	1.00E+00	8.29E-01	1.00E+00	1.54E-01	1.00E+00	alanine aminopeptidase activity	F
GO:0016289	22	8.99E-01	1.00E+00	5.32E-01	1.00E+00	9.39E-01	1.00E+00	5.76E-01	1.00E+00	7.51E-01	1.00E+00	1.84E-01	1.00E+00	7.09E-01	1.00E+00	6.04E-01	1.00E+00	CoA hydrolase activity	F
GO:0016290	16	9.53E-01	1.00E+00	2.45E-01	1.00E+00	8.97E-01	1.00E+00	3.75E-01	1.00E+00	8.85E-01	1.00E+00	2.38E-02	1.00E+00	9.13E-01	1.00E+00	5.66E-01	1.00E+00	palmitoyl-CoA hydrolase activity	F
GO:0016298	81	7.74E-02	1.00E+00	3.42E-02	1.00E+00	2.33E-01	1.00E+00	3.68E-01	1.00E+00	6.04E-02	1.00E+00	2.53E-01	1.00E+00	1.79E-01	1.00E+00	7.00E-03	4.28E-01	lipase activity	F
GO:0016301	992	3.80E-11	2.57E-03	1.66E-25	0.00E+00	1.11E-11	7.08E-04	5.50E-18	0.00E+00	3.65E-07	9.59E-04	1.52E-15	0.00E+00	2.30E-03	8.40E-02	1.16E-13	0.00E+00	kinase activity	F
GO:0016303	11	6.44E-01	1.00E+00	1.55E-01	1.00E+00	4.57E-01	1.00E+00	9.91E-02	1.00E+00	4.63E-01	1.00E+00	2.95E-01	1.00E+00	9.04E-01	1.00E+00	2.50E-01	1.00E+00	phosphatidylinositol 3-kinase activity	F
GO:0016310	871	1.68E-05	7.00E-03	5.33E-14	0.00E+00	8.82E-06	2.91E-03	9.12E-10	0.00E+00	1.45E-03	1.20E-01	6.98E-09	8.78E-04	2.95E-02	8.38E-01	1.70E-09	0.00E+00	phosphorylation	P
GO:0016311	150	2.48E-03	2.12E-01	3.41E-05	7.00E-03	4.79E-03	3.08E-01	1.81E-04	1.30E-02	1.38E-01	1.00E+00	9.56E-03	5.03E-01	2.05E-03	8.40E-02	2.18E-03	7.90E-02	dephosphorylation	P

GO:0016323	140	4.82E-02	1.00E+00	2.87E-03	1.88E-01	2.26E-01	1.00E+00	5.21E-02	1.00E+00	2.92E-01	1.00E+00	1.53E-02	6.68E-01	1.72E-02	4.88E-01	7.24E-03	4.28E-01	basolateral plasma membrane	C
GO:0016324	105	8.93E-01	1.00E+00	1.56E-01	1.00E+00	9.69E-01	1.00E+00	3.07E-01	1.00E+00	9.74E-01	1.00E+00	6.17E-01	1.00E+00	2.37E-01	1.00E+00	3.26E-02	1.00E+00	apical plasma membrane	C
GO:0016327	123	3.43E-02	1.00E+00	5.91E-02	1.00E+00	3.75E-01	1.00E+00	3.82E-01	1.00E+00	2.67E-01	1.00E+00	4.67E-01	1.00E+00	2.73E-03	8.40E-02	6.79E-04	6.00E-02	apicolateral plasma membrane	C
GO:0016331	69	2.66E-01	1.00E+00	2.14E-01	1.00E+00	5.15E-01	1.00E+00	4.71E-01	1.00E+00	9.58E-02	1.00E+00	3.88E-01	1.00E+00	3.11E-01	1.00E+00	3.40E-02	1.00E+00	morphogenesis of embryonic epithelium	P
GO:0016337	226	1.00E+00	1.00E+00	9.50E-01	1.00E+00	9.96E-01	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.77E-01	1.00E+00	5.19E-01	1.00E+00	cell-cell adhesion	P
GO:0016338	23	1.26E-01	1.00E+00	3.33E-01	1.00E+00	3.01E-01	1.00E+00	2.73E-01	1.00E+00	4.32E-01	1.00E+00	7.87E-01	1.00E+00	3.07E-02	8.38E-01	1.38E-01	1.00E+00	calcium-independent cell-cell adhesion	P
GO:0016339	12	9.95E-01	1.00E+00	9.94E-01	1.00E+00	6.94E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	1.74E-01	1.00E+00	calcium-dependent cell-cell adhesion	P
GO:0016358	41	1.37E-01	1.00E+00	8.26E-02	1.00E+00	3.17E-01	1.00E+00	3.26E-01	1.00E+00	2.66E-01	1.00E+00	1.98E-01	1.00E+00	1.14E-01	1.00E+00	3.58E-02	1.00E+00	dendrite development	P
GO:0016363	41	3.30E-05	7.00E-03	9.59E-06	4.51E-03	2.23E-06	2.00E-03	5.00E-05	1.07E-02	5.98E-03	3.75E-01	2.23E-03	1.27E-01	1.36E-02	4.78E-01	2.52E-02	9.99E-01	nuclear matrix	C
GO:0016407	67	4.96E-04	4.40E-02	1.11E-03	9.65E-02	5.99E-04	4.90E-02	1.52E-03	9.60E-02	2.23E-03	1.20E-01	6.13E-03	4.21E-01	9.83E-02	1.00E+00	4.96E-02	1.00E+00	acetyltransferase activity	F
GO:0016408	13	3.58E-02	1.00E+00	1.04E-01	1.00E+00	7.80E-02	1.00E+00	3.22E-01	1.00E+00	1.38E-01	1.00E+00	3.40E-01	1.00E+00	2.69E-02	8.38E-01	2.13E-02	9.99E-01	C-acyltransferase activity	F
GO:0016409	17	1.64E-01	1.00E+00	3.09E-02	1.00E+00	3.74E-01	1.00E+00	1.27E-01	1.00E+00	1.12E-01	1.00E+00	4.06E-02	1.00E+00	2.04E-01	1.00E+00	2.66E-01	1.00E+00	palmitoyltransferase activity	F
GO:0016410	68	1.85E-03	2.12E-01	1.59E-03	9.65E-02	4.64E-03	3.08E-01	3.86E-03	2.88E-01	8.53E-03	6.92E-01	1.54E-02	6.68E-01	8.76E-02	1.00E+00	7.64E-03	4.28E-01	N-acyltransferase activity	F
GO:0016411	14	9.53E-02	1.00E+00	3.50E-01	1.00E+00	4.08E-02	1.00E+00	2.03E-01	1.00E+00	7.36E-02	1.00E+00	5.00E-01	1.00E+00	5.53E-01	1.00E+00	4.27E-01	1.00E+00	acylglycerol O-acyltransferase activity	F
GO:0016439	29	4.40E-01	1.00E+00	3.07E-01	1.00E+00	8.96E-01	1.00E+00	7.16E-01	1.00E+00	6.37E-01	1.00E+00	3.03E-01	1.00E+00	1.13E-01	1.00E+00	2.65E-01	1.00E+00	tRNA-pseudouridine synthase activity	F
GO:0016444	28	2.24E-01	1.00E+00	2.21E-03	1.71E-01	4.26E-01	1.00E+00	3.86E-03	2.88E-01	3.51E-01	1.00E+00	2.21E-01	1.00E+00	1.50E-01	1.00E+00	1.51E-02	6.56E-01	somatic cell DNA recombination	P
GO:0016445	30	2.47E-01	1.00E+00	8.52E-03	4.69E-01	4.44E-01	1.00E+00	7.11E-03	4.92E-01	3.27E-01	1.00E+00	3.02E-01	1.00E+00	2.10E-01	1.00E+00	3.76E-02	1.00E+00	somatic diversification of immunoglobulins	P
GO:0016447	28	2.24E-01	1.00E+00	2.21E-03	1.71E-01	4.26E-01	1.00E+00	3.86E-03	2.88E-01	3.51E-01	1.00E+00	2.21E-01	1.00E+00	1.50E-01	1.00E+00	1.51E-02	6.56E-01	somatic recombination of immunoglobulin g	P
GO:0016458	34	2.63E-04	1.90E-02	3.17E-06	3.92E-03	1.11E-03	7.90E-02	2.19E-05	9.57E-03	2.79E-03	2.13E-01	8.78E-03	5.03E-01	1.87E-02	6.36E-01	1.60E-04	1.60E-02	gene silencing	P
GO:0016459	58	1.04E-01	1.00E+00	6.28E-02	1.00E+00	4.86E-01	1.00E+00	3.24E-01	1.00E+00	1.80E-01	1.00E+00	6.41E-01	1.00E+00	4.68E-02	1.00E+00	8.52E-04	6.00E-02	myosin complex	C
GO:0016462	754	6.11E-11	2.57E-03	5.46E-15	0.00E+00	1.14E-09	9.80E-04	1.25E-11	0.00E+00	3.80E-08	9.59E-04	5.63E-11	6.20E-04	1.16E-03	6.14E-02	2.92E-06	2.00E-03	pyrophosphatase activity	F
GO:0016469	69	4.90E-02	1.00E+00	2.10E-01	1.00E+00	1.48E-01	1.00E+00	4.82E-01	1.00E+00	2.36E-02	1.00E+00	1.06E-01	1.00E+00	2.69E-01	1.00E+00	3.91E-01	1.00E+00	proton-transporting two-sector ATPase com	C
GO:0016477	361	3.12E-01	1.00E+00	2.24E-01	1.00E+00	8.43E-01	1.00E+00	6.48E-01	1.00E+00	3.99E-01	1.00E+00	5.48E-01	1.00E+00	5.61E-02	1.00E+00	6.08E-03	4.28E-01	cell migration	P
GO:0016481	335	9.26E-11	2.57E-03	1.06E-09	8.90E-04	4.58E-11	7.08E-04	1.13E-08	8.93E-04	6.03E-05	2.40E-02	1.98E-05	5.87E-03	1.56E-06	8.23E-04	1.69E-06	2.00E-03	negative regulation of transcription	P
GO:0016485	110	1.94E-01	1.00E+00	6.78E-03	3.12E-01	1.61E-01	1.00E+00	4.25E-02	1.00E+00	1.15E-01	1.00E+00	2.74E-02	1.00E+00	7.52E-01	1.00E+00	2.54E-02	9.99E-01	protein processing	P
GO:0016486	10	6.02E-01	1.00E+00	2.50E-01	1.00E+00	4.92E-01	1.00E+00	2.40E-01	1.00E+00	7.19E-01	1.00E+00	7.34E-01	1.00E+00	9.54E-01	1.00E+00	2.07E-01	1.00E+00	peptide hormone processing	P
GO:0016491	978	3.72E-02	1.00E+00	1.16E-01	1.00E+00	1.84E-01	1.00E+00	3.15E-01	1.00E+00	5.69E-02	1.00E+00	1.74E-02	6.68E-01	1.32E-01	1.00E+00	3.82E-01	1.00E+00	oxidoreductase activity	F
GO:0016493	37	6.34E-01	1.00E+00	7.21E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	4.91E-01	1.00E+00	2.97E-01	1.00E+00	1.33E-01	1.00E+00	2.96E-01	1.00E+00	C-C chemokine receptor activity	F
GO:0016494	33	6.96E-01	1.00E+00	8.59E-01	1.00E+00	9.81E-01	1.00E+00	9.99E-01	1.00E+00	7.93E-01	1.00E+00	6.73E-01	1.00E+00	2.07E-01	1.00E+00	4.01E-01	1.00E+00	C-X-C chemokine receptor activity	F
GO:0016500	27	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	9.72E-01	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	6.20E-01	1.00E+00	protein-hormone receptor activity	F
GO:0016502	139	9.67E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.05E-01	1.00E+00	9.64E-01	1.00E+00	4.11E-01	1.00E+00	4.38E-01	1.00E+00	nucleotide receptor activity	F
GO:0016503	186	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	pheromone receptor activity	F
GO:0016504	15	3.19E-02	1.00E+00	7.74E-02	1.00E+00	8.26E-02	1.00E+00	1.30E-01	1.00E+00	3.55E-02	1.00E+00	1.57E-02	6.68E-01	1.91E-01	1.00E+00	4.40E-01	1.00E+00	protease activator activity	F
GO:0016525	20	8.59E-01	1.00E+00	5.99E-01	1.00E+00	9.95E-01	1.00E+00	6.43E-01	1.00E+00	5.33E-01	1.00E+00	4.01E-01	1.00E+00	6.52E-01	1.00E+00	6.17E-01	1.00E+00	negative regulation of angiogenesis	P
GO:0016528	31	1.17E-01	1.00E+00	1.35E-01	1.00E+00	1.96E-01	1.00E+00	1.75E-01	1.00E+00	1.27E-01	1.00E+00	1.45E-01	1.00E+00	3.38E-01	1.00E+00	3.63E-01	1.00E+00	sarcoplasm	C
GO:0016529	28	8.86E-02	1.00E+00	1.06E-01	1.00E+00	2.06E-01	1.00E+00	1.20E-01	1.00E+00	8.40E-02	1.00E+00	1.88E-01	1.00E+00	2.37E-01	1.00E+00	2.82E-01	1.00E+00	sarcoplasmic reticulum	C
GO:0016538	10	5.20E-02	1.00E+00	7.36E-01	1.00E+00	1.68E-02	1.00E+00	2.87E-01	1.00E+00	7.96E-02	1.00E+00	5.53E-01	1.00E+00	2.95E-01	1.00E+00	1.00E+00	1.00E+00	cyclin-dependent protein kinase regulator a	F
GO:0016540	65	1.71E-01	1.00E+00	4.27E-03	1.88E-01	1.82E-01	1.00E+00	6.01E-02	1.00E+00	1.12E-01	1.00E+00	1.68E-02	6.68E-01	5.15E-01	1.00E+00	1.27E-02	4.76E-01	protein autoprocessing	P
GO:0016563	252	3.99E-06	3.02E-03	2.23E-08	9.59E-04	4.06E-06	2.91E-03	1.06E-07	2.89E-03	4.37E-04	4.90E-02	1.10E-04	1.30E-02	1.19E-02	3.39E-01	1.25E-04	1.60E-02	transcriptional activator activity	F
GO:0016564	193	1.86E-05	7.00E-03	4.62E-06	4.51E-03	8.37E-05	1.16E-02	4.06E-05	9.57E-03	2.19E-02	1.00E+00	6.81E-03	4.21E-01	2.22E-04	1.20E-02	4.35E-05	7.00E-03	transcriptional repressor activity	F
GO:0016566	19	3.91E-01	1.00E+00	8.76E-01	1.00E+00	7.74E-01	1.00E+00	8.85E-01	1.00E+00	4.87E-01	1.00E+00	6.11E-01	1.00E+00	1.64E-01	1.00E+00	9.19E-01	1.00E+00	specific transcriptional repressor activity	F
GO:0016567	100	4.26E-05	9.52E-03	7.56E-07	3.92E-03	4.04E-06	2.91E-03	1.31E-05	2.89E-03	7.19E-03	6.92E-01	1.25E-06	2.00E-03	5.58E-02	1.00E+00	2.74E-02	9.99E-01	protein ubiquitination	P
GO:0016568	192	9.52E-16	0.00E+00	5.37E-21	0.00E+00	1.16E-14	7.08E-04	2.19E-20	0.00E+00	5.20E-09	0.00E+00	2.41E-12	6.20E-04	6.54E-05	8.00E-03	5.76E-09	0.00E+00	chromatin modification	P
GO:0016569	55	1.49E-04	1.43E-02	6.69E-07	3.92E-03	2.66E-05	3.00E-03	6.85E-07	2.89E-03	1.08E-02	6.92E-01	4.02E-04	2.33E-02	6.59E-02	1.00E+00	5.93E-04	3.00E-02	covalent chromatin modification	P
GO:0016570	51	8.24E-04	8.86E-02	7.47E-06	4.51E-03	1.39E-04	1.16E-02	6.46E-06	2.89E-03	2.44E-02	1.00E+00	7.67E-04	4.48E-02	1.78E-01	1.00E+00	3.73E-03	1.27E-01	histone modification	P
GO:0016571	18	2.02E-04	1.72E-02	7.41E-07	3.92E-03	1.13E-04	1.16E-02	1.13E-05	2.89E-03	4.33E-03	2.13E-01	4.33E-04	2.33E-02	2.49E-02	8.38E-01	2.99E-03	1.27E-01	histone methylation	P
GO:0016573	12	1.50E-01	1.00E+00	2.92E-02	1.00E+00	8.82E-02	1.00E+00	5.00E-02	1.00E+00	5.66E-01	1.00E+00	6.95E-02	1.00E+00	6.55E-01	1.00E+00	4.45E-02	1.00E+00	histone acetylation	P
GO:0016575	12	1.12E-01	1.00E+00	1.29E-01	1.00E+00	9.74E-02	1.00E+00	1.10E-01	1.00E+00	2.47E-02	1.00E+00	1.80E-01	1.00E+00	6.30E-01	1.00E+00	3.69E-01	1.00E+00	histone deacetylation	P
GO:0016579	11	4.16E-01	1.00E+00	1.88E-01	1.00E+00	2.91E-01	1.00E+00	6.05E-03	2.88E-01	2.74E-01	1.00E+00	3.18E-01	1.00E+00	8.72E-01	1.00E+00	6.00E-01	1.00E+00	protein deubiquitination	P
GO:0016581	11	2.94E-02	1.00E+00	1.07E-05	4.51E-03	1.36E-02	6.53E-01	1.61E-05	9.57E-03	2.21E-01	1.00E+00	8.48E-03	5.03E-01	3.67E-02	8.38E-01	1.85E-03	7.90E-02	NuRD complex	C
GO:0016585	24	2.43E-03	2.12E-01	1.42E-04	1.50E-02	4.48E-02	1.00E+00	4.90E-05	1.07E-02	8.28E-03	6.92E-01	9.81E-03	5.03E-01	7.26E-03	2.75E-01	1.13E-02	4.76E-01	chromatin remodeling complex	C
GO:0016591	75	9.76E-06	7.00E-03	3.45E-04	4.40E-02	3.88E-07	2.00E-03	1.71E-04	1.30E-02	3.20E-03	2.13E-01	3.47E-03	1.51E-01	3.34E-02	8.38E-01	1.50E-01	1.00E+00	DNA-directed RNA polymerase II, holoenzy	C
GO:0016597	16	9.57E-01	1.00E+00	9.06E-01	1.00E+00	8.93E-01	1.00E+00	9.42E-01	1.00E+00	9.93E-01	1.00E+00	7.63E-01	1.00E+00	9.21E-01	1.00E+00	6.43E-01	1.00E+00	amino acid binding	F
GO:0016599	17	3.51E-02	1.00E+00	2.33E-02	1.00E+00	3.99E-02	1.00E+00	6.30E-03	3.33E-01	1.29E-01	1.00E+00	7.63E-02	1.00E+00	5.16E-02	1.00E+00	2.13E-01	1.00E+00	caveolar membrane	C
GO:0016601	19	6.19E-02	1.00E+00	8.43E-02	1.00E+00	3.49E-01	1.00E+00	4.30E-02	1.00E+00	1.19E-02	6.92E-01	1.09E-01	1.00E+00	1.39E-01	1.00E+00	7.41E-01	1.00E+00	Rac protein signal transduction	P
GO:0016604	125	7.51E-14	0.00E+00	4.70E-16	0.00E+00	8.73E-13	7.08E-04	8.84E-14	0.00E+00	7.00E-10	0.00E+00	5.21E-12	6.20E-04	1.02E-04	8.00E-03	1.01E-03	6.00E-02	nuclear body	C
GO:0016605	24	9.36E-05	1.43E-02	2.01E-05	7.00E-03	4.14E-04	4.00E-02	5.56E-04	4.20E-02	1.31E-03	1.20E-01	2.51E-05	5.87E-03	4.04E-02	1.00E+00	4.05E-02	1.00E+00	PML body	C
GO:0016607	84	2.51E-09	2.57E-03	8.55E-12	0.00E+00	7.80E-08	9.80E-04	1.83E-09	0.00E+00	3.98E-08	9.59E-04	2.48E-09	8.78E-04	1.36E-03	6.14E-02	2.69E-03	8.32E-02	nuclear speck	C
GO:0016614	149	3.75E-02	1.00E+00	3.38E-02	1.00E+00	1.01E-01	1.00E+00	9.47E-02	1.00E+00	2.08E-02	7.90E-01	3.69E-03	1.80E-01	2.30E-01	1.00E+00	2.72E-01	1.00E+00	oxidoreductase activity, acting on CH-OH g	F
GO:0016616	132	2.89E-02	1.00E+00	3.88E-02	1.00E+00	1.81E-01	1.00E+00	1.51E-01	1.00E+00	1.24E-02	6.92E-01	2.84E-03	1.44E-01	1.39E-01	1.00E+00	3.05E-01	1.00E+00	oxidoreductase activity, acting on the CH-O	F
GO:0016620	55	8.21E-01	1.00E+00	6.27E-01	1.00E+00	6.86E-01	1.00E+00	8.27E-01	1.00E+00	9.81E-01	1.00E+00	3.48E-01	1.00E+00	4.75E-01	1.00E+00	4.41E-01	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016627	92	6.15E-03	3.09E-01	6.54E-03	3.12E-01	1.43E-02	6.53E-01	2.77E-02	1.00E+00	1.38E-02	6.92E-01	3.48E-03	1.51E-01	7.87E-02	1.00E+00	1.69E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016628	59	1.10E-01	1.00E+00	3.53E-02	1.00E+00	1.59E-01	1.00E+00	1.01E-01	1.00E+00	2.30E-01	1.00E+00	1.67E-02	6.68E-01	1.03E-01	1.00E+00	2.07E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016634	10	3.33E-01	1.00E+00	4.26E-01	1.00E+00	5.55E-01	1.00E+00	5.18E-01	1.00E+00	2.53E-01	1.00E+00	2.49E-01	1.00E+00	1.85E-01	1.00E+00	7.94E-01	1.00E+00	oxidoreductase activity, acting on the CH-C	F
GO:0016638	22	2.57E-01	1.00E+00	6.19E-01	1.00E+00	4.71E-01	1.00E+00	6.49E-01	1.00E+00	2.06E-01	1.00E+00	2.37E-01	1.00E+00	2.41E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016641	20	4.20E-01	1.00E+00	7.81E-01	1.00E+00	6.69E-01	1.00E+00	8.17E-01	1.00E+00	2.90E-01	1.00E+00	2.43E-01	1.00E+00	3.92E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016645	26	4.83E-02	1.00E+00	5.39E-02	1.00E+00	1.87E-01	1.00E+00	4.28E-02	1.00E+00	8.88E-02	1.00E+00	4.94E-02	1.00E+00	1.01E-01	1.00E+00	2.97E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016646	16	6.12E-02	1.00E+00	1.08E-01	1.00E+00	1.19E-01	1.00E+00	2.58E-01	1.00E+00	8.91E-02	1.00E+00	5.49E-02	1.00E+00	1.34E-01	1.00E+00	2.40E-01	1.00E+00	oxidoreductase activity, acting on the CH-N	F
GO:0016651	69	1.36E-02	6.08E-01	1.76E-01	1.00E+00	3.67E-02	1.00E+00	4.29E-01	1.00E+00	1.04E-01	1.00E+00	9.61E-02	1.00E+00	2.89E-02	8.38E-01	3.32E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016655	44	1.21E-01	1.00E+00	4.90E-01	1.00E+00	1.94E-01	1.00E+00	6.40E-01	1.00E+00	2.04E-01	1.00E+00	3.30E-01	1.00E+00	2.67E-01	1.00E+00	5.26E-01	1.00E+00	oxidoreductase activity, acting on NADH or	F
GO:0016667	20	3.63E-03	2.12E-01	2.80E-02	1.00E+00	6.68E-03	4.69E-01	6.32E-02	1.00E+00	7.46E-02	1.00E+00	3.51E-02	1.00E+00	2.89E-02	8.38E-01	3.48E-01	1.00E+00	oxidoreductase activity, acting on sulfur gro	F
GO:0016675	30	1.65E-01	1.00E+00	2.39E-01	1.00E+00	8.87E-02	1.00E+00	5.95E-02	1.00E+00	2.03E-01	1.00E+00	2.69E-01	1.00E+00	5.78E-01	1.00E+00	6.57E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016676	30	1.65E-01	1.00E+00	2.39E-01	1.00E+00	8.87E-02	1.00E+00	5.95E-02	1.00E+00	2.03E-01	1.00E+00	2.69E-01	1.00E+00	5.78E-01	1.00E+00	6.57E-01	1.00E+00	oxidoreductase activity, acting on heme gro	F
GO:0016679	13	5.88E-02	1.00E+00	1.81E-01	1.00E+00	3.40E-01	1.00E+00	1.97E-01	1.00E+00	1.24E-01	1.00E+00	2.69E-01	1.00E+00	2.50E-02	8.38E-01	2.37E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F
GO:0016681	13	5.88E-02	1.00E+00	1.81E-01	1.00E+00	3.40E-01	1.00E+00	1.97E-01	1.00E+00	1.24E-01	1.00E+00	2.69E-01	1.00E+00	2.50E-02	8.38E-01	2.37E-01	1.00E+00	oxidoreductase activity, acting on diphenols	F

GO:0016684	50	3.52E-02	1.00E+00	1.16E-01	1.00E+00	7.08E-02	1.00E+00	1.02E-01	1.00E+00	1.92E-01	1.00E+00	2.13E-01	1.00E+00	1.59E-02	4.88E-01	2.48E-01	1.00E+00	oxidoreductase activity, acting on peroxide a	F
GO:0016701	62	1.24E-01	1.00E+00	7.05E-04	5.90E-02	1.08E-01	1.00E+00	2.16E-03	1.39E-01	2.71E-01	1.00E+00	1.08E-02	5.03E-01	3.28E-01	1.00E+00	6.14E-02	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016702	61	1.97E-01	1.00E+00	1.02E-03	9.65E-02	1.65E-01	1.00E+00	2.51E-03	1.39E-01	3.98E-01	1.00E+00	1.82E-02	6.68E-01	3.57E-01	1.00E+00	5.40E-02	1.00E+00	oxidoreductase activity, acting on single dor	F
GO:0016705	168	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.93E-01	1.00E+00	9.30E-01	1.00E+00	9.89E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016706	24	2.83E-01	1.00E+00	1.45E-02	6.07E-01	2.00E-01	1.00E+00	6.74E-02	1.00E+00	7.68E-01	1.00E+00	2.70E-03	1.44E-01	2.18E-01	1.00E+00	1.47E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016709	35	8.37E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.46E-01	1.00E+00	3.75E-01	1.00E+00	9.99E-01	1.00E+00	9.07E-01	1.00E+00	9.87E-01	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016712	71	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	oxidoreductase activity, acting on paired do	F
GO:0016740	1983	2.27E-20	0.00E+00	1.78E-36	0.00E+00	7.12E-21	0.00E+00	1.16E-26	0.00E+00	1.04E-13	0.00E+00	7.84E-24	0.00E+00	1.19E-04	8.00E-03	1.58E-16	0.00E+00	transferase activity	F
GO:0016741	202	3.40E-05	7.00E-03	6.22E-05	7.00E-03	1.63E-05	3.00E-03	4.07E-05	9.57E-03	6.62E-04	1.20E-01	8.74E-05	1.10E-02	8.58E-02	1.00E+00	2.18E-01	1.00E+00	transferase activity, transferring one-carbon	F
GO:0016746	209	5.71E-06	3.62E-03	9.10E-08	3.92E-03	2.49E-05	3.00E-03	1.35E-05	2.89E-03	1.16E-04	2.70E-02	4.47E-06	2.90E-03	3.54E-02	8.38E-01	2.04E-03	7.90E-02	transferase activity, transferring acyl groups	F
GO:0016747	194	3.20E-06	3.02E-03	3.57E-07	3.92E-03	2.07E-05	3.00E-03	2.84E-05	9.57E-03	6.37E-05	2.40E-02	1.69E-05	5.87E-03	2.55E-02	8.38E-01	3.89E-03	1.34E-01	transferase activity, transferring groups othe	F
GO:0016755	22	5.08E-01	1.00E+00	1.52E-01	1.00E+00	3.84E-01	1.00E+00	2.98E-01	1.00E+00	5.54E-01	1.00E+00	2.45E-02	1.00E+00	6.96E-01	1.00E+00	6.85E-01	1.00E+00	transferase activity, transferring amino-acyl	F
GO:0016757	248	1.01E-01	1.00E+00	2.83E-02	1.00E+00	1.59E-01	1.00E+00	1.48E-01	1.00E+00	1.27E-01	1.00E+00	2.93E-02	1.00E+00	2.80E-01	1.00E+00	3.70E-02	1.00E+00	transferase activity, transferring glycosyl gro	F
GO:0016758	164	4.50E-01	1.00E+00	3.19E-01	1.00E+00	4.72E-01	1.00E+00	4.67E-01	1.00E+00	3.62E-01	1.00E+00	1.85E-01	1.00E+00	6.07E-01	1.00E+00	3.48E-01	1.00E+00	transferase activity, transferring hexosyl gro	F
GO:0016763	47	1.34E-03	8.86E-02	3.18E-03	1.88E-01	1.48E-02	6.53E-01	7.07E-03	4.92E-01	8.15E-04	1.20E-01	2.53E-02	1.00E+00	1.41E-01	1.00E+00	2.52E-02	9.99E-01	transferase activity, transferring pentosyl gr	F
GO:0016765	61	2.12E-01	1.00E+00	2.96E-01	1.00E+00	1.61E-01	1.00E+00	5.51E-01	1.00E+00	1.96E-01	1.00E+00	5.56E-02	1.00E+00	7.05E-01	1.00E+00	7.70E-01	1.00E+00	transferase activity, transferring alkyl or aryl	F
GO:0016769	34	1.11E-01	1.00E+00	9.39E-03	4.69E-01	1.89E-01	1.00E+00	5.91E-02	1.00E+00	2.32E-01	1.00E+00	6.47E-03	4.21E-01	2.06E-01	1.00E+00	3.03E-02	9.99E-01	transferase activity, transferring nitrogenous	F
GO:0016772	1136	8.54E-15	0.00E+00	4.77E-29	0.00E+00	9.11E-17	0.00E+00	7.39E-23	0.00E+00	3.62E-09	0.00E+00	8.21E-16	0.00E+00	7.48E-04	3.44E-02	6.86E-15	0.00E+00	transferase activity, transferring phosphorus	F
GO:0016773	836	1.11E-07	2.57E-03	3.03E-17	0.00E+00	6.90E-08	9.80E-04	9.83E-13	0.00E+00	4.11E-05	6.33E-03	1.07E-09	6.20E-04	7.31E-03	2.75E-01	8.99E-11	0.00E+00	phosphotransferase activity, alcohol group a	F
GO:0016775	34	6.15E-01	1.00E+00	3.91E-01	1.00E+00	7.20E-01	1.00E+00	4.38E-01	1.00E+00	5.10E-01	1.00E+00	7.36E-01	1.00E+00	6.35E-01	1.00E+00	1.15E-01	1.00E+00	phosphotransferase activity, nitrogenous gr	F
GO:0016776	34	9.48E-03	6.08E-01	9.65E-05	1.50E-02	3.22E-02	1.00E+00	1.55E-03	9.60E-02	8.55E-03	6.92E-01	6.18E-04	3.20E-02	1.58E-01	1.00E+00	1.61E-02	6.56E-01	phosphotransferase activity, phosphate gro	F
GO:0016779	120	1.63E-05	7.00E-03	2.14E-04	2.40E-02	8.84E-08	2.00E-03	1.70E-05	9.57E-03	1.30E-03	1.20E-01	5.28E-02	1.00E+00	4.51E-02	1.00E+00	1.26E-02	4.76E-01	nucleotidyltransferase activity	F
GO:0016780	18	2.07E-01	1.00E+00	1.23E-01	1.00E+00	8.57E-02	1.00E+00	6.26E-02	1.00E+00	3.28E-01	1.00E+00	6.08E-01	1.00E+00	7.60E-01	1.00E+00	5.12E-01	1.00E+00	phosphotransferase activity, for other substi	F
GO:0016782	63	1.00E+00	1.00E+00	7.96E-01	1.00E+00	1.00E+00	1.00E+00	7.09E-01	1.00E+00	9.96E-01	1.00E+00	7.55E-01	1.00E+00	1.00E+00	1.00E+00	6.86E-01	1.00E+00	transferase activity, transferring sulfur-conta	F
GO:0016787	2528	2.54E-15	0.00E+00	1.04E-22	0.00E+00	2.32E-12	7.08E-04	8.94E-16	0.00E+00	3.01E-11	0.00E+00	2.74E-14	6.20E-04	1.38E-05	3.63E-03	8.29E-14	0.00E+00	hydrolase activity	F
GO:0016788	691	6.59E-07	2.76E-03	1.43E-12	0.00E+00	1.75E-05	3.00E-03	8.89E-09	8.93E-04	3.60E-05	6.33E-03	3.73E-06	2.90E-03	8.14E-03	2.75E-01	2.09E-09	0.00E+00	hydrolase activity, acting on ester bonds	F
GO:0016789	132	3.69E-01	1.00E+00	1.30E-01	1.00E+00	5.33E-01	1.00E+00	5.54E-01	1.00E+00	2.94E-01	1.00E+00	3.57E-01	1.00E+00	5.28E-01	1.00E+00	2.61E-02	9.99E-01	carboxylic ester hydrolase activity	F
GO:0016790	99	1.56E-01	1.00E+00	1.78E-04	1.80E-02	2.89E-02	1.00E+00	9.05E-05	1.30E-02	2.64E-01	1.00E+00	5.89E-03	4.21E-01	8.31E-01	1.00E+00	5.24E-03	2.01E-01	thiolester hydrolase activity	F
GO:0016791	255	3.38E-06	3.02E-03	8.17E-09	8.90E-04	5.60E-05	9.82E-03	1.24E-06	2.89E-03	2.60E-03	1.29E-01	7.45E-05	1.10E-02	5.02E-05	8.00E-03	2.27E-05	7.00E-03	phosphoric monoester hydrolase activity	F
GO:0016796	21	3.12E-01	1.00E+00	4.93E-02	1.00E+00	2.12E-01	1.00E+00	1.00E-01	1.00E+00	3.29E-01	1.00E+00	5.27E-02	1.00E+00	8.94E-01	1.00E+00	1.89E-01	1.00E+00	exonuclease activity, active with either ribo-	F
GO:0016798	139	2.89E-02	1.00E+00	2.28E-01	1.00E+00	7.77E-03	6.41E-01	5.70E-01	1.00E+00	2.53E-02	1.00E+00	8.00E-02	1.00E+00	4.03E-01	1.00E+00	3.32E-01	1.00E+00	hydrolase activity, acting on glycosyl bonds	F
GO:0016799	19	2.78E-01	1.00E+00	6.73E-01	1.00E+00	1.17E-01	1.00E+00	5.09E-01	1.00E+00	7.27E-01	1.00E+00	9.18E-01	1.00E+00	4.01E-01	1.00E+00	1.83E-01	1.00E+00	hydrolase activity, hydrolyzing N-glycosyl cc	F
GO:0016805	15	1.71E-01	1.00E+00	1.53E-01	1.00E+00	7.84E-02	1.00E+00	8.19E-02	1.00E+00	5.58E-01	1.00E+00	3.83E-01	1.00E+00	1.82E-01	1.00E+00	4.57E-01	1.00E+00	dipeptidase activity	F
GO:0016806	12	2.15E-01	1.00E+00	2.55E-01	1.00E+00	2.10E-01	1.00E+00	1.91E-01	1.00E+00	5.28E-01	1.00E+00	2.43E-01	1.00E+00	1.12E-01	1.00E+00	4.24E-01	1.00E+00	dipeptidyl-peptidase and tripeptidyl-peptida	F
GO:0016810	112	2.42E-04	1.90E-02	1.26E-02	6.07E-01	2.74E-03	1.35E-01	1.21E-02	6.47E-01	7.33E-03	6.92E-01	1.27E-01	1.00E+00	6.03E-04	3.44E-02	3.53E-02	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016811	54	4.44E-03	2.14E-01	3.40E-03	1.88E-01	4.22E-03	2.20E-01	1.95E-03	1.39E-01	3.10E-02	1.00E+00	1.46E-01	1.00E+00	5.29E-02	1.00E+00	5.62E-02	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016812	10	3.68E-01	1.00E+00	6.55E-01	1.00E+00	6.53E-01	1.00E+00	6.38E-01	1.00E+00	1.67E-01	1.00E+00	7.61E-01	1.00E+00	3.71E-01	1.00E+00	1.35E-01	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016813	14	5.22E-02	1.00E+00	7.20E-01	1.00E+00	2.27E-01	1.00E+00	8.08E-01	1.00E+00	1.29E-01	1.00E+00	5.29E-01	1.00E+00	1.74E-02	4.88E-01	6.87E-01	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016814	25	4.54E-02	1.00E+00	2.56E-02	1.00E+00	7.31E-02	1.00E+00	2.92E-02	1.00E+00	9.83E-02	1.00E+00	1.16E-01	1.00E+00	5.30E-02	1.00E+00	2.44E-02	9.99E-01	hydrolase activity, acting on carbon-nitroger	F
GO:0016817	760	3.67E-11	2.57E-03	2.23E-15	0.00E+00	8.01E-10	7.95E-04	5.87E-12	0.00E+00	2.12E-08	9.59E-04	3.75E-11	6.20E-04	1.21E-03	6.14E-02	1.45E-06	2.00E-03	hydrolase activity, acting on acid anhydrides	F
GO:0016818	759	3.71E-11	2.57E-03	3.33E-15	0.00E+00	9.51E-10	7.95E-04	8.08E-12	0.00E+00	2.01E-08	9.59E-04	5.64E-11	6.20E-04	1.21E-03	6.14E-02	1.57E-06	2.00E-03	hydrolase activity, acting on acid anhydrides	F
GO:0016820	137	2.12E-01	1.00E+00	3.50E-02	1.00E+00	2.29E-01	1.00E+00	2.09E-01	1.00E+00	4.95E-01	1.00E+00	1.24E-02	5.03E-01	3.66E-01	1.00E+00	2.28E-01	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016829	166	5.56E-03	3.09E-01	1.79E-03	9.65E-02	3.12E-02	1.00E+00	5.38E-02	1.00E+00	5.76E-03	3.75E-01	3.67E-03	1.80E-01	2.54E-01	1.00E+00	9.01E-03	4.28E-01	lyase activity	F
GO:0016830	47	3.55E-03	2.12E-01	5.34E-04	4.74E-02	1.00E-02	6.53E-01	1.01E-02	5.72E-01	3.93E-03	2.13E-01	1.02E-02	5.03E-01	4.17E-01	1.00E+00	6.49E-03	4.28E-01	carbon-carbon lyase activity	F
GO:0016831	33	2.39E-02	1.00E+00	2.57E-03	1.80E-01	1.73E-02	1.00E+00	8.07E-03	4.92E-01	3.32E-02	1.00E+00	4.43E-02	1.00E+00	7.97E-01	1.00E+00	1.19E-02	4.76E-01	carboxy-lyase activity	F
GO:0016835	59	1.44E-01	1.00E+00	3.36E-01	1.00E+00	1.94E-01	1.00E+00	7.61E-01	1.00E+00	1.60E-01	1.00E+00	1.50E-01	1.00E+00	4.54E-01	1.00E+00	4.56E-01	1.00E+00	carbon-oxygen lyase activity	F
GO:0016836	49	1.69E-01	1.00E+00	2.02E-01	1.00E+00	2.96E-01	1.00E+00	5.63E-01	1.00E+00	1.28E-01	1.00E+00	7.02E-02	1.00E+00	4.29E-01	1.00E+00	3.45E-01	1.00E+00	hydro-lyase activity	F
GO:0016846	15	6.99E-02	1.00E+00	1.70E-01	1.00E+00	4.35E-02	1.00E+00	2.45E-01	1.00E+00	1.50E-01	1.00E+00	9.64E-02	1.00E+00	2.81E-01	1.00E+00	5.02E-01	1.00E+00	carbon-sulfur lyase activity	F
GO:0016849	23	4.75E-01	1.00E+00	5.09E-01	1.00E+00	9.37E-01	1.00E+00	5.98E-01	1.00E+00	2.77E-01	1.00E+00	7.68E-01	1.00E+00	1.63E-01	1.00E+00	1.84E-01	1.00E+00	phosphorus-oxygen lyase activity	F
GO:0016853	187	3.53E-04	3.10E-02	5.45E-05	7.00E-03	7.65E-04	4.90E-02	5.07E-05	1.07E-02	6.02E-03	3.75E-01	9.04E-03	5.03E-01	3.36E-02	8.38E-01	2.97E-03	1.27E-01	isomerase activity	F
GO:0016854	15	2.25E-01	1.00E+00	4.00E-01	1.00E+00	2.78E-01	1.00E+00	2.80E-01	1.00E+00	8.43E-02	1.00E+00	5.77E-01	1.00E+00	4.26E-01	1.00E+00	5.55E-01	1.00E+00	racemase and epimerase activity	F
GO:0016859	39	1.00E-04	1.43E-02	7.84E-03	4.16E-01	8.42E-03	6.53E-01	4.52E-03	2.88E-01	5.34E-04	4.90E-02	1.68E-01	1.00E+00	7.29E-04	3.44E-02	7.18E-02	1.00E+00	cis-trans isomerase activity	F
GO:0016860	41	4.14E-01	1.00E+00	3.31E-02	1.00E+00	9.62E-02	1.00E+00	2.10E-02	9.37E-01	8.10E-01	1.00E+00	1.39E-01	1.00E+00	6.93E-01	1.00E+00	2.86E-02	9.99E-01	intramolecular oxidoreductase activity	F
GO:0016863	14	9.16E-01	1.00E+00	8.28E-01	1.00E+00	6.59E-01	1.00E+00	7.66E-01	1.00E+00	9.33E-01	1.00E+00	8.26E-01	1.00E+00	9.98E-01	1.00E+00	5.91E-01	1.00E+00	intramolecular oxidoreductase activity, trans	F
GO:0016866	47	1.82E-01	1.00E+00	2.06E-02	1.00E+00	2.78E-01	1.00E+00	8.15E-02	1.00E+00	3.93E-01	1.00E+00	4.25E-02	1.00E+00	1.08E-01	1.00E+00	8.83E-02	1.00E+00	intramolecular transferase activity	F
GO:0016868	10	2.39E-01	1.00E+00	1.99E-02	1.00E+00	3.75E-01	1.00E+00	3.03E-02	1.00E+00	2.82E-01	1.00E+00	6.28E-03	4.21E-01	2.56E-01	1.00E+00	5.31E-01	1.00E+00	intramolecular transferase activity, phospho	F
GO:0016874	424	2.39E-12	0.00E+00	2.08E-19	0.00E+00	1.51E-11	7.08E-04	4.38E-17	0.00E+00	1.29E-08	0.00E+00	3.34E-12	6.20E-04	4.92E-04	3.44E-02	8.51E-07	2.00E-03	ligase activity	F
GO:0016875	70	1.01E-05	7.00E-03	7.63E-05	1.50E-02	1.64E-04	1.16E-02	6.87E-05	1.30E-02	1.08E-04	2.70E-02	2.03E-04	2.33E-02	2.53E-02	8.38E-01	1.20E-01	1.00E+00	ligase activity, forming carbon-oxygen bond	F
GO:0016876	70	1.01E-05	7.00E-03	7.63E-05	1.50E-02	1.64E-04	1.16E-02	6.87E-05	1.30E-02	1.08E-04	2.70E-02	2.03E-04	2.33E-02	2.53E-02	8.38E-01	1.20E-01	1.00E+00	ligase activity, forming aminoacyl-tRNA and	F
GO:0016877	27	1.96E-01	1.00E+00	5.66E-02	1.00E+00	3.94E-01	1.00E+00	1.22E-01	1.00E+00	5.15E-01	1.00E+00	2.71E-01	1.00E+00	1.32E-02	4.78E-01	4.91E-02	1.00E+00	ligase activity, forming carbon-sulfur bonds	F
GO:0016878	15	5.05E-01	1.00E+00	1.89E-01	1.00E+00	6.80E-01	1.00E+00	2.83E-01	1.00E+00	6.32E-01	1.00E+00	2.28E-01	1.00E+00	1.68E-01	1.00E+00	2.20E-01	1.00E+00	acid-thiol ligase activity	F
GO:0016879	241	7.16E-08	2.57E-03	1.04E-11	0.00E+00	5.28E-08	9.80E-04	1.05E-10	0.00E+00	4.02E-05	6.33E-03	3.82E-07	1.65E-03	4.06E-03	2.23E-01	8.33E-05	1.60E-02	ligase activity, forming carbon-nitrogen bonc	F
GO:0016881	200	6.42E-08	2.57E-03	4.25E-12	0.00E+00	4.81E-08	9.80E-04	2.39E-11	0.00E+00	1.70E-05	5.37E-03	1.10E-08	8.78E-04	6.56E-03	2.75E-01	6.14E-04	3.00E-02	acid-amino acid ligase activity	F
GO:0016884	11	2.35E-01	1.00E+00	3.66E-01	1.00E+00	1.44E-01	1.00E+00	1.98E-01	1.00E+00	3.40E-01	1.00E+00	9.97E-01	1.00E+00	5.52E-01	1.00E+00	1.60E-01	1.00E+00	carbon-nitrogen ligase activity, with glutamir	F
GO:0016887	363	3.27E-05	7.00E-03	8.04E-08	3.92E-03	2.13E-05	3.00E-03	8.73E-07	2.89E-03	2.10E-03	1.20E-01	3.25E-06	2.90E-03	1.37E-01	1.00E+00	9.09E-03	4.28E-01	ATPase activity	F
GO:0016891	21	3.24E-02	1.00E+00	9.97E-03	4.69E-01	1.46E-01	1.00E+00	1.62E-01	1.00E+00	8.54E-02	1.00E+00	6.35E-02	1.00E+00	8.01E-02	1.00E+00	3.39E-03	1.27E-01	endoribonuclease activity, producing 5'-pho	F
GO:0016892	24	9.71E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.13E-01	1.00E+00	5.13E-01	1.00E+00	9.39E-01	1.00E+00	9.96E-01	1.00E+00	endoribonuclease activity, producing 3'-pho	F
GO:0016893	27	3.66E-02	1.00E+00	1.34E-02	6.07E-01	2.21E-01	1.00E+00	1.01E-01	1.00E+00	1.49E-01	1.00E+00	6.26E-02	1.00E+00	2.66E-02	8.38E-01	1.80E-02	6.56E-01	endonuclease activity, active with either ribo	F
GO:0016894	26	8.05E-01	1.00E+00	9.95E-01	1.00E+00	9.34E-01	1.00E+00	9.99E-01	1.00E+00	4.74E-01	1.00E+00	4.75E-01	1.00E+00	8.43E-01	1.00E+00	9.83E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016896	13	1.10E-01	1.00E+00	8.64E-02	1.00E+00	5.42E-02	1.00E+00	2.49E-01	1.00E+00	2.50E-01	1.00E+00	2.71E-02	1.00E+00	5.10E-01	1.00E+00	1.93E-01	1.00E+00	exoribonuclease activity, producing 5'-phos	F
GO:0016903	65	8.32E-01	1.00E+00	7.08E-01	1.00E+00	6.92E-01	1.00E+00	8.49E-01	1.00E+00	9.48E-01	1.00E+00	5.19E-01	1.00E+00	5.86E-01	1.00E+00	5.25E-01	1.00E+00	oxidoreductase activity, acting on the aldeh	F
GO:0016917	78	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	GABA receptor activity	F
GO:0016918	11	5.90E-01	1.00E+00	2.93E-01	1.00E+00	6.73E-01	1.00E+00	3.31E-01	1.00E+00	7.74E-01	1.00E+00	4.55E-01	1.00E+00	3.61E-01	1.00E+00	1.36E-01	1.00E+00	retinal binding	F
GO:0016986	22	2.46E-01	1.00E+00	1.98E-01	1.00E+00	1.11E-01	1.00E+00	5.16E-02	1.00E+00	5.34E-01	1.00E+00	3.57E-01	1.00E+00	2.06E-01	1.00E+00	4.89E-01	1.00E+00	transcription initiation factor activity	F
GO:0016998	17	7.97E-01	1.00E+00	4.51E-01	1.00E+00	9.10E-01	1.00E+00	8.01E-01	1.00E+00	4.31E-01	1.00E+00	1.17E-01	1.00E+00	9.52E-01	1.00E+00	8.53E-01	1.00E+00	cell wall catabolism	P

GO:0017004	20	8.31E-01	1.00E+00	5.54E-01	1.00E+00	7.06E-01	1.00E+00	4.36E-01	1.00E+00	8.85E-01	1.00E+00	4.21E-01	1.00E+00	8.94E-01	1.00E+00	9.38E-01	1.00E+00	cytochrome complex assembly	P
GO:0017015	26	8.46E-02	1.00E+00	1.71E-01	1.00E+00	2.25E-01	1.00E+00	2.16E-01	1.00E+00	8.59E-02	1.00E+00	4.18E-01	1.00E+00	1.30E-01	1.00E+00	6.97E-02	1.00E+00	regulation of transforming growth factor beta	P
GO:0017016	58	1.00E-01	1.00E+00	1.49E-03	9.65E-02	4.62E-01	1.00E+00	1.47E-02	6.47E-01	2.25E-01	1.00E+00	1.94E-02	7.56E-01	3.40E-02	8.38E-01	1.45E-03	6.00E-02	Ras GTPase binding	F
GO:0017017	13	9.55E-01	1.00E+00	7.55E-01	1.00E+00	6.48E-01	1.00E+00	9.59E-01	1.00E+00	9.99E-01	1.00E+00	6.71E-01	1.00E+00	4.90E-01	1.00E+00	5.91E-01	1.00E+00	MAP kinase phosphatase activity	F
GO:0017022	17	5.73E-01	1.00E+00	5.64E-02	1.00E+00	8.20E-01	1.00E+00	6.78E-02	1.00E+00	6.32E-01	1.00E+00	5.82E-02	1.00E+00	2.19E-01	1.00E+00	2.44E-01	1.00E+00	myosin binding	F
GO:0017038	100	2.73E-06	3.02E-03	3.13E-08	9.59E-04	3.63E-05	9.82E-03	2.62E-06	2.89E-03	1.65E-04	4.90E-02	8.64E-04	4.48E-02	5.51E-03	2.23E-01	3.22E-05	7.00E-03	protein import	P
GO:0017046	12	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.64E-01	1.00E+00	2.57E-01	1.00E+00	peptide hormone binding	F
GO:0017048	24	5.48E-02	1.00E+00	8.81E-03	4.69E-01	5.50E-01	1.00E+00	6.31E-02	1.00E+00	2.84E-02	1.00E+00	4.26E-02	1.00E+00	2.35E-01	1.00E+00	1.89E-02	7.36E-01	Rho GTPase binding	F
GO:0017053	10	3.78E-01	1.00E+00	4.29E-01	1.00E+00	4.91E-01	1.00E+00	6.17E-01	1.00E+00	3.53E-01	1.00E+00	4.95E-01	1.00E+00	5.75E-01	1.00E+00	2.68E-01	1.00E+00	transcriptional repressor complex	C
GO:0017076	1987	9.76E-30	0.00E+00	2.80E-45	0.00E+00	1.98E-27	0.00E+00	5.65E-33	0.00E+00	8.23E-18	0.00E+00	8.08E-31	0.00E+00	5.41E-09	0.00E+00	2.10E-19	0.00E+00	purine nucleotide binding	F
GO:0017110	10	3.79E-02	1.00E+00	1.15E-02	6.07E-01	1.65E-01	1.00E+00	2.06E-02	9.37E-01	8.53E-03	6.92E-01	9.68E-02	1.00E+00	1.12E-01	1.00E+00	2.95E-01	1.00E+00	nucleoside-diphosphatase activity	F
GO:0017111	725	6.84E-11	2.57E-03	5.76E-15	0.00E+00	5.25E-10	7.95E-04	1.93E-11	0.00E+00	4.77E-08	9.59E-04	2.30E-11	6.20E-04	1.96E-03	8.40E-02	4.35E-06	2.91E-03	nucleoside-triphosphatase activity	F
GO:0017124	26	1.72E-01	1.00E+00	2.25E-01	1.00E+00	2.48E-01	1.00E+00	6.95E-02	1.00E+00	4.97E-01	1.00E+00	9.26E-01	1.00E+00	2.03E-01	1.00E+00	2.37E-01	1.00E+00	SH3 domain binding	F
GO:0017127	10	4.40E-01	1.00E+00	9.05E-01	1.00E+00	6.69E-01	1.00E+00	8.67E-01	1.00E+00	1.54E-01	1.00E+00	9.42E-01	1.00E+00	6.94E-01	1.00E+00	6.67E-01	1.00E+00	cholesterol transporter activity	F
GO:0017137	22	5.21E-01	1.00E+00	1.82E-02	1.00E+00	6.35E-01	1.00E+00	1.71E-01	1.00E+00	8.18E-01	1.00E+00	2.40E-02	1.00E+00	7.32E-02	1.00E+00	6.31E-03	4.28E-01	Rab GTPase binding	F
GO:0017144	12	4.63E-01	1.00E+00	9.55E-01	1.00E+00	8.54E-01	1.00E+00	9.74E-01	1.00E+00	4.04E-01	1.00E+00	9.88E-01	1.00E+00	2.46E-01	1.00E+00	3.82E-02	1.00E+00	drug metabolism	P
GO:0017145	10	4.16E-01	1.00E+00	3.43E-01	1.00E+00	2.31E-01	1.00E+00	6.85E-01	1.00E+00	4.37E-01	1.00E+00	9.47E-02	1.00E+00	8.02E-01	1.00E+00	6.02E-01	1.00E+00	stem cell division	P
GO:0017148	38	6.76E-04	8.86E-02	3.49E-04	4.40E-02	1.56E-03	9.50E-02	2.14E-02	9.37E-01	3.97E-02	1.00E+00	6.02E-03	4.21E-01	4.72E-03	2.23E-01	9.32E-03	4.28E-01	negative regulation of protein biosynthesis	P
GO:0017153	67	8.15E-01	1.00E+00	6.31E-01	1.00E+00	9.16E-01	1.00E+00	8.87E-01	1.00E+00	8.21E-01	1.00E+00	5.31E-01	1.00E+00	5.29E-01	1.00E+00	3.38E-01	1.00E+00	sodium:dicarboxylate symporter activity	F
GO:0017156	23	1.88E-01	1.00E+00	1.95E-01	1.00E+00	3.15E-01	1.00E+00	3.66E-01	1.00E+00	4.33E-01	1.00E+00	2.05E-01	1.00E+00	2.98E-02	8.38E-01	1.88E-01	1.00E+00	calcium ion-dependent exocytosis	P
GO:0017157	23	2.03E-01	1.00E+00	5.88E-03	3.08E-01	2.23E-01	1.00E+00	1.23E-02	6.47E-01	4.47E-01	1.00E+00	3.61E-02	1.00E+00	1.20E-01	1.00E+00	6.03E-02	1.00E+00	regulation of exocytosis	P
GO:0018024	24	1.25E-04	1.43E-02	4.96E-08	9.59E-04	3.42E-05	9.82E-03	3.87E-06	2.89E-03	3.71E-03	2.13E-01	1.03E-04	1.10E-02	9.39E-02	1.00E+00	6.99E-05	7.00E-03	histone-lysine N-methyltransferase activity	F
GO:0018105	18	1.14E-01	1.00E+00	1.41E-01	1.00E+00	1.21E-01	1.00E+00	1.53E-01	1.00E+00	2.34E-01	1.00E+00	7.72E-02	1.00E+00	1.02E-01	1.00E+00	3.36E-01	1.00E+00	peptidyl-serine phosphorylation	P
GO:0018107	10	3.80E-01	1.00E+00	3.42E-01	1.00E+00	4.87E-01	1.00E+00	4.75E-01	1.00E+00	4.04E-01	1.00E+00	2.76E-01	1.00E+00	2.15E-01	1.00E+00	4.12E-01	1.00E+00	peptidyl-threonine phosphorylation	P
GO:0018108	75	7.96E-01	1.00E+00	1.25E-02	6.07E-01	7.43E-01	1.00E+00	2.28E-01	1.00E+00	7.78E-01	1.00E+00	8.06E-02	1.00E+00	6.02E-01	1.00E+00	5.20E-04	3.00E-02	peptidyl-tyrosine phosphorylation	P
GO:0018149	14	9.97E-01	1.00E+00	5.22E-01	1.00E+00	1.00E+00	1.00E+00	8.27E-01	1.00E+00	8.48E-01	1.00E+00	1.29E-01	1.00E+00	9.94E-01	1.00E+00	8.54E-01	1.00E+00	peptide cross-linking	P
GO:0018193	147	1.05E-02	6.08E-01	1.54E-06	3.92E-03	3.70E-02	1.00E+00	2.88E-04	4.20E-02	3.14E-02	1.00E+00	5.91E-04	3.20E-02	2.51E-02	8.38E-01	1.09E-06	2.00E-03	peptidyl-amino acid modification	P
GO:0018195	10	6.69E-03	3.15E-01	2.99E-01	1.00E+00	1.56E-01	1.00E+00	3.42E-01	1.00E+00	2.70E-02	1.00E+00	5.20E-01	1.00E+00	7.87E-03	2.75E-01	1.14E-01	1.00E+00	peptidyl-arginine modification	P
GO:0018209	21	1.96E-01	1.00E+00	1.07E-01	1.00E+00	2.03E-01	1.00E+00	1.98E-01	1.00E+00	3.75E-01	1.00E+00	1.59E-01	1.00E+00	1.11E-01	1.00E+00	1.28E-01	1.00E+00	peptidyl-serine modification	P
GO:0018210	13	5.82E-01	1.00E+00	2.53E-01	1.00E+00	6.68E-01	1.00E+00	5.63E-01	1.00E+00	5.92E-01	1.00E+00	4.80E-01	1.00E+00	2.45E-01	1.00E+00	1.39E-01	1.00E+00	peptidyl-threonine modification	P
GO:0018212	75	7.96E-01	1.00E+00	1.25E-02	6.07E-01	7.43E-01	1.00E+00	2.28E-01	1.00E+00	7.78E-01	1.00E+00	8.06E-02	1.00E+00	6.02E-01	1.00E+00	5.20E-04	3.00E-02	peptidyl-tyrosine modification	P
GO:0018298	15	7.91E-01	1.00E+00	6.82E-01	1.00E+00	6.52E-01	1.00E+00	9.89E-01	1.00E+00	9.91E-01	1.00E+00	3.08E-01	1.00E+00	2.38E-01	1.00E+00	5.00E-01	1.00E+00	protein-chromophore linkage	P
GO:0018342	10	8.44E-01	1.00E+00	6.17E-01	1.00E+00	8.66E-01	1.00E+00	4.66E-01	1.00E+00	4.73E-01	1.00E+00	7.63E-01	1.00E+00	1.00E+00	1.00E+00	6.33E-01	1.00E+00	protein prenylation	P
GO:0018958	83	6.31E-01	1.00E+00	1.86E-01	1.00E+00	5.60E-01	1.00E+00	4.54E-01	1.00E+00	5.30E-01	1.00E+00	8.49E-02	1.00E+00	7.40E-01	1.00E+00	2.21E-01	1.00E+00	phenol metabolism	P
GO:0019001	388	9.97E-07	2.76E-03	8.67E-09	8.90E-04	6.12E-05	9.82E-03	1.11E-06	2.89E-03	3.10E-06	1.69E-03	3.91E-07	1.65E-03	3.95E-03	2.23E-01	6.12E-04	3.00E-02	guanyl nucleotide binding	F
GO:0019012	18	2.90E-01	1.00E+00	9.58E-02	1.00E+00	2.03E-01	1.00E+00	5.07E-02	1.00E+00	3.48E-01	1.00E+00	9.68E-02	1.00E+00	3.01E-01	1.00E+00	6.22E-01	1.00E+00	virion	C
GO:0019028	17	2.58E-01	1.00E+00	8.48E-02	1.00E+00	1.88E-01	1.00E+00	4.56E-02	1.00E+00	3.04E-01	1.00E+00	8.55E-02	1.00E+00	3.06E-01	1.00E+00	5.84E-01	1.00E+00	viral capsid	C
GO:0019048	11	2.42E-01	1.00E+00	3.48E-01	1.00E+00	3.93E-01	1.00E+00	6.69E-01	1.00E+00	4.93E-01	1.00E+00	3.91E-01	1.00E+00	1.35E-01	1.00E+00	2.49E-01	1.00E+00	virus-host interaction	P
GO:0019058	18	3.99E-01	1.00E+00	5.78E-02	1.00E+00	7.56E-01	1.00E+00	2.38E-01	1.00E+00	6.08E-01	1.00E+00	1.99E-01	1.00E+00	7.31E-02	1.00E+00	8.42E-02	1.00E+00	viral infectious cycle	P
GO:0019098	19	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	9.83E-01	1.00E+00	9.48E-01	1.00E+00	7.76E-01	1.00E+00	reproductive behavior	P
GO:0019104	10	1.20E-01	1.00E+00	4.31E-01	1.00E+00	4.54E-02	1.00E+00	5.44E-01	1.00E+00	2.71E-01	1.00E+00	7.34E-01	1.00E+00	4.73E-01	1.00E+00	1.11E-01	1.00E+00	DNA N-glycosylase activity	F
GO:0019199	124	9.33E-01	1.00E+00	7.02E-01	1.00E+00	8.79E-01	1.00E+00	9.67E-01	1.00E+00	8.34E-01	1.00E+00	6.44E-01	1.00E+00	7.94E-01	1.00E+00	7.42E-02	1.00E+00	transmembrane receptor protein kinase acti	F
GO:0019200	36	1.24E-03	8.86E-02	1.97E-03	1.30E-01	4.64E-02	1.00E+00	3.38E-03	1.76E-01	1.27E-02	6.92E-01	9.11E-03	5.03E-01	1.74E-02	4.88E-01	1.39E-01	1.00E+00	carbohydrate kinase activity	F
GO:0019201	17	3.98E-02	1.00E+00	2.33E-02	1.00E+00	8.31E-02	1.00E+00	6.55E-02	1.00E+00	4.31E-02	1.00E+00	3.25E-02	1.00E+00	9.08E-02	1.00E+00	7.02E-02	1.00E+00	nucleotide kinase activity	F
GO:0019205	42	7.52E-05	1.41E-02	1.22E-06	3.92E-03	6.97E-04	4.90E-02	2.22E-04	1.30E-02	2.42E-04	4.90E-02	3.97E-05	9.66E-03	1.02E-02	2.75E-01	7.72E-04	6.00E-02	nucleobase, nucleoside, nucleotide kinase a	F
GO:0019207	95	1.68E-01	1.00E+00	1.29E-02	6.07E-01	2.29E-01	1.00E+00	9.46E-03	5.72E-01	6.20E-01	1.00E+00	6.67E-02	1.00E+00	6.62E-02	1.00E+00	1.17E-01	1.00E+00	kinase regulator activity	F
GO:0019208	48	4.94E-02	1.00E+00	3.20E-02	1.00E+00	6.90E-02	1.00E+00	9.35E-02	1.00E+00	4.63E-02	1.00E+00	1.12E-01	1.00E+00	1.65E-01	1.00E+00	1.17E-02	4.76E-01	phosphatase regulator activity	F
GO:0019209	17	2.43E-02	1.00E+00	1.08E-02	4.69E-01	1.94E-01	1.00E+00	2.87E-02	1.00E+00	1.20E-01	1.00E+00	2.35E-02	1.00E+00	1.61E-02	4.88E-01	2.08E-01	1.00E+00	kinase activator activity	F
GO:0019210	26	4.30E-01	1.00E+00	1.88E-02	1.00E+00	2.09E-01	1.00E+00	1.83E-02	9.37E-01	9.25E-01	1.00E+00	3.63E-02	1.00E+00	4.88E-01	1.00E+00	1.51E-01	1.00E+00	kinase inhibitor activity	F
GO:0019212	22	1.00E-01	1.00E+00	2.82E-02	1.00E+00	2.02E-01	1.00E+00	2.89E-02	1.00E+00	5.80E-02	1.00E+00	1.01E-01	1.00E+00	2.45E-01	1.00E+00	4.49E-02	1.00E+00	phosphatase inhibitor activity	F
GO:0019213	22	1.03E-02	6.08E-01	3.49E-02	1.00E+00	3.16E-02	1.00E+00	1.43E-02	6.47E-01	1.48E-02	6.92E-01	2.93E-01	1.00E+00	7.67E-02	1.00E+00	2.73E-01	1.00E+00	deacetylase activity	F
GO:0019216	38	3.80E-02	1.00E+00	6.97E-03	3.12E-01	1.28E-01	1.00E+00	1.23E-02	6.47E-01	1.54E-01	1.00E+00	8.69E-03	5.03E-01	7.63E-02	1.00E+00	9.05E-02	1.00E+00	regulation of lipid metabolism	P
GO:0019217	13	8.21E-02	1.00E+00	1.02E-02	4.69E-01	2.34E-02	1.00E+00	2.25E-02	9.37E-01	1.43E-01	1.00E+00	2.45E-02	1.00E+00	5.88E-01	1.00E+00	7.11E-02	1.00E+00	regulation of fatty acid metabolism	P
GO:0019218	17	2.39E-01	1.00E+00	3.08E-01	1.00E+00	5.75E-01	1.00E+00	4.47E-01	1.00E+00	3.73E-01	1.00E+00	1.70E-01	1.00E+00	8.40E-02	1.00E+00	6.41E-01	1.00E+00	regulation of steroid metabolism	P
GO:0019219	2572	8.02E-27	0.00E+00	1.61E-36	0.00E+00	9.50E-27	0.00E+00	6.84E-36	0.00E+00	2.66E-19	0.00E+00	9.18E-26	0.00E+00	2.54E-06	1.00E-03	1.28E-10	0.00E+00	regulation of nucleobase, nucleoside, nucle	P
GO:0019220	125	3.96E-01	1.00E+00	9.52E-02	1.00E+00	4.62E-01	1.00E+00	1.74E-01	1.00E+00	8.91E-01	1.00E+00	3.66E-01	1.00E+00	3.62E-02	8.38E-01	3.67E-02	1.00E+00	regulation of phosphate metabolism	P
GO:0019221	55	1.00E+00	1.00E+00	9.40E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	9.94E-01	1.00E+00	7.53E-01	1.00E+00	1.00E+00	1.00E+00	7.28E-01	1.00E+00	cytokine and chemokine mediated signaling	P
GO:0019222	2990	2.10E-33	0.00E+00	0.00E+00	0.00E+00	4.21E-31	0.00E+00	6.93E-42	0.00E+00	1.48E-22	0.00E+00	5.90E-32	0.00E+00	6.60E-10	0.00E+00	5.31E-16	0.00E+00	regulation of metabolism	P
GO:0019226	294	7.66E-01	1.00E+00	5.45E-01	1.00E+00	9.67E-01	1.00E+00	9.49E-01	1.00E+00	7.58E-01	1.00E+00	2.09E-01	1.00E+00	1.95E-01	1.00E+00	6.50E-02	1.00E+00	transmission of nerve impulse	P
GO:0019229	15	9.95E-01	1.00E+00	6.25E-01	1.00E+00	9.85E-01	1.00E+00	9.49E-01	1.00E+00	1.00E+00	1.00E+00	5.47E-01	1.00E+00	5.19E-01	1.00E+00	1.49E-01	1.00E+00	regulation of vasoconstriction	P
GO:0019233	33	9.13E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.04E-01	1.00E+00	1.00E+00	1.00E+00	4.46E-01	1.00E+00	7.27E-01	1.00E+00	sensory perception of pain	P
GO:0019236	19	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to pheromone	P
GO:0019239	22	3.35E-01	1.00E+00	1.29E-01	1.00E+00	2.49E-01	1.00E+00	1.20E-01	1.00E+00	4.70E-01	1.00E+00	1.94E-01	1.00E+00	3.57E-01	1.00E+00	1.53E-01	1.00E+00	deaminase activity	F
GO:0019290	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	siderophore biosynthesis	P
GO:0019318	188	7.27E-04	8.86E-02	5.20E-05	7.00E-03	1.70E-03	9.50E-02	1.90E-02	9.37E-01	2.70E-02	1.00E+00	7.20E-07	2.00E-03	1.69E-02	4.88E-01	4.46E-02	1.00E+00	hexose metabolism	P
GO:0019319	29	5.51E-02	1.00E+00	4.14E-03	1.88E-01	1.11E-01	1.00E+00	1.53E-02	6.47E-01	2.42E-01	1.00E+00	8.72E-02	1.00E+00	3.29E-02	8.38E-01	3.95E-02	1.00E+00	hexose biosynthesis	P
GO:0019320	75	1.21E-03	8.86E-02	5.18E-05	7.00E-03	6.68E-04	4.90E-02	3.65E-02	1.00E+00	5.71E-03	3.75E-01	1.98E-06	2.00E-03	2.99E-01	1.00E+00	3.98E-02	1.00E+00	hexose catabolism	P
GO:0019321	11	6.71E-02	1.00E+00	1.44E-01	1.00E+00	1.60E-01	1.00E+00	9.42E-02	1.00E+00	4.80E-01	1.00E+00	1.36E-01	1.00E+00	6.70E-02	1.00E+00	4.93E-01	1.00E+00	pentose metabolism	P
GO:0019362	26	7.46E-04	8.86E-02	1.61E-01	1.00E+00	1.00E-02	6.53E-01	4.82E-01	1.00E+00	1.04E-02	6.92E-01	7.19E-02	1.00E+00	6.03E-02	1.00E+00	4.02E-01	1.00E+00	pyridine nucleotide metabolism	P
GO:0019363	12	7.96E-02	1.00E+00	5.39E-01	1.00E+00	5.58E-01	1.00E+00	9.60E-01	1.00E+00	6.13E-02	1.00E+00	6.84E-01	1.00E+00	1.45E-01	1.00E+00	1.87E-01	1.00E+00	pyridine nucleotide biosynthesis	P
GO:0019370	17	5.97E-01	1.00E+00	4.18E-01	1.00E+00	7.60E-01	1.00E+00	4.41E-01	1.00E+00	2.45E-01	1.00E+00	2.60E-01	1.00E+00	6.95E-01	1.00E+00	7.54E-01	1.00E+00	leukotriene biosynthesis	P
GO:0019395	25	6.60E-03	3.15E-01	4.72E-02	1.00E+00	1.42E-02	6.53E-01	3.54E-01	1.00E+00	3.90E-02	1.00E+00	4.12E-02	1.00E+00	3.14E-01	1.00E+00	2.44E-01	1.00E+00	fatty acid oxidation	P
GO:0019438	59	4.07E-01	1.00E+00	3.61E-02	1.00E+00	4.69E-01	1.00E+00	3.55E-01	1.00E+00	3.33E-01	1.00E+00	4.74E-03	2.66E-01	6.23E-01	1.00E+00	1.23E-01	1.00E+00	aromatic compound biosynthesis	P
GO:0019439	15	7.15E-01	1.00E+00	5.63E-01	1.00E+00	9.78E-01	1.00E+00	9.94E-01	1.00E+00	7.45E-01	1.00E+00	6.49E-01	1.00E+00	4.18E-01	1.00E+00	2.67E-01	1.00E+00	aromatic compound catabolism	P
GO:0019538	3830	4.96E-43	0.00E+00	0.00E+00	0.00E+00	7.26E-39	0.00E+00	0.00E+00	0.00E+00	1.56E-25	0.00E+00	2.59E-35	0.00E+00	5.32E-16	0.00E+00	9.60E-30	0.00E+00	protein metabolism	P

GO:0019540	47	4.01E-01	1.00E+00	4.96E-02	1.00E+00	3.53E-01	1.00E+00	2.65E-01	1.00E+00	4.50E-01	1.00E+00	1.22E-02	5.03E-01	5.56E-01	1.00E+00	1.33E-01	1.00E+00	siderophore biosynthesis from catechol	P
GO:0019717	63	6.71E-02	1.00E+00	1.44E-02	6.07E-01	7.85E-02	1.00E+00	5.08E-02	1.00E+00	1.25E-01	1.00E+00	2.10E-02	7.56E-01	3.66E-01	1.00E+00	6.36E-02	1.00E+00	synaptosome	C
GO:0019722	33	3.85E-03	2.12E-01	1.40E-02	6.07E-01	1.49E-02	6.53E-01	1.52E-01	1.00E+00	2.68E-02	1.00E+00	6.07E-02	1.00E+00	1.04E-02	2.75E-01	7.55E-04	6.00E-02	calcium-mediated signaling	P
GO:0019724	128	6.85E-01	1.00E+00	8.44E-01	1.00E+00	7.22E-01	1.00E+00	2.78E-01	1.00E+00	9.77E-01	1.00E+00	9.92E-01	1.00E+00	2.46E-01	1.00E+00	7.63E-01	1.00E+00	B cell mediated immunity	P
GO:0019725	275	1.32E-03	8.86E-02	1.46E-04	1.50E-02	3.58E-02	1.00E+00	2.90E-03	1.61E-01	6.65E-02	1.00E+00	2.32E-03	1.27E-01	5.41E-04	3.44E-02	5.05E-03	2.01E-01	cell homeostasis	P
GO:0019748	97	1.02E-01	1.00E+00	9.61E-02	1.00E+00	4.91E-02	1.00E+00	2.50E-01	1.00E+00	2.74E-01	1.00E+00	1.56E-01	1.00E+00	3.20E-01	1.00E+00	5.15E-02	1.00E+00	secondary metabolism	P
GO:0019751	36	6.49E-03	3.15E-01	1.36E-02	6.07E-01	1.40E-02	6.53E-01	4.88E-03	2.88E-01	2.53E-02	1.00E+00	1.15E-01	1.00E+00	1.32E-01	1.00E+00	2.13E-01	1.00E+00	polyol metabolism	P
GO:0019752	642	4.34E-06	3.02E-03	3.48E-10	0.00E+00	2.70E-04	4.00E-02	7.79E-06	2.89E-03	9.40E-04	1.20E-01	2.08E-08	8.78E-04	6.73E-05	8.00E-03	4.18E-06	2.91E-03	carboxylic acid metabolism	P
GO:0019783	71	9.55E-03	6.08E-01	4.18E-05	7.00E-03	3.31E-04	4.00E-02	1.77E-06	2.89E-03	7.64E-02	1.00E+00	1.51E-02	6.68E-01	5.88E-01	1.00E+00	3.18E-03	1.27E-01	small conjugating protein-specific protease	F
GO:0019787	178	2.61E-08	2.57E-03	9.76E-12	0.00E+00	1.13E-08	9.80E-04	2.51E-10	0.00E+00	2.59E-06	1.69E-03	9.38E-10	6.20E-04	1.56E-02	4.88E-01	1.07E-03	6.00E-02	small conjugating protein ligase activity	F
GO:0019814	10	9.98E-01	1.00E+00	9.85E-01	1.00E+00	9.24E-01	1.00E+00	9.26E-01	1.00E+00	9.98E-01	1.00E+00	9.72E-01	1.00E+00	9.92E-01	1.00E+00	9.87E-01	1.00E+00	immunoglobulin complex	C
GO:0019825	18	7.62E-01	1.00E+00	9.55E-02	1.00E+00	3.37E-01	1.00E+00	3.91E-02	1.00E+00	9.90E-01	1.00E+00	2.06E-01	1.00E+00	5.66E-01	1.00E+00	3.65E-01	1.00E+00	oxygen binding	F
GO:0019827	18	1.53E-02	1.00E+00	5.02E-02	1.00E+00	1.06E-02	6.53E-01	6.04E-02	1.00E+00	1.29E-01	1.00E+00	1.33E-01	1.00E+00	2.14E-01	1.00E+00	3.01E-01	1.00E+00	stem cell maintenance	P
GO:0019829	55	3.57E-02	1.00E+00	8.10E-02	1.00E+00	4.36E-02	1.00E+00	2.28E-01	1.00E+00	4.13E-02	1.00E+00	1.25E-01	1.00E+00	4.80E-01	1.00E+00	1.79E-01	1.00E+00	cation-transporting ATPase activity	F
GO:0019835	27	5.88E-01	1.00E+00	8.99E-01	1.00E+00	9.04E-01	1.00E+00	8.98E-01	1.00E+00	3.60E-01	1.00E+00	7.86E-01	1.00E+00	4.16E-01	1.00E+00	8.90E-01	1.00E+00	cytolysis	P
GO:0019838	89	9.93E-01	1.00E+00	9.95E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	8.98E-01	1.00E+00	9.61E-01	1.00E+00	9.88E-01	1.00E+00	7.83E-01	1.00E+00	growth factor binding	F
GO:0019840	17	8.88E-01	1.00E+00	3.85E-01	1.00E+00	9.70E-01	1.00E+00	3.88E-01	1.00E+00	9.72E-01	1.00E+00	6.26E-01	1.00E+00	4.33E-01	1.00E+00	1.53E-01	1.00E+00	isoprenoid binding	F
GO:0019841	11	5.34E-01	1.00E+00	2.38E-01	1.00E+00	7.62E-01	1.00E+00	1.71E-01	1.00E+00	7.56E-01	1.00E+00	5.02E-01	1.00E+00	2.35E-01	1.00E+00	1.64E-01	1.00E+00	retinol binding	F
GO:0019842	148	5.46E-03	3.09E-01	1.47E-02	6.07E-01	4.82E-02	1.00E+00	1.53E-02	6.47E-01	5.36E-02	1.00E+00	1.46E-02	6.68E-01	6.90E-03	2.75E-01	4.02E-01	1.00E+00	vitamin binding	F
GO:0019843	21	8.47E-06	3.62E-03	2.65E-04	4.40E-02	2.84E-05	3.00E-03	3.15E-06	2.89E-03	2.91E-05	6.33E-03	2.12E-03	1.27E-01	8.24E-02	1.00E+00	7.28E-01	1.00E+00	rRNA binding	F
GO:0019861	91	8.26E-01	1.00E+00	3.20E-01	1.00E+00	7.94E-01	1.00E+00	5.81E-01	1.00E+00	6.94E-01	1.00E+00	5.82E-01	1.00E+00	7.99E-01	1.00E+00	8.03E-02	1.00E+00	flagellum	C
GO:0019865	11	3.03E-01	1.00E+00	1.29E-01	1.00E+00	1.99E-01	1.00E+00	1.56E-01	1.00E+00	9.68E-01	1.00E+00	2.57E-01	1.00E+00	1.50E-01	1.00E+00	1.17E-01	1.00E+00	immunoglobulin binding	F
GO:0019866	334	1.28E-09	2.57E-03	2.86E-09	8.90E-04	2.80E-07	2.00E-03	1.76E-07	2.89E-03	1.22E-08	0.00E+00	1.08E-06	2.00E-03	8.85E-04	3.44E-02	2.97E-04	3.00E-02	organelle inner membrane	C
GO:0019867	81	1.38E-03	8.86E-02	6.43E-07	3.92E-03	2.42E-02	1.00E+00	1.13E-04	1.30E-02	5.76E-03	3.75E-01	9.52E-05	1.10E-02	2.71E-03	8.40E-02	1.44E-03	6.00E-02	outer membrane	C
GO:0019882	83	4.45E-01	1.00E+00	8.15E-01	1.00E+00	2.71E-01	1.00E+00	4.42E-01	1.00E+00	3.34E-01	1.00E+00	1.38E-01	1.00E+00	6.07E-01	1.00E+00	1.00E+00	1.00E+00	antigen processing and presentation	P
GO:0019884	24	5.07E-02	1.00E+00	1.38E-01	1.00E+00	1.13E-01	1.00E+00	8.47E-02	1.00E+00	1.29E-01	1.00E+00	1.01E-01	1.00E+00	1.86E-01	1.00E+00	8.42E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019886	16	2.93E-02	1.00E+00	8.09E-02	1.00E+00	1.52E-01	1.00E+00	1.14E-01	1.00E+00	1.90E-01	1.00E+00	6.31E-02	1.00E+00	6.99E-02	1.00E+00	6.58E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019887	75	1.66E-01	1.00E+00	2.25E-02	1.00E+00	1.51E-01	1.00E+00	1.57E-02	6.47E-01	6.78E-01	1.00E+00	9.02E-02	1.00E+00	1.06E-01	1.00E+00	1.83E-01	1.00E+00	protein kinase regulator activity	F
GO:0019888	45	3.81E-02	1.00E+00	2.04E-02	1.00E+00	6.45E-02	1.00E+00	6.78E-02	1.00E+00	3.93E-02	1.00E+00	6.28E-02	1.00E+00	1.15E-01	1.00E+00	1.45E-02	4.76E-01	protein phosphatase regulator activity	F
GO:0019897	60	1.00E-01	1.00E+00	3.41E-02	1.00E+00	2.37E-01	1.00E+00	2.30E-01	1.00E+00	3.19E-01	1.00E+00	1.16E-01	1.00E+00	5.91E-02	1.00E+00	3.84E-03	1.34E-01	extrinsic to plasma membrane	C
GO:0019898	93	8.43E-02	1.00E+00	9.24E-03	4.69E-01	4.92E-01	1.00E+00	2.82E-01	1.00E+00	3.62E-01	1.00E+00	1.02E-01	1.00E+00	8.96E-03	2.75E-01	3.59E-04	3.00E-02	extrinsic to membrane	C
GO:0019899	251	3.78E-06	3.02E-03	7.94E-11	0.00E+00	1.98E-03	9.50E-02	5.47E-10	0.00E+00	3.46E-03	2.13E-01	1.17E-06	2.00E-03	1.53E-06	8.23E-04	8.84E-05	1.60E-02	enzyme binding	F
GO:0019900	96	1.55E-02	1.00E+00	4.76E-04	4.74E-02	1.51E-01	1.00E+00	3.99E-04	4.20E-02	1.14E-01	1.00E+00	2.51E-03	1.27E-01	2.14E-03	8.40E-02	1.02E-01	1.00E+00	kinase binding	F
GO:0019901	80	1.26E-02	6.08E-01	1.34E-03	9.65E-02	1.29E-01	1.00E+00	1.31E-03	9.40E-02	6.40E-02	1.00E+00	2.37E-03	1.27E-01	6.07E-03	2.75E-01	2.52E-01	1.00E+00	protein kinase binding	F
GO:0019902	16	1.10E-01	1.00E+00	1.14E-02	6.07E-01	3.44E-03	2.03E-01	1.47E-02	6.47E-01	3.23E-01	1.00E+00	7.54E-02	1.00E+00	5.92E-01	1.00E+00	2.50E-02	9.99E-01	phosphatase binding	F
GO:0019903	12	8.84E-02	1.00E+00	2.79E-02	1.00E+00	8.58E-03	6.53E-01	1.66E-02	6.47E-01	2.20E-01	1.00E+00	1.32E-01	1.00E+00	4.98E-01	1.00E+00	7.55E-02	1.00E+00	protein phosphatase binding	F
GO:0019904	142	3.73E-06	3.02E-03	1.06E-05	4.51E-03	2.43E-05	3.00E-03	6.43E-05	1.30E-02	1.25E-03	1.20E-01	5.12E-04	3.20E-02	1.08E-04	8.00E-03	1.39E-02	4.76E-01	protein domain specific binding	F
GO:0019905	26	2.18E-01	1.00E+00	5.88E-01	1.00E+00	9.24E-01	1.00E+00	8.19E-01	1.00E+00	2.48E-01	1.00E+00	7.80E-01	1.00E+00	5.06E-02	1.00E+00	1.70E-01	1.00E+00	syntaxin binding	F
GO:0019915	12	1.66E-01	1.00E+00	2.53E-02	1.00E+00	3.30E-01	1.00E+00	1.02E-01	1.00E+00	2.45E-01	1.00E+00	7.76E-02	1.00E+00	1.96E-01	1.00E+00	1.06E-01	1.00E+00	sequestering of lipid	P
GO:0019932	161	6.28E-02	1.00E+00	3.28E-02	1.00E+00	2.75E-01	1.00E+00	3.45E-01	1.00E+00	9.46E-02	1.00E+00	1.13E-01	1.00E+00	2.80E-02	8.38E-01	5.04E-04	3.00E-02	second-messenger-mediated signaling	P
GO:0019933	69	7.37E-01	1.00E+00	7.05E-01	1.00E+00	9.35E-01	1.00E+00	9.32E-01	1.00E+00	6.41E-01	1.00E+00	5.97E-01	1.00E+00	2.79E-01	1.00E+00	2.35E-01	1.00E+00	cAMP-mediated signaling	P
GO:0019935	74	6.40E-01	1.00E+00	6.00E-01	1.00E+00	9.13E-01	1.00E+00	8.92E-01	1.00E+00	5.01E-01	1.00E+00	5.30E-01	1.00E+00	2.99E-01	1.00E+00	1.93E-01	1.00E+00	cyclic-nucleotide-mediated signaling	P
GO:0019941	162	3.22E-05	7.00E-03	6.72E-10	8.90E-04	6.13E-07	2.00E-03	2.31E-10	0.00E+00	5.45E-03	3.75E-01	3.59E-06	2.90E-03	1.69E-01	1.00E+00	3.72E-04	3.00E-02	modification-dependent protein catabolism	P
GO:0019953	364	2.51E-04	1.90E-02	6.36E-04	5.90E-02	3.02E-04	4.00E-02	3.81E-03	2.88E-01	1.84E-02	7.90E-01	3.42E-03	1.51E-01	4.41E-03	2.23E-01	3.53E-02	1.00E+00	sexual reproduction	P
GO:0019955	111	9.71E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.39E-01	1.00E+00	9.74E-01	1.00E+00	5.20E-01	1.00E+00	6.48E-01	1.00E+00	cytokine binding	F
GO:0019956	50	7.39E-01	1.00E+00	7.93E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	5.99E-01	1.00E+00	4.70E-01	1.00E+00	1.57E-01	1.00E+00	3.60E-01	1.00E+00	chemokine binding	F
GO:0019957	37	6.34E-01	1.00E+00	7.21E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	4.91E-01	1.00E+00	2.97E-01	1.00E+00	1.33E-01	1.00E+00	2.96E-01	1.00E+00	C-C chemokine binding	F
GO:0019958	34	7.29E-01	1.00E+00	8.99E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	7.77E-01	1.00E+00	7.29E-01	1.00E+00	2.23E-01	1.00E+00	4.63E-01	1.00E+00	C-X-C chemokine binding	F
GO:0019959	11	9.29E-02	1.00E+00	1.29E-01	1.00E+00	8.89E-01	1.00E+00	8.55E-01	1.00E+00	4.08E-01	1.00E+00	1.57E-01	1.00E+00	2.13E-02	6.36E-01	2.84E-02	9.99E-01	interleukin-8 binding	F
GO:0019965	58	9.95E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.85E-01	1.00E+00	5.78E-01	1.00E+00	7.39E-01	1.00E+00	interleukin binding	F
GO:0019966	30	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	interleukin-1 binding	F
GO:0019992	55	3.64E-01	1.00E+00	6.83E-02	1.00E+00	2.24E-01	1.00E+00	1.63E-01	1.00E+00	8.40E-01	1.00E+00	2.79E-01	1.00E+00	6.14E-02	1.00E+00	7.42E-02	1.00E+00	diacylglycerol binding	F
GO:0020037	203	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.70E-01	1.00E+00	6.95E-01	1.00E+00	heme binding	F
GO:0021510	37	1.56E-01	1.00E+00	8.82E-01	1.00E+00	3.89E-01	1.00E+00	9.42E-01	1.00E+00	2.14E-01	1.00E+00	8.09E-01	1.00E+00	5.39E-02	1.00E+00	6.02E-01	1.00E+00	spinal cord development	P
GO:0021515	25	3.33E-01	1.00E+00	9.85E-01	1.00E+00	5.73E-01	1.00E+00	9.93E-01	1.00E+00	5.30E-01	1.00E+00	9.91E-01	1.00E+00	1.06E-01	1.00E+00	7.01E-01	1.00E+00	cell differentiation in spinal cord	P
GO:0021516	11	5.57E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	9.94E-01	1.00E+00	7.04E-01	1.00E+00	9.92E-01	1.00E+00	1.28E-01	1.00E+00	9.82E-01	1.00E+00	dorsal spinal cord development	P
GO:0021517	17	2.25E-01	1.00E+00	9.07E-01	1.00E+00	4.35E-01	1.00E+00	9.64E-01	1.00E+00	3.43E-01	1.00E+00	9.45E-01	1.00E+00	1.05E-01	1.00E+00	6.01E-01	1.00E+00	ventral spinal cord development	P
GO:0021522	15	2.23E-01	1.00E+00	9.50E-01	1.00E+00	4.61E-01	1.00E+00	9.92E-01	1.00E+00	2.82E-01	1.00E+00	9.93E-01	1.00E+00	1.13E-01	1.00E+00	5.49E-01	1.00E+00	spinal cord motor neuron differentiation	P
GO:0021532	13	1.51E-01	1.00E+00	4.83E-01	1.00E+00	4.07E-01	1.00E+00	5.28E-01	1.00E+00	3.39E-01	1.00E+00	4.36E-01	1.00E+00	8.33E-02	1.00E+00	5.16E-01	1.00E+00	neural tube patterning	P
GO:0021533	14	1.40E-01	1.00E+00	5.72E-01	1.00E+00	2.51E-01	1.00E+00	5.96E-01	1.00E+00	2.29E-01	1.00E+00	4.12E-01	1.00E+00	1.32E-01	1.00E+00	4.13E-01	1.00E+00	cell differentiation in hindbrain	P
GO:0021534	10	3.94E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	2.16E-01	1.00E+00	9.48E-01	1.00E+00	2.50E-01	1.00E+00	5.74E-01	1.00E+00	cell proliferation in hindbrain	P
GO:0021536	30	9.41E-01	1.00E+00	9.20E-01	1.00E+00	9.63E-01	1.00E+00	9.90E-01	1.00E+00	9.66E-01	1.00E+00	7.41E-01	1.00E+00	4.52E-01	1.00E+00	7.79E-01	1.00E+00	diencephalon development	P
GO:0021537	53	3.82E-01	1.00E+00	4.30E-01	1.00E+00	3.35E-01	1.00E+00	3.99E-01	1.00E+00	4.20E-01	1.00E+00	5.22E-01	1.00E+00	4.85E-01	1.00E+00	4.57E-01	1.00E+00	telencephalon development	P
GO:0021543	38	4.46E-01	1.00E+00	2.07E-01	1.00E+00	4.52E-01	1.00E+00	2.36E-01	1.00E+00	3.11E-01	1.00E+00	2.86E-01	1.00E+00	6.79E-01	1.00E+00	3.00E-01	1.00E+00	pallium development	P
GO:0021545	13	9.61E-01	1.00E+00	8.65E-01	1.00E+00	8.88E-01	1.00E+00	7.04E-01	1.00E+00	9.91E-01	1.00E+00	8.47E-01	1.00E+00	8.17E-01	1.00E+00	9.82E-01	1.00E+00	cranial nerve development	P
GO:0021549	26	1.90E-01	1.00E+00	7.90E-01	1.00E+00	6.11E-01	1.00E+00	7.36E-01	1.00E+00	2.30E-01	1.00E+00	5.81E-01	1.00E+00	7.16E-02	1.00E+00	6.80E-01	1.00E+00	cerebellum development	P
GO:0021575	19	4.56E-02	1.00E+00	5.16E-01	1.00E+00	4.19E-01	1.00E+00	5.43E-01	1.00E+00	6.58E-02	1.00E+00	3.70E-01	1.00E+00	2.60E-02	8.38E-01	3.84E-01	1.00E+00	hindbrain morphogenesis	P
GO:0021587	18	3.84E-02	1.00E+00	4.52E-01	1.00E+00	3.55E-01	1.00E+00	4.64E-01	1.00E+00	4.41E-02	1.00E+00	3.54E-01	1.00E+00	3.85E-02	8.54E-01	3.53E-01	1.00E+00	cerebellum morphogenesis	P
GO:0021675	19	9.38E-01	1.00E+00	8.14E-01	1.00E+00	8.73E-01	1.00E+00	5.95E-01	1.00E+00	9.41E-01	1.00E+00	8.52E-01	1.00E+00	8.52E-01	1.00E+00	9.38E-01	1.00E+00	nerve development	P
GO:0021680	11	3.64E-01	1.00E+00	3.89E-01	1.00E+00	5.90E-01	1.00E+00	3.32E-01	1.00E+00	6.12E-01	1.00E+00	3.29E-01	1.00E+00	1.83E-01	1.00E+00	4.31E-01	1.00E+00	cerebellar Purkinje cell layer development	P
GO:0021695	20	6.08E-02	1.00E+00	5.03E-01	1.00E+00	3.14E-01	1.00E+00	4.12E-01	1.00E+00	8.73E-02	1.00E+00	3.56E-01	1.00E+00	6.88E-02	1.00E+00	5.17E-01	1.00E+00	cerebellar cortex development	P
GO:0021696	17	1.92E-02	1.00E+00	3.71E-01	1.00E+00	2.78E-01	1.00E+00	4.04E-01	1.00E+00	2.74E-02	1.00E+00	2.81E-01	1.00E+00	3.09E-02	8.38E-01	3.09E-01	1.00E+00	cerebellar cortex morphogenesis	P
GO:0021697	13	8.17E-02	1.00E+00	4.81E-01	1.00E+00	2.57E-01	1.00E+00	4.67E-01	1.00E+00	7.85E-02	1.00E+00	3.81E-01	1.00E+00	9.98E-02	1.00E+00	3.69E-01	1.00E+00	cerebellar cortex formation	P
GO:0021700	92	6.71E-02	1.00E+00	9.95E-02	1.00E+00	9.88E-02	1.00E+00	7.21E-01	1.00E+00	5.67E-01	1.00E+00	1.68E-01	1.00E+00	3.68E-02	8.38E-01	2.19E-02	9.99E-01	developmental maturation	P
GO:0021761	20	2.51E-01	1.00E+00	7.23E-02	1.00E+00	2.91E-01	1.00E+00	6.19E-02	1.00E+00	2.81E-01	1.00E+00	3.05E-01	1.00E+00	2.75E-01	1.00E+00	1.02E-01	1.00E+00	limbic system development	P

GO:0021766	16	1.40E-01	1.00E+00	3.70E-02	1.00E+00	2.32E-01	1.00E+00	7.06E-02	1.00E+00	1.40E-01	1.00E+00	1.58E-01	1.00E+00	1.89E-01	1.00E+00	4.40E-02	1.00E+00	hippocampus development	P
GO:0021782	17	6.61E-01	1.00E+00	6.37E-01	1.00E+00	4.46E-01	1.00E+00	5.89E-01	1.00E+00	7.29E-01	1.00E+00	4.56E-01	1.00E+00	6.57E-01	1.00E+00	8.52E-01	1.00E+00	glial cell development	P
GO:0021795	14	7.12E-01	1.00E+00	5.24E-01	1.00E+00	8.31E-01	1.00E+00	4.03E-01	1.00E+00	8.23E-01	1.00E+00	7.57E-01	1.00E+00	3.39E-01	1.00E+00	5.10E-01	1.00E+00	cerebral cortex cell migration	P
GO:0021846	12	9.19E-01	1.00E+00	8.76E-01	1.00E+00	6.92E-01	1.00E+00	9.47E-01	1.00E+00	7.89E-01	1.00E+00	7.10E-01	1.00E+00	1.00E+00	1.00E+00	7.89E-01	1.00E+00	cell proliferation in the forebrain	P
GO:0021872	13	7.73E-01	1.00E+00	7.10E-01	1.00E+00	6.17E-01	1.00E+00	7.54E-01	1.00E+00	7.16E-01	1.00E+00	4.80E-01	1.00E+00	9.90E-01	1.00E+00	9.11E-01	1.00E+00	generation of neurons in the forebrain	P
GO:0021879	11	8.11E-01	1.00E+00	6.63E-01	1.00E+00	6.52E-01	1.00E+00	6.33E-01	1.00E+00	8.93E-01	1.00E+00	5.19E-01	1.00E+00	9.80E-01	1.00E+00	8.50E-01	1.00E+00	forebrain neuron differentiation	P
GO:0021885	17	8.78E-01	1.00E+00	7.20E-01	1.00E+00	9.31E-01	1.00E+00	5.92E-01	1.00E+00	9.63E-01	1.00E+00	8.87E-01	1.00E+00	3.79E-01	1.00E+00	6.55E-01	1.00E+00	forebrain cell migration	P
GO:0021895	13	2.56E-01	1.00E+00	4.57E-01	1.00E+00	2.12E-01	1.00E+00	4.71E-01	1.00E+00	5.25E-01	1.00E+00	3.16E-01	1.00E+00	3.51E-01	1.00E+00	8.10E-01	1.00E+00	cerebral cortex neuron differentiation	P
GO:0021915	62	1.38E-01	1.00E+00	4.51E-02	1.00E+00	4.05E-01	1.00E+00	8.73E-02	1.00E+00	5.86E-02	1.00E+00	1.13E-01	1.00E+00	1.60E-01	1.00E+00	3.11E-02	9.99E-01	neural tube development	P
GO:0021924	10	3.94E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	2.16E-01	1.00E+00	9.48E-01	1.00E+00	2.50E-01	1.00E+00	5.74E-01	1.00E+00	cell proliferation in the external granule laye	P
GO:0021930	10	3.94E-01	1.00E+00	9.64E-01	1.00E+00	9.95E-01	1.00E+00	9.80E-01	1.00E+00	2.16E-01	1.00E+00	9.48E-01	1.00E+00	2.50E-01	1.00E+00	5.74E-01	1.00E+00	granule cell precursor proliferation	P
GO:0021953	34	1.52E-01	1.00E+00	4.69E-01	1.00E+00	3.40E-01	1.00E+00	4.44E-01	1.00E+00	2.84E-01	1.00E+00	5.34E-01	1.00E+00	5.82E-02	1.00E+00	4.36E-01	1.00E+00	central nervous system neuron differentiatic	P
GO:0021954	30	1.75E-01	1.00E+00	4.51E-01	1.00E+00	2.05E-01	1.00E+00	3.87E-01	1.00E+00	3.96E-01	1.00E+00	5.19E-01	1.00E+00	7.84E-02	1.00E+00	5.24E-01	1.00E+00	central nervous system neuron developmer	P
GO:0021955	14	6.82E-02	1.00E+00	1.39E-01	1.00E+00	5.75E-02	1.00E+00	1.65E-01	1.00E+00	1.55E-01	1.00E+00	3.53E-01	1.00E+00	5.32E-02	1.00E+00	9.34E-02	1.00E+00	central nervous system neuron axonogenes	P
GO:0021983	24	9.56E-01	1.00E+00	8.97E-01	1.00E+00	9.51E-01	1.00E+00	9.96E-01	1.00E+00	9.96E-01	1.00E+00	5.87E-01	1.00E+00	4.39E-01	1.00E+00	7.66E-01	1.00E+00	pituitary gland development	P
GO:0021987	29	3.07E-01	1.00E+00	1.61E-01	1.00E+00	3.05E-01	1.00E+00	2.18E-01	1.00E+00	3.00E-01	1.00E+00	1.72E-01	1.00E+00	4.08E-01	1.00E+00	2.87E-01	1.00E+00	cerebral cortex development	P
GO:0022008	438	1.13E-01	1.00E+00	3.05E-01	1.00E+00	5.92E-01	1.00E+00	6.01E-01	1.00E+00	1.58E-01	1.00E+00	5.56E-01	1.00E+00	3.08E-02	8.38E-01	4.17E-02	1.00E+00	neurogenesis	P
GO:0022029	16	8.08E-01	1.00E+00	6.67E-01	1.00E+00	8.89E-01	1.00E+00	5.24E-01	1.00E+00	9.34E-01	1.00E+00	8.41E-01	1.00E+00	3.02E-01	1.00E+00	6.66E-01	1.00E+00	telencephalon cell migration	P
GO:0022037	31	8.99E-02	1.00E+00	8.47E-01	1.00E+00	3.80E-01	1.00E+00	7.43E-01	1.00E+00	1.17E-01	1.00E+00	5.54E-01	1.00E+00	4.18E-02	1.00E+00	8.36E-01	1.00E+00	metencephalon development	P
GO:0030001	604	2.35E-01	1.00E+00	5.64E-03	3.08E-01	6.42E-01	1.00E+00	1.25E-01	1.00E+00	5.96E-01	1.00E+00	3.65E-02	1.00E+00	3.54E-02	8.38E-01	1.56E-03	6.00E-02	metal ion transport	P
GO:0030003	156	3.18E-02	1.00E+00	1.21E-02	6.07E-01	4.26E-01	1.00E+00	5.18E-02	1.00E+00	2.50E-01	1.00E+00	4.89E-02	1.00E+00	2.62E-03	8.40E-02	2.33E-02	9.99E-01	cation homeostasis	P
GO:0030004	18	7.69E-02	1.00E+00	6.54E-02	1.00E+00	2.61E-01	1.00E+00	5.90E-02	1.00E+00	5.05E-02	1.00E+00	1.22E-01	1.00E+00	2.21E-01	1.00E+00	2.42E-01	1.00E+00	monovalent inorganic cation homeostasis	P
GO:0030005	138	1.12E-01	1.00E+00	3.60E-02	1.00E+00	5.25E-01	1.00E+00	1.31E-01	1.00E+00	4.77E-01	1.00E+00	1.01E-01	1.00E+00	1.02E-02	2.75E-01	2.78E-02	9.99E-01	di-, tri-valent inorganic cation homeostasis	P
GO:0030010	13	3.35E-01	1.00E+00	5.50E-02	1.00E+00	2.02E-01	1.00E+00	9.54E-02	1.00E+00	7.11E-01	1.00E+00	1.09E-01	1.00E+00	2.66E-01	1.00E+00	1.85E-01	1.00E+00	establishment of cell polarity	P
GO:0030016	83	3.14E-01	1.00E+00	6.95E-02	1.00E+00	6.68E-01	1.00E+00	2.34E-01	1.00E+00	2.34E-01	1.00E+00	2.72E-01	1.00E+00	4.53E-01	1.00E+00	1.41E-02	4.76E-01	myofibril	C
GO:0030017	74	3.06E-01	1.00E+00	7.18E-02	1.00E+00	5.17E-01	1.00E+00	1.68E-01	1.00E+00	2.17E-01	1.00E+00	2.92E-01	1.00E+00	6.54E-01	1.00E+00	2.76E-02	9.99E-01	sarcomere	C
GO:0030018	36	3.02E-01	1.00E+00	2.20E-01	1.00E+00	2.12E-01	1.00E+00	2.34E-01	1.00E+00	2.46E-01	1.00E+00	5.47E-01	1.00E+00	7.14E-01	1.00E+00	1.32E-01	1.00E+00	Z disc	C
GO:0030027	56	1.55E-02	1.00E+00	1.80E-03	9.65E-02	3.44E-02	1.00E+00	2.20E-02	9.37E-01	4.84E-02	1.00E+00	2.94E-03	1.44E-01	4.36E-02	1.00E+00	5.99E-03	4.28E-01	lamellipodium	C
GO:0030029	231	2.08E-05	7.00E-03	1.56E-09	8.90E-04	1.39E-02	6.53E-01	1.50E-04	1.30E-02	1.66E-02	6.92E-01	3.18E-05	9.52E-03	1.66E-06	8.23E-04	1.60E-10	0.00E+00	actin filament-based process	P
GO:0030030	334	5.11E-02	1.00E+00	1.02E-02	4.69E-01	3.09E-01	1.00E+00	2.45E-01	1.00E+00	5.90E-02	1.00E+00	4.75E-02	1.00E+00	8.04E-02	1.00E+00	5.23E-04	3.00E-02	cell projection organization and biogenesis	P
GO:0030031	82	1.12E-03	8.86E-02	2.38E-05	7.00E-03	1.14E-02	6.53E-01	2.81E-03	1.61E-01	6.63E-03	6.92E-01	2.64E-04	2.33E-02	2.17E-02	6.36E-01	7.07E-05	7.00E-03	cell projection biogenesis	P
GO:0030032	18	6.07E-02	1.00E+00	1.30E-03	9.65E-02	1.13E-01	1.00E+00	1.72E-03	1.24E-01	3.55E-02	1.00E+00	6.30E-03	4.21E-01	3.93E-01	1.00E+00	3.44E-03	1.27E-01	lamellipodium biogenesis	P
GO:0030035	15	3.27E-02	1.00E+00	7.98E-02	1.00E+00	3.65E-01	1.00E+00	1.35E-01	1.00E+00	1.05E-01	1.00E+00	2.96E-01	1.00E+00	1.40E-02	4.78E-01	1.85E-02	7.36E-01	microspike biogenesis	P
GO:0030036	210	2.82E-05	7.00E-03	6.59E-09	8.90E-04	1.30E-02	6.53E-01	1.28E-04	1.30E-02	1.57E-02	6.92E-01	5.49E-05	9.66E-03	9.46E-06	2.94E-03	5.81E-09	0.00E+00	actin cytoskeleton organization and biogene	P
GO:0030041	37	3.05E-02	1.00E+00	8.22E-03	4.16E-01	1.22E-01	1.00E+00	5.83E-02	1.00E+00	2.46E-01	1.00E+00	2.02E-01	1.00E+00	1.67E-02	4.88E-01	7.45E-04	6.00E-02	actin filament polymerization	P
GO:0030042	23	1.14E-01	1.00E+00	3.06E-03	1.88E-01	4.29E-01	1.00E+00	5.37E-02	1.00E+00	2.44E-01	1.00E+00	3.76E-02	1.00E+00	8.37E-02	1.00E+00	1.03E-02	4.76E-01	actin filament depolymerization	P
GO:0030048	16	2.09E-01	1.00E+00	5.51E-03	3.08E-01	1.92E-01	1.00E+00	1.05E-01	1.00E+00	2.62E-01	1.00E+00	1.15E-02	5.03E-01	2.44E-01	1.00E+00	1.85E-03	7.90E-02	actin filament-based movement	P
GO:0030054	474	7.83E-02	1.00E+00	2.30E-02	1.00E+00	8.21E-01	1.00E+00	6.10E-01	1.00E+00	1.93E-01	1.00E+00	1.08E-01	1.00E+00	1.81E-03	8.40E-02	8.83E-06	7.00E-03	cell junction	C
GO:0030055	49	4.03E-02	1.00E+00	3.58E-02	1.00E+00	4.42E-01	1.00E+00	1.94E-01	1.00E+00	2.06E-02	7.90E-01	9.03E-02	1.00E+00	2.18E-02	6.36E-01	5.10E-03	2.01E-01	cell-matrix junction	C
GO:0030057	16	5.68E-01	1.00E+00	5.58E-01	1.00E+00	6.38E-01	1.00E+00	7.34E-01	1.00E+00	7.85E-01	1.00E+00	4.34E-01	1.00E+00	4.44E-01	1.00E+00	2.89E-01	1.00E+00	desmosome	C
GO:0030072	47	2.13E-01	1.00E+00	1.64E-01	1.00E+00	3.78E-01	1.00E+00	4.70E-01	1.00E+00	4.30E-01	1.00E+00	2.76E-01	1.00E+00	3.39E-02	8.38E-01	2.61E-02	9.99E-01	peptide hormone secretion	P
GO:0030073	41	1.55E-01	1.00E+00	1.76E-01	1.00E+00	2.47E-01	1.00E+00	4.48E-01	1.00E+00	2.90E-01	1.00E+00	3.83E-01	1.00E+00	5.55E-02	1.00E+00	1.95E-02	7.36E-01	insulin secretion	P
GO:0030097	273	4.26E-03	2.14E-01	2.47E-02	1.00E+00	8.28E-04	4.90E-02	3.73E-02	1.00E+00	6.90E-01	1.00E+00	3.77E-01	1.00E+00	7.77E-04	3.44E-02	1.97E-02	7.36E-01	hemopoiesis	P
GO:0030098	118	8.08E-02	1.00E+00	2.86E-02	1.00E+00	1.25E-01	1.00E+00	1.16E-01	1.00E+00	7.33E-01	1.00E+00	4.00E-01	1.00E+00	8.54E-03	2.75E-01	5.81E-03	4.28E-01	lymphocyte differentiation	P
GO:0030099	130	9.31E-03	6.08E-01	2.33E-01	1.00E+00	2.65E-03	1.07E-01	1.03E-01	1.00E+00	7.43E-01	1.00E+00	5.78E-01	1.00E+00	1.18E-03	6.14E-02	3.57E-01	1.00E+00	myeloid cell differentiation	P
GO:0030100	48	6.86E-01	1.00E+00	8.68E-02	1.00E+00	4.49E-01	1.00E+00	1.59E-01	1.00E+00	8.98E-01	1.00E+00	1.86E-01	1.00E+00	5.70E-01	1.00E+00	1.01E-01	1.00E+00	regulation of endocytosis	P
GO:0030101	12	6.80E-01	1.00E+00	3.72E-01	1.00E+00	5.97E-01	1.00E+00	3.60E-01	1.00E+00	6.50E-01	1.00E+00	4.15E-01	1.00E+00	7.34E-01	1.00E+00	4.70E-01	1.00E+00	natural killer cell activation	P
GO:0030111	28	6.32E-02	1.00E+00	1.57E-01	1.00E+00	2.59E-01	1.00E+00	2.85E-01	1.00E+00	4.89E-02	1.00E+00	3.33E-01	1.00E+00	1.52E-01	1.00E+00	8.21E-02	1.00E+00	regulation of Wnt receptor signaling pathwa	P
GO:0030117	61	2.62E-06	3.02E-03	3.59E-08	9.59E-04	9.97E-05	1.16E-02	1.12E-08	8.93E-04	2.74E-03	2.13E-01	1.11E-05	5.87E-03	4.86E-04	3.44E-02	1.10E-02	4.76E-01	membrane coat	C
GO:0030118	39	5.24E-04	4.40E-02	1.07E-05	4.51E-03	1.35E-03	7.90E-02	4.73E-05	1.07E-02	5.08E-02	1.00E+00	2.05E-04	2.33E-02	3.07E-03	8.78E-02	3.96E-02	1.00E+00	clathrin coat	C
GO:0030119	28	1.84E-03	2.12E-01	4.26E-04	4.74E-02	6.21E-03	4.69E-01	5.83E-04	4.20E-02	1.67E-01	1.00E+00	2.13E-03	1.27E-01	2.05E-03	8.40E-02	1.87E-01	1.00E+00	membrane coat adaptor complex	C
GO:0030120	30	3.74E-04	3.10E-02	1.78E-05	4.51E-03	6.23E-03	4.69E-01	2.03E-04	1.30E-02	1.98E-02	7.90E-01	6.00E-06	5.87E-03	1.93E-02	6.36E-01	1.49E-02	6.56E-01	vesicle coat	C
GO:0030125	16	6.71E-03	3.15E-01	7.09E-04	5.90E-02	9.55E-03	6.53E-01	3.37E-02	1.00E+00	1.04E-01	1.00E+00	3.70E-05	9.66E-03	4.80E-02	1.00E+00	4.19E-02	1.00E+00	clathrin vesicle coat	C
GO:0030131	28	1.84E-03	2.12E-01	4.26E-04	4.74E-02	6.21E-03	4.69E-01	5.83E-04	4.20E-02	1.67E-01	1.00E+00	2.13E-03	1.27E-01	2.05E-03	8.40E-02	1.87E-01	1.00E+00	clathrin adaptor complex	C
GO:0030133	41	3.67E-03	2.12E-01	3.32E-03	1.88E-01	3.08E-02	1.00E+00	1.36E-02	6.47E-01	1.23E-02	6.92E-01	2.35E-02	1.00E+00	2.88E-02	8.38E-01	3.31E-02	1.00E+00	transport vesicle	C
GO:0030135	120	2.42E-03	2.12E-01	9.65E-06	4.51E-03	2.56E-02	1.00E+00	8.16E-04	6.90E-02	6.03E-02	1.00E+00	6.33E-05	9.66E-03	2.52E-03	8.40E-02	8.28E-04	6.00E-02	coated vesicle	C
GO:0030136	103	1.62E-02	1.00E+00	5.15E-04	4.74E-02	4.70E-02	1.00E+00	2.78E-02	1.00E+00	1.75E-01	1.00E+00	8.50E-04	4.48E-02	9.18E-03	2.75E-01	4.86E-03	2.01E-01	clathrin-coated vesicle	C
GO:0030137	11	1.93E-03	2.12E-01	1.40E-04	1.50E-02	1.11E-01	1.00E+00	2.86E-06	2.89E-03	8.90E-03	6.92E-01	2.80E-03	1.44E-01	6.20E-03	2.75E-01	1.49E-02	6.56E-01	COPI-coated vesicle	C
GO:0030139	22	1.27E-01	1.00E+00	3.16E-02	1.00E+00	5.50E-02	1.00E+00	4.81E-02	1.00E+00	6.38E-01	1.00E+00	1.31E-01	1.00E+00	5.73E-02	1.00E+00	2.25E-02	9.99E-01	endocytic vesicle	C
GO:0030140	19	1.58E-02	1.00E+00	1.75E-02	7.63E-01	5.31E-02	1.00E+00	9.31E-02	1.00E+00	6.80E-02	1.00E+00	2.74E-02	1.00E+00	4.71E-02	1.00E+00	5.66E-02	1.00E+00	trans-Golgi network transport vesicle	C
GO:0030141	56	2.97E-02	1.00E+00	1.07E-02	4.69E-01	7.21E-02	1.00E+00	4.15E-02	1.00E+00	4.84E-02	1.00E+00	3.43E-02	1.00E+00	1.69E-01	1.00E+00	2.95E-02	9.99E-01	secretory granule	C
GO:0030145	140	1.03E-02	6.08E-01	1.69E-04	1.50E-02	6.23E-03	4.69E-01	8.58E-04	6.90E-02	4.25E-01	1.00E+00	5.03E-02	1.00E+00	4.58E-02	1.00E+00	1.11E-04	1.60E-02	manganese ion binding	F
GO:0030148	20	2.51E-02	1.00E+00	9.16E-03	4.69E-01	7.41E-02	1.00E+00	4.46E-01	1.00E+00	2.09E-01	1.00E+00	1.59E-03	1.22E-01	3.04E-02	8.38E-01	1.02E-01	1.00E+00	sphingolipid biosynthesis	P
GO:0030149	11	2.17E-03	2.12E-01	3.43E-02	1.00E+00	9.11E-03	6.53E-01	8.79E-02	1.00E+00	8.78E-03	6.92E-01	5.85E-03	4.21E-01	2.87E-02	8.38E-01	2.65E-01	1.00E+00	sphingolipid catabolism	P
GO:0030154	1418	9.25E-07	2.76E-03	2.34E-04	2.40E-02	9.77E-05	1.16E-02	7.60E-03	4.92E-01	2.05E-02	7.90E-01	4.46E-02	1.00E+00	1.09E-07	0.00E+00	6.40E-05	7.00E-03	cell differentiation	P
GO:0030155	65	2.18E-01	1.00E+00	2.66E-01	1.00E+00	5.63E-01	1.00E+00	5.30E-01	1.00E+00	2.14E-01	1.00E+00	1.43E-01	1.00E+00	9.33E-02	1.00E+00	3.77E-01	1.00E+00	regulation of cell adhesion	P
GO:0030162	15	3.22E-01	1.00E+00	4.02E-01	1.00E+00	1.60E-01	1.00E+00	4.46E-01	1.00E+00	1.74E-01	1.00E+00	5.45E-01	1.00E+00	8.02E-01	1.00E+00	3.48E-01	1.00E+00	regulation of proteolysis	P
GO:0030163	228	1.79E-08	2.57E-03	4.88E-11	0.00E+00	1.15E-08	9.80E-04	8.76E-12	0.00E+00	6.53E-05	2.40E-02	1.39E-05	5.87E-03	1.98E-02	6.36E-01	1.73E-05	7.00E-03	protein catabolism	P
GO:0030165	29	4.67E-01	1.00E+00	3.17E-01	1.00E+00	8.17E-01	1.00E+00	1.87E-01	1.00E+00	3.39E-01	1.00E+00	3.77E-01	1.00E+00	3.07E-01	1.00E+00	5.40E-01	1.00E+00	PDZ domain binding	F
GO:0030166	22	9.27E-01	1.00E+00	9.05E-01	1.00E+00	1.00E+00	1.00E+00	4.99E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	2.35E-01	1.00E+00	3.63E-01	1.00E+00	proteoglycan biosynthesis	P
GO:0030168	16	2.52E-01	1.00E+00	2.35E-01	1.00E+00	2.58E-01	1.00E+00	2.01E-01	1.00E+00	6.03E-01	1.00E+00	5.55E-01	1.00E+00	1.20E-01	1.00E+00	1.84E-01	1.00E+00	platelet activation	P
GO:0030169	14	1.14E-01	1.00E+00	1.47E-01	1.00E+00	2.47E-01	1.00E+00	1.68E-01	1.00E+00	1.66E-01	1.00E+00	6.91E-01	1.00E+00	9.06E-02	1.00E+00	1.11E-01	1.00E+00	low-density lipoprotein binding	F
GO:0030170	63	6.68E-02	1.00E+00	9.47E-02	1.00E+00	1.16E-01	1.00E+00	1.30E-01	1.00E+00	1.53E-01	1.00E+00	4.17E-02	1.00E+00	9.98E-02	1.00E+00	5.29E-01	1.00E+00	pyridoxal phosphate binding	F
GO:0030173	32	1.63E-01	1.00E+00	1.95E-01	1.00E+00	2.50E-01	1.00E+00	5.44E-01	1.00E+00	2.27E-01	1.00E+00	1.69E-01	1.00E+00	5.30E-02	1.00E+00	1.49E-01	1.00E+00	integral to Golgi membrane	C
GO:0030175	18	2.71E-01	1.00E+00	6.95E-02	1.00E+00	4.55E-01	1.00E+00	1.11E-01	1.00E+00	5.58E-01	1.00E+00	1.16E-01	1.00E+00	6.03E-02	1.00E+00	4.98E-02	1.00E+00	filopodium	C

GO:0030176	33	4.30E-02	1.00E+00	3.01E-04	4.40E-02	7.64E-02	1.00E+00	2.74E-03	1.61E-01	1.04E-01	1.00E+00	1.50E-03	9.30E-02	4.18E-02	1.00E+00	2.43E-02	9.99E-01	integral to endoplasmic reticulum membran	C
GO:0030178	20	1.05E-01	1.00E+00	1.13E-01	1.00E+00	5.21E-01	1.00E+00	4.29E-01	1.00E+00	7.35E-02	1.00E+00	1.82E-01	1.00E+00	2.17E-01	1.00E+00	6.05E-02	1.00E+00	negative regulation of Wnt receptor signalin	P
GO:0030182	358	4.20E-01	1.00E+00	6.14E-01	1.00E+00	9.03E-01	1.00E+00	7.81E-01	1.00E+00	3.49E-01	1.00E+00	8.68E-01	1.00E+00	1.57E-01	1.00E+00	9.46E-02	1.00E+00	neuron differentiation	P
GO:0030183	55	7.09E-01	1.00E+00	5.06E-01	1.00E+00	8.26E-01	1.00E+00	5.22E-01	1.00E+00	9.46E-01	1.00E+00	9.32E-01	1.00E+00	2.53E-01	1.00E+00	1.46E-01	1.00E+00	B cell differentiation	P
GO:0030193	13	3.08E-01	1.00E+00	3.88E-01	1.00E+00	2.67E-01	1.00E+00	8.19E-01	1.00E+00	2.71E-01	1.00E+00	3.78E-01	1.00E+00	4.76E-01	1.00E+00	2.45E-01	1.00E+00	regulation of blood coagulation	P
GO:0030198	83	7.32E-01	1.00E+00	2.39E-01	1.00E+00	9.21E-01	1.00E+00	7.81E-01	1.00E+00	9.62E-01	1.00E+00	4.43E-01	1.00E+00	1.76E-01	1.00E+00	1.28E-02	4.76E-01	extracellular matrix organization and biogen	P
GO:0030199	14	5.34E-01	1.00E+00	4.79E-01	1.00E+00	9.74E-01	1.00E+00	7.80E-01	1.00E+00	4.03E-01	1.00E+00	4.70E-01	1.00E+00	2.98E-01	1.00E+00	1.20E-01	1.00E+00	collagen fibril organization	P
GO:0030203	31	7.34E-02	1.00E+00	2.91E-01	1.00E+00	5.12E-01	1.00E+00	4.54E-02	1.00E+00	6.70E-02	1.00E+00	3.61E-01	1.00E+00	9.46E-02	1.00E+00	8.31E-01	1.00E+00	glycosaminoglycan metabolism	P
GO:0030216	37	8.54E-01	1.00E+00	5.07E-01	1.00E+00	7.61E-01	1.00E+00	5.75E-01	1.00E+00	9.38E-01	1.00E+00	3.80E-01	1.00E+00	8.12E-01	1.00E+00	4.32E-01	1.00E+00	keratinocyte differentiation	P
GO:0030217	72	1.16E-02	6.08E-01	1.03E-02	4.69E-01	6.94E-02	1.00E+00	1.08E-01	1.00E+00	1.65E-01	1.00E+00	1.35E-01	1.00E+00	6.59E-04	3.44E-02	9.40E-03	4.28E-01	T cell differentiation	P
GO:0030218	52	2.44E-02	1.00E+00	1.04E-01	1.00E+00	1.85E-02	1.00E+00	3.69E-02	1.00E+00	7.30E-01	1.00E+00	4.49E-01	1.00E+00	3.86E-03	2.23E-01	1.15E-01	1.00E+00	erythrocyte differentiation	P
GO:0030225	12	2.16E-01	1.00E+00	4.52E-01	1.00E+00	2.20E-01	1.00E+00	3.66E-01	1.00E+00	2.52E-01	1.00E+00	3.02E-01	1.00E+00	4.87E-01	1.00E+00	9.80E-01	1.00E+00	macrophage differentiation	P
GO:0030234	830	1.53E-02	1.00E+00	6.65E-06	4.51E-03	1.29E-01	1.00E+00	1.40E-04	1.30E-02	2.85E-01	1.00E+00	4.25E-05	9.66E-03	1.14E-03	6.14E-02	2.06E-03	7.90E-02	enzyme regulator activity	F
GO:0030238	12	8.88E-01	1.00E+00	4.47E-01	1.00E+00	8.12E-01	1.00E+00	8.58E-01	1.00E+00	9.93E-01	1.00E+00	5.13E-01	1.00E+00	3.57E-01	1.00E+00	1.20E-01	1.00E+00	male sex determination	P
GO:0030239	18	1.36E-01	1.00E+00	1.58E-01	1.00E+00	2.68E-01	1.00E+00	2.98E-01	1.00E+00	5.28E-01	1.00E+00	1.55E-01	1.00E+00	4.89E-02	1.00E+00	2.06E-01	1.00E+00	myofibril assembly	P
GO:0030246	345	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.97E-01	1.00E+00	4.40E-01	1.00E+00	carbohydrate binding	F
GO:0030247	95	9.19E-01	1.00E+00	8.19E-01	1.00E+00	8.62E-01	1.00E+00	9.53E-01	1.00E+00	8.45E-01	1.00E+00	8.38E-01	1.00E+00	9.51E-01	1.00E+00	3.01E-01	1.00E+00	polysaccharide binding	F
GO:0030258	37	5.25E-02	1.00E+00	7.78E-03	4.16E-01	7.03E-02	1.00E+00	1.08E-02	5.72E-01	7.36E-02	1.00E+00	3.52E-02	1.00E+00	3.27E-01	1.00E+00	5.32E-02	1.00E+00	lipid modification	P
GO:0030261	24	6.00E-03	3.09E-01	1.20E-06	3.92E-03	7.98E-04	4.90E-02	6.58E-09	8.93E-04	9.53E-02	1.00E+00	1.69E-02	6.68E-01	1.68E-01	1.00E+00	4.17E-03	2.01E-01	chromosome condensation	P
GO:0030262	17	6.72E-04	8.86E-02	4.28E-04	4.74E-02	1.25E-03	7.90E-02	1.21E-05	2.89E-03	2.42E-03	1.20E-01	7.66E-03	4.21E-01	4.87E-02	1.00E+00	3.09E-01	1.00E+00	apoptotic nuclear changes	P
GO:0030278	39	3.59E-01	1.00E+00	8.85E-01	1.00E+00	6.65E-01	1.00E+00	9.91E-01	1.00E+00	3.41E-01	1.00E+00	5.41E-01	1.00E+00	2.28E-01	1.00E+00	6.82E-01	1.00E+00	regulation of ossification	P
GO:0030279	13	4.08E-01	1.00E+00	6.29E-01	1.00E+00	6.03E-01	1.00E+00	8.60E-01	1.00E+00	8.59E-01	1.00E+00	5.43E-01	1.00E+00	1.72E-01	1.00E+00	1.60E-01	1.00E+00	negative regulation of ossification	P
GO:0030282	37	2.03E-01	1.00E+00	5.54E-01	1.00E+00	5.15E-01	1.00E+00	8.42E-01	1.00E+00	1.95E-01	1.00E+00	2.11E-01	1.00E+00	8.47E-02	1.00E+00	6.67E-01	1.00E+00	bone mineralization	P
GO:0030286	37	4.25E-01	1.00E+00	1.09E-01	1.00E+00	5.36E-01	1.00E+00	2.62E-01	1.00E+00	4.58E-01	1.00E+00	4.79E-01	1.00E+00	3.23E-01	1.00E+00	1.62E-01	1.00E+00	dynein complex	C
GO:0030288	22	9.64E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	9.92E-01	1.00E+00	8.53E-01	1.00E+00	1.00E+00	1.00E+00	8.08E-01	1.00E+00	6.73E-01	1.00E+00	periplasmic space (sensu Proteobacteria)	C
GO:0030295	11	5.90E-02	1.00E+00	2.56E-03	1.80E-01	2.30E-01	1.00E+00	1.25E-02	6.47E-01	2.00E-01	1.00E+00	2.10E-02	7.56E-01	8.24E-02	1.00E+00	2.03E-01	1.00E+00	protein kinase activator activity	F
GO:0030301	15	3.09E-01	1.00E+00	5.51E-01	1.00E+00	3.36E-01	1.00E+00	5.38E-01	1.00E+00	5.92E-01	1.00E+00	6.19E-01	1.00E+00	1.23E-01	1.00E+00	4.19E-01	1.00E+00	cholesterol transport	P
GO:0030308	48	5.36E-03	3.09E-01	6.29E-03	3.08E-01	5.01E-03	3.08E-01	2.17E-02	9.37E-01	1.84E-01	1.00E+00	9.13E-02	1.00E+00	2.71E-02	8.38E-01	4.50E-03	2.01E-01	negative regulation of cell growth	P
GO:0030312	26	9.63E-01	1.00E+00	9.33E-01	1.00E+00	9.94E-01	1.00E+00	9.64E-01	1.00E+00	8.93E-01	1.00E+00	9.91E-01	1.00E+00	8.19E-01	1.00E+00	3.47E-01	1.00E+00	external encapsulating structure	C
GO:0030313	24	9.68E-01	1.00E+00	9.88E-01	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	8.44E-01	1.00E+00	9.99E-01	1.00E+00	8.42E-01	1.00E+00	4.08E-01	1.00E+00	cell envelope	C
GO:0030315	18	8.20E-01	1.00E+00	8.34E-01	1.00E+00	9.00E-01	1.00E+00	7.87E-01	1.00E+00	9.89E-01	1.00E+00	7.73E-01	1.00E+00	2.75E-01	1.00E+00	8.66E-01	1.00E+00	T-tubule	C
GO:0030316	21	5.44E-01	1.00E+00	7.16E-01	1.00E+00	2.61E-01	1.00E+00	8.12E-01	1.00E+00	8.94E-01	1.00E+00	4.85E-01	1.00E+00	5.04E-01	1.00E+00	9.18E-01	1.00E+00	osteoclast differentiation	P
GO:0030317	30	7.52E-01	1.00E+00	7.98E-01	1.00E+00	5.97E-01	1.00E+00	8.95E-01	1.00E+00	7.65E-01	1.00E+00	8.09E-01	1.00E+00	9.10E-01	1.00E+00	6.24E-01	1.00E+00	sperm motility	P
GO:0030318	19	2.72E-01	1.00E+00	6.59E-01	1.00E+00	2.24E-01	1.00E+00	6.22E-01	1.00E+00	2.79E-01	1.00E+00	6.27E-01	1.00E+00	3.44E-01	1.00E+00	5.79E-01	1.00E+00	melanocyte differentiation	P
GO:0030321	10	9.62E-01	1.00E+00	9.86E-01	1.00E+00	9.07E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.30E-01	1.00E+00	4.14E-01	1.00E+00	transepithelial chloride transport	P
GO:0030323	94	4.77E-01	1.00E+00	5.21E-01	1.00E+00	3.22E-01	1.00E+00	5.02E-01	1.00E+00	7.80E-01	1.00E+00	7.23E-01	1.00E+00	2.43E-01	1.00E+00	1.86E-01	1.00E+00	respiratory tube development	P
GO:0030324	92	4.63E-01	1.00E+00	5.06E-01	1.00E+00	3.16E-01	1.00E+00	4.81E-01	1.00E+00	7.71E-01	1.00E+00	7.40E-01	1.00E+00	2.19E-01	1.00E+00	1.47E-01	1.00E+00	lung development	P
GO:0030325	10	1.00E+00	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	9.42E-01	1.00E+00	9.48E-01	1.00E+00	9.15E-01	1.00E+00	1.00E+00	1.00E+00	7.52E-01	1.00E+00	adrenal gland development	P
GO:0030326	85	8.15E-01	1.00E+00	9.71E-01	1.00E+00	8.18E-01	1.00E+00	9.82E-01	1.00E+00	8.46E-01	1.00E+00	9.76E-01	1.00E+00	5.90E-01	1.00E+00	6.58E-01	1.00E+00	embryonic limb morphogenesis	P
GO:0030330	17	5.91E-02	1.00E+00	1.26E-02	6.07E-01	2.35E-02	1.00E+00	6.16E-02	1.00E+00	5.91E-02	1.00E+00	4.81E-02	1.00E+00	5.04E-01	1.00E+00	4.53E-02	1.00E+00	DNA damage response, signal transduction	P
GO:0030334	87	5.35E-01	1.00E+00	1.74E-01	1.00E+00	8.03E-01	1.00E+00	3.06E-01	1.00E+00	7.14E-01	1.00E+00	3.14E-01	1.00E+00	2.12E-01	1.00E+00	9.07E-02	1.00E+00	regulation of cell migration	P
GO:0030335	37	8.20E-01	1.00E+00	3.88E-01	1.00E+00	9.32E-01	1.00E+00	6.29E-01	1.00E+00	9.70E-01	1.00E+00	6.33E-01	1.00E+00	3.04E-01	1.00E+00	1.62E-01	1.00E+00	positive regulation of cell migration	P
GO:0030336	24	3.29E-01	1.00E+00	1.40E-01	1.00E+00	6.10E-01	1.00E+00	7.43E-02	1.00E+00	2.63E-01	1.00E+00	1.78E-01	1.00E+00	5.45E-01	1.00E+00	5.14E-01	1.00E+00	negative regulation of cell migration	P
GO:0030374	21	3.98E-01	1.00E+00	8.19E-02	1.00E+00	8.11E-02	1.00E+00	3.51E-02	1.00E+00	1.63E-01	1.00E+00	1.79E-01	1.00E+00	9.35E-01	1.00E+00	6.54E-01	1.00E+00	ligand-dependent nuclear receptor transcrip	F
GO:0030375	12	5.37E-01	1.00E+00	3.29E-01	1.00E+00	1.95E-01	1.00E+00	1.61E-01	1.00E+00	3.33E-01	1.00E+00	2.74E-01	1.00E+00	8.48E-01	1.00E+00	8.53E-01	1.00E+00	thyroid hormone receptor coactivator activit	F
GO:0030384	61	2.06E-04	1.72E-02	1.20E-04	1.50E-02	2.15E-03	9.50E-02	4.52E-04	4.20E-02	1.29E-03	1.20E-01	6.39E-04	3.20E-02	1.84E-02	6.36E-01	7.97E-03	4.28E-01	phosphoinositide metabolism	P
GO:0030414	224	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.07E-01	1.00E+00	9.98E-01	1.00E+00	protease inhibitor activity	F
GO:0030424	84	5.33E-01	1.00E+00	7.83E-01	1.00E+00	7.14E-01	1.00E+00	9.85E-01	1.00E+00	5.58E-01	1.00E+00	6.86E-01	1.00E+00	3.52E-01	1.00E+00	2.66E-01	1.00E+00	axon	C
GO:0030425	78	7.59E-01	1.00E+00	1.12E-01	1.00E+00	9.78E-01	1.00E+00	1.90E-01	1.00E+00	8.33E-01	1.00E+00	4.89E-02	1.00E+00	2.63E-01	1.00E+00	2.81E-01	1.00E+00	dendrite	C
GO:0030426	34	7.44E-02	1.00E+00	1.81E-02	1.00E+00	1.53E-01	1.00E+00	1.29E-01	1.00E+00	4.96E-01	1.00E+00	3.17E-02	1.00E+00	5.19E-02	1.00E+00	1.50E-01	1.00E+00	growth cone	C
GO:0030427	34	7.44E-02	1.00E+00	1.81E-02	1.00E+00	1.53E-01	1.00E+00	1.29E-01	1.00E+00	4.96E-01	1.00E+00	3.17E-02	1.00E+00	5.19E-02	1.00E+00	1.50E-01	1.00E+00	site of polarized growth	C
GO:0030433	11	7.43E-02	1.00E+00	7.27E-06	4.51E-03	9.23E-02	1.00E+00	1.59E-03	9.60E-02	1.66E-01	1.00E+00	2.30E-02	1.00E+00	3.01E-01	1.00E+00	1.50E-01	1.00E+00	ER-associated protein catabolism	P
GO:0030496	10	2.90E-02	1.00E+00	1.83E-01	1.00E+00	4.72E-02	1.00E+00	1.92E-01	1.00E+00	3.82E-01	1.00E+00	1.49E-01	1.00E+00	5.22E-02	1.00E+00	3.15E-01	1.00E+00	midbody	C
GO:0030500	25	5.68E-01	1.00E+00	6.79E-01	1.00E+00	8.17E-01	1.00E+00	9.03E-01	1.00E+00	2.91E-01	1.00E+00	4.61E-01	1.00E+00	5.18E-01	1.00E+00	5.35E-01	1.00E+00	regulation of bone mineralization	P
GO:0030501	13	8.14E-01	1.00E+00	3.48E-01	1.00E+00	5.65E-01	1.00E+00	8.92E-01	1.00E+00	9.36E-01	1.00E+00	2.07E-01	1.00E+00	3.88E-01	1.00E+00	1.59E-01	1.00E+00	positive regulation of bone mineralization	P
GO:0030509	42	3.46E-01	1.00E+00	2.86E-01	1.00E+00	4.20E-01	1.00E+00	8.98E-01	1.00E+00	6.66E-01	1.00E+00	2.23E-01	1.00E+00	1.40E-01	1.00E+00	6.97E-02	1.00E+00	BMP signaling pathway	P
GO:0030510	21	2.92E-01	1.00E+00	4.92E-01	1.00E+00	4.06E-01	1.00E+00	9.98E-01	1.00E+00	3.90E-01	1.00E+00	7.53E-01	1.00E+00	2.64E-01	1.00E+00	4.19E-02	1.00E+00	regulation of BMP signaling pathway	P
GO:0030512	11	1.81E-02	1.00E+00	1.36E-01	1.00E+00	6.46E-02	1.00E+00	1.55E-01	1.00E+00	2.99E-02	1.00E+00	1.80E-01	1.00E+00	6.05E-02	1.00E+00	1.11E-01	1.00E+00	negative regulation of transforming growth f	P
GO:0030514	14	2.54E-01	1.00E+00	2.92E-01	1.00E+00	3.88E-01	1.00E+00	9.85E-01	1.00E+00	3.72E-01	1.00E+00	4.64E-01	1.00E+00	1.59E-01	1.00E+00	3.35E-02	1.00E+00	negative regulation of BMP signaling pathw	P
GO:0030516	15	1.26E-01	1.00E+00	2.73E-01	1.00E+00	3.74E-01	1.00E+00	4.10E-01	1.00E+00	2.38E-01	1.00E+00	5.92E-01	1.00E+00	2.20E-01	1.00E+00	9.05E-02	1.00E+00	regulation of axon extension	P
GO:0030518	24	1.80E-02	1.00E+00	6.97E-03	3.12E-01	1.94E-02	1.00E+00	1.31E-02	6.47E-01	1.17E-01	1.00E+00	1.09E-01	1.00E+00	8.51E-02	1.00E+00	3.46E-02	1.00E+00	steroid hormone receptor signaling pathway	P
GO:0030521	13	4.24E-02	1.00E+00	7.28E-03	3.12E-01	3.69E-03	2.20E-01	1.45E-02	6.47E-01	2.07E-01	1.00E+00	1.22E-01	1.00E+00	3.53E-01	1.00E+00	3.39E-02	1.00E+00	androgen receptor signaling pathway	P
GO:0030522	34	1.82E-02	1.00E+00	1.43E-02	6.07E-01	5.37E-02	1.00E+00	3.04E-02	1.00E+00	3.83E-02	1.00E+00	9.84E-02	1.00E+00	5.76E-02	1.00E+00	7.78E-02	1.00E+00	intracellular receptor-mediated signaling pa	P
GO:0030528	1412	3.59E-11	2.57E-03	1.36E-11	0.00E+00	4.74E-10	7.95E-04	2.20E-10	0.00E+00	7.34E-07	1.69E-03	2.70E-07	1.65E-03	3.28E-05	4.00E-03	3.85E-05	7.00E-03	transcription regulator activity	F
GO:0030529	743	1.01E-24	0.00E+00	1.13E-12	0.00E+00	9.42E-24	0.00E+00	6.90E-14	0.00E+00	5.95E-19	0.00E+00	1.46E-09	8.78E-04	5.02E-06	1.00E-03	4.83E-03	2.01E-01	ribonucleoprotein complex	C
GO:0030532	15	8.57E-05	1.43E-02	2.86E-02	1.00E+00	1.19E-02	6.53E-01	4.77E-03	2.88E-01	6.12E-06	1.69E-03	5.64E-02	1.00E+00	6.68E-03	2.75E-01	9.64E-01	1.00E+00	small nuclear ribonucleoprotein complex	C
GO:0030534	82	6.46E-01	1.00E+00	3.93E-01	1.00E+00	9.65E-01	1.00E+00	8.10E-01	1.00E+00	8.36E-01	1.00E+00	2.56E-01	1.00E+00	1.13E-01	1.00E+00	1.02E-01	1.00E+00	adult behavior	P
GO:0030539	11	8.90E-01	1.00E+00	9.95E-01	1.00E+00	9.42E-01	1.00E+00	9.29E-01	1.00E+00	6.11E-01	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	9.47E-01	1.00E+00	male genitalia development	P
GO:0030545	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	receptor regulator activity	F
GO:0030551	26	6.75E-01	1.00E+00	8.22E-01	1.00E+00	7.85E-01	1.00E+00	8.47E-01	1.00E+00	6.64E-01	1.00E+00	6.53E-01	1.00E+00	4.46E-01	1.00E+00	7.50E-01	1.00E+00	cyclic nucleotide binding	F
GO:0030552	18	4.79E-01	1.00E+00	4.69E-01	1.00E+00	6.13E-01	1.00E+00	5.19E-01	1.00E+00	5.69E-01	1.00E+00	3.96E-01	1.00E+00	2.78E-01	1.00E+00	5.03E-01	1.00E+00	cAMP binding	F
GO:0030554	1661	9.56E-27	0.00E+00	3.66E-40	0.00E+00	5.04E-25	0.00E+00	1.70E-28	0.00E+00	1.46E-14	0.00E+00	1.97E-26	0.00E+00	5.36E-09	0.00E+00	1.16E-18	0.00E+00	adenyl nucleotide binding	F
GO:0030574	17	2.77E-01	1.00E+00	8.57E-01	1.00E+00	3.87E-01	1.00E+00	9.18E-01	1.00E+00	6.00E-01	1.00E+00	8.89E-01	1.00E+00	1.27E-01	1.00E+00	5.60E-01	1.00E+00	collagen catabolism	P
GO:0030593	16	5.19E-01	1.00E+00	1.90E-01	1.00E+00	8.72E-01	1.00E+00	4.44E-01	1.00E+00	2.21E-01	1.00E+00	2.81E-01	1.00E+00	4.61E-01	1.00E+00	8.87E-02	1.00E+00	neutrophil chemotaxis	P
GO:0030594	239	7.88E-01	1.00E+00	8.23E-01	1.00E+00	9.84E-01	1.00E+00	9.27E-01	1.00E+00	7.28E-01	1.00E+00	8.80E-01	1.00E+00	1.73E-01	1.00E+00	2.41E-01	1.00E+00	neurotransmitter receptor activity	F

GO:0030595	30	2.03E-01	1.00E+00	3.15E-01	1.00E+00	3.84E-01	1.00E+00	4.18E-01	1.00E+00	2.57E-01	1.00E+00	3.73E-01	1.00E+00	9.63E-02	1.00E+00	1.73E-01	1.00E+00	leukocyte chemotaxis	P
GO:0030641	13	2.03E-02	1.00E+00	2.48E-02	1.00E+00	1.60E-01	1.00E+00	9.70E-03	5.72E-01	7.60E-03	6.92E-01	1.55E-01	1.00E+00	1.15E-01	1.00E+00	1.39E-01	1.00E+00	hydrogen ion homeostasis	P
GO:0030658	17	8.21E-02	1.00E+00	3.40E-02	1.00E+00	1.03E-01	1.00E+00	1.01E-01	1.00E+00	3.13E-01	1.00E+00	3.14E-02	1.00E+00	1.32E-01	1.00E+00	1.50E-01	1.00E+00	transport vesicle membrane	C
GO:0030659	94	4.21E-04	3.10E-02	2.21E-05	7.00E-03	2.44E-03	1.07E-01	1.46E-04	1.30E-02	1.60E-02	6.92E-01	3.35E-04	2.33E-02	8.47E-03	2.75E-01	5.68E-03	4.28E-01	cytoplasmic vesicle membrane	C
GO:0030660	19	2.68E-02	1.00E+00	1.74E-02	7.63E-01	4.69E-02	1.00E+00	8.45E-02	1.00E+00	1.94E-01	1.00E+00	9.03E-03	5.03E-01	7.48E-02	1.00E+00	1.30E-01	1.00E+00	Golgi-associated vesicle membrane	C
GO:0030662	33	1.49E-03	1.29E-01	4.17E-05	7.00E-03	1.45E-02	6.53E-01	7.03E-04	4.20E-02	5.74E-02	1.00E+00	5.04E-05	9.66E-03	1.44E-02	4.78E-01	8.77E-03	4.28E-01	coated vesicle membrane	C
GO:0030665	19	2.13E-02	1.00E+00	1.92E-03	1.30E-01	2.76E-02	1.00E+00	7.20E-02	1.00E+00	2.29E-01	1.00E+00	8.43E-04	4.48E-02	3.60E-02	8.38E-01	2.36E-02	9.99E-01	clathrin coated vesicle membrane	C
GO:0030667	11	2.98E-01	1.00E+00	5.10E-02	1.00E+00	2.18E-01	1.00E+00	9.73E-02	1.00E+00	3.74E-01	1.00E+00	3.64E-02	1.00E+00	5.39E-01	1.00E+00	1.89E-01	1.00E+00	secretory granule membrane	C
GO:0030672	16	6.14E-01	1.00E+00	4.78E-01	1.00E+00	6.08E-01	1.00E+00	5.22E-01	1.00E+00	5.01E-01	1.00E+00	3.47E-01	1.00E+00	5.02E-01	1.00E+00	5.11E-01	1.00E+00	synaptic vesicle membrane	C
GO:0030674	35	2.58E-02	1.00E+00	1.19E-02	6.07E-01	1.13E-01	1.00E+00	2.64E-03	1.61E-01	4.20E-02	1.00E+00	9.62E-02	1.00E+00	9.18E-02	1.00E+00	4.36E-02	1.00E+00	protein binding, bridging	F
GO:0030693	16	4.93E-01	1.00E+00	8.33E-01	1.00E+00	7.23E-01	1.00E+00	9.31E-01	1.00E+00	3.88E-01	1.00E+00	6.26E-01	1.00E+00	4.60E-01	1.00E+00	7.34E-01	1.00E+00	caspase activity	F
GO:0030695	368	4.38E-02	1.00E+00	3.64E-07	3.92E-03	1.62E-01	1.00E+00	8.57E-05	1.30E-02	4.22E-01	1.00E+00	2.80E-06	2.90E-03	2.20E-02	6.36E-01	7.47E-04	6.00E-02	GTPase regulator activity	F
GO:0030705	135	2.76E-05	7.00E-03	8.57E-06	4.51E-03	4.75E-06	2.91E-03	6.47E-04	4.20E-02	1.78E-03	1.20E-01	2.06E-04	2.33E-02	3.85E-03	2.23E-01	4.51E-04	3.00E-02	cytoskeleton-dependent intracellular transp	P
GO:0030728	11	8.71E-01	1.00E+00	9.91E-01	1.00E+00	8.17E-01	1.00E+00	9.32E-01	1.00E+00	7.93E-01	1.00E+00	1.00E+00	1.00E+00	7.99E-01	1.00E+00	9.89E-01	1.00E+00	ovulation	P
GO:0030799	16	1.58E-01	1.00E+00	1.44E-01	1.00E+00	5.20E-01	1.00E+00	3.39E-01	1.00E+00	1.48E-01	1.00E+00	2.01E-01	1.00E+00	8.96E-02	1.00E+00	7.03E-02	1.00E+00	regulation of cyclic nucleotide metabolism	P
GO:0030801	10	9.64E-02	1.00E+00	9.74E-02	1.00E+00	3.57E-01	1.00E+00	2.14E-01	1.00E+00	9.14E-02	1.00E+00	1.25E-01	1.00E+00	1.15E-01	1.00E+00	7.11E-02	1.00E+00	positive regulation of cyclic nucleotide meta	P
GO:0030802	12	8.36E-02	1.00E+00	2.29E-01	1.00E+00	3.48E-01	1.00E+00	2.67E-01	1.00E+00	9.60E-02	1.00E+00	4.80E-01	1.00E+00	4.47E-02	1.00E+00	1.05E-01	1.00E+00	regulation of cyclic nucleotide biosynthesis	P
GO:0030808	12	8.36E-02	1.00E+00	2.29E-01	1.00E+00	3.48E-01	1.00E+00	2.67E-01	1.00E+00	9.60E-02	1.00E+00	4.80E-01	1.00E+00	4.47E-02	1.00E+00	1.05E-01	1.00E+00	regulation of nucleotide biosynthesis	P
GO:0030814	11	2.20E-01	1.00E+00	8.14E-02	1.00E+00	5.00E-01	1.00E+00	3.68E-01	1.00E+00	3.29E-01	1.00E+00	1.44E-01	1.00E+00	4.97E-02	1.00E+00	1.92E-02	7.36E-01	regulation of cAMP metabolism	P
GO:0030832	54	8.49E-03	6.08E-01	7.99E-04	8.10E-02	8.85E-02	1.00E+00	1.40E-02	6.47E-01	1.31E-01	1.00E+00	2.60E-02	1.00E+00	9.47E-03	2.75E-01	3.33E-04	3.00E-02	regulation of actin filament length	P
GO:0030833	28	1.81E-02	1.00E+00	3.64E-02	1.00E+00	4.96E-02	1.00E+00	1.24E-01	1.00E+00	2.08E-01	1.00E+00	1.71E-01	1.00E+00	2.54E-02	8.38E-01	5.20E-03	2.01E-01	regulation of actin filament polymerization	P
GO:0030834	23	1.14E-01	1.00E+00	3.06E-03	1.88E-01	4.29E-01	1.00E+00	5.37E-02	1.00E+00	2.44E-01	1.00E+00	3.76E-02	1.00E+00	8.37E-02	1.00E+00	1.03E-02	4.76E-01	regulation of actin filament depolymerizatio	P
GO:0030835	21	6.57E-02	1.00E+00	3.57E-03	1.88E-01	3.55E-01	1.00E+00	5.68E-02	1.00E+00	1.54E-01	1.00E+00	2.47E-02	1.00E+00	7.47E-02	1.00E+00	1.07E-02	4.76E-01	negative regulation of actin filament depoly	P
GO:0030855	56	6.16E-01	1.00E+00	2.04E-01	1.00E+00	5.10E-01	1.00E+00	6.76E-01	1.00E+00	9.09E-01	1.00E+00	3.06E-01	1.00E+00	2.85E-01	1.00E+00	7.90E-03	4.28E-01	epithelial cell differentiation	P
GO:0030856	10	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	4.71E-01	1.00E+00	regulation of epithelial cell differentiation	P
GO:0030863	32	3.90E-02	1.00E+00	5.74E-07	3.92E-03	1.51E-02	6.53E-01	1.29E-04	1.30E-02	2.25E-01	1.00E+00	6.92E-03	4.21E-01	2.41E-01	1.00E+00	7.07E-04	6.00E-02	cortical cytoskeleton	C
GO:0030864	22	2.46E-01	1.00E+00	2.58E-03	1.80E-01	9.45E-02	1.00E+00	4.31E-03	2.88E-01	4.95E-01	1.00E+00	6.96E-02	1.00E+00	6.39E-01	1.00E+00	6.65E-02	1.00E+00	cortical actin cytoskeleton	C
GO:0030865	14	2.25E-02	1.00E+00	1.69E-03	9.65E-02	3.85E-02	1.00E+00	6.24E-02	1.00E+00	5.40E-02	1.00E+00	5.43E-03	3.43E-01	2.30E-01	1.00E+00	1.82E-02	6.56E-01	cortical cytoskeleton organization and biogg	P
GO:0030866	11	3.76E-02	1.00E+00	6.75E-03	3.12E-01	8.66E-02	1.00E+00	1.42E-01	1.00E+00	6.03E-02	1.00E+00	1.23E-02	5.03E-01	2.70E-01	1.00E+00	2.19E-02	9.99E-01	cortical actin cytoskeleton organization and	P
GO:0030867	10	2.07E-01	1.00E+00	1.45E-01	1.00E+00	2.31E-01	1.00E+00	1.91E-01	1.00E+00	9.32E-01	1.00E+00	1.13E-01	1.00E+00	3.22E-02	8.38E-01	3.84E-01	1.00E+00	rough endoplasmic reticulum membrane	C
GO:0030878	12	7.59E-01	1.00E+00	9.97E-01	1.00E+00	8.77E-01	1.00E+00	9.88E-01	1.00E+00	6.96E-01	1.00E+00	9.07E-01	1.00E+00	7.25E-01	1.00E+00	1.00E+00	1.00E+00	thyroid gland development	P
GO:0030879	29	6.52E-01	1.00E+00	8.17E-01	1.00E+00	7.45E-01	1.00E+00	9.58E-01	1.00E+00	7.94E-01	1.00E+00	5.72E-01	1.00E+00	4.27E-01	1.00E+00	7.08E-01	1.00E+00	mammary gland development	P
GO:0030880	16	1.44E-05	7.00E-03	1.26E-02	6.07E-01	1.91E-09	9.80E-04	2.41E-03	1.39E-01	2.37E-03	1.20E-01	4.46E-02	1.00E+00	1.28E-01	1.00E+00	3.65E-01	1.00E+00	RNA polymerase complex	C
GO:0030888	29	9.48E-01	1.00E+00	3.46E-01	1.00E+00	9.99E-01	1.00E+00	4.46E-01	1.00E+00	8.37E-01	1.00E+00	9.13E-01	1.00E+00	4.95E-01	1.00E+00	8.43E-02	1.00E+00	regulation of B cell proliferation	P
GO:0030890	20	8.85E-01	1.00E+00	3.49E-01	1.00E+00	9.98E-01	1.00E+00	5.13E-01	1.00E+00	7.66E-01	1.00E+00	1.00E+00	1.00E+00	3.91E-01	1.00E+00	4.46E-02	1.00E+00	positive regulation of B cell proliferation	P
GO:0030894	10	3.12E-03	2.12E-01	4.01E-03	1.88E-01	4.16E-03	2.20E-01	3.29E-03	1.76E-01	6.70E-04	1.20E-01	1.18E-01	1.00E+00	9.51E-02	1.00E+00	2.28E-01	1.00E+00	replisome	C
GO:0030900	142	4.39E-01	1.00E+00	5.73E-01	1.00E+00	6.49E-01	1.00E+00	7.34E-01	1.00E+00	5.49E-01	1.00E+00	3.63E-01	1.00E+00	1.66E-01	1.00E+00	6.28E-01	1.00E+00	forebrain development	P
GO:0030901	14	3.39E-01	1.00E+00	9.29E-01	1.00E+00	7.39E-01	1.00E+00	9.70E-01	1.00E+00	3.55E-01	1.00E+00	8.74E-01	1.00E+00	1.06E-01	1.00E+00	6.99E-01	1.00E+00	midbrain development	P
GO:0030902	57	6.08E-01	1.00E+00	9.99E-01	1.00E+00	7.50E-01	1.00E+00	9.97E-01	1.00E+00	6.59E-01	1.00E+00	9.85E-01	1.00E+00	2.13E-01	1.00E+00	9.02E-01	1.00E+00	hindbrain development	P
GO:0030955	108	9.72E-01	1.00E+00	8.37E-01	1.00E+00	9.87E-01	1.00E+00	9.19E-01	1.00E+00	9.95E-01	1.00E+00	5.64E-01	1.00E+00	3.96E-01	1.00E+00	4.91E-01	1.00E+00	potassium ion binding	F
GO:0030968	16	7.75E-02	1.00E+00	1.65E-02	7.63E-01	2.20E-01	1.00E+00	1.26E-02	6.47E-01	1.12E-01	1.00E+00	1.53E-01	1.00E+00	6.59E-02	1.00E+00	7.47E-02	1.00E+00	unfolded protein response	P
GO:0030983	12	5.32E-01	1.00E+00	1.51E-01	1.00E+00	5.90E-01	1.00E+00	3.48E-01	1.00E+00	6.99E-01	1.00E+00	8.90E-02	1.00E+00	5.39E-01	1.00E+00	1.45E-01	1.00E+00	mismatched DNA binding	F
GO:0031012	326	7.98E-01	1.00E+00	6.28E-01	1.00E+00	9.83E-01	1.00E+00	9.67E-01	1.00E+00	6.94E-01	1.00E+00	4.85E-01	1.00E+00	2.11E-01	1.00E+00	8.53E-02	1.00E+00	extracellular matrix	C
GO:0031016	26	3.29E-01	1.00E+00	9.84E-01	1.00E+00	4.79E-01	1.00E+00	9.93E-01	1.00E+00	1.21E-01	1.00E+00	9.72E-01	1.00E+00	4.04E-01	1.00E+00	5.38E-01	1.00E+00	pancreas development	P
GO:0031018	16	4.72E-01	1.00E+00	9.92E-01	1.00E+00	6.05E-01	1.00E+00	1.00E+00	1.00E+00	2.18E-01	1.00E+00	9.16E-01	1.00E+00	5.96E-01	1.00E+00	7.83E-01	1.00E+00	endocrine pancreas development	P
GO:0031023	16	4.24E-03	2.14E-01	9.82E-05	1.50E-02	1.08E-03	7.90E-02	4.53E-04	4.20E-02	5.21E-02	1.00E+00	2.23E-03	1.27E-01	4.03E-01	1.00E+00	6.48E-02	1.00E+00	microtubule organizing center organization	P
GO:0031032	12	4.94E-01	1.00E+00	4.85E-02	1.00E+00	7.17E-01	1.00E+00	5.50E-02	1.00E+00	9.71E-01	1.00E+00	2.29E-01	1.00E+00	7.48E-02	1.00E+00	7.39E-02	1.00E+00	actomyosin structure organization and biog	P
GO:0031047	12	1.25E-02	6.08E-01	5.24E-04	4.74E-02	7.09E-03	4.69E-01	1.01E-03	9.40E-02	2.04E-02	7.90E-01	6.19E-02	1.00E+00	3.95E-01	1.00E+00	2.40E-03	7.90E-02	RNA-mediated gene silencing	P
GO:0031069	17	5.91E-01	1.00E+00	6.72E-01	1.00E+00	9.40E-01	1.00E+00	8.10E-01	1.00E+00	6.12E-01	1.00E+00	6.34E-01	1.00E+00	1.24E-01	1.00E+00	1.24E-01	1.00E+00	hair follicle morphogenesis	P
GO:0031072	64	1.02E-02	6.08E-01	1.81E-03	9.65E-02	3.03E-02	1.00E+00	1.28E-03	9.40E-02	6.66E-03	6.92E-01	2.02E-02	7.56E-01	1.88E-01	1.00E+00	6.03E-02	1.00E+00	heat shock protein binding	F
GO:0031090	1437	9.47E-29	0.00E+00	7.36E-36	0.00E+00	5.98E-19	0.00E+00	8.86E-25	0.00E+00	4.36E-21	0.00E+00	3.43E-24	0.00E+00	1.73E-12	0.00E+00	1.25E-14	0.00E+00	organelle membrane	C
GO:0031098	53	3.96E-01	1.00E+00	4.65E-01	1.00E+00	5.18E-01	1.00E+00	7.04E-01	1.00E+00	4.45E-01	1.00E+00	6.20E-01	1.00E+00	4.42E-01	1.00E+00	1.54E-01	1.00E+00	stress-activated protein kinase signaling pa	P
GO:0031099	28	1.51E-01	1.00E+00	2.28E-01	1.00E+00	4.54E-01	1.00E+00	2.54E-01	1.00E+00	3.75E-02	1.00E+00	2.72E-01	1.00E+00	7.07E-01	1.00E+00	1.20E-01	1.00E+00	regeneration	P
GO:0031105	13	1.44E-01	1.00E+00	1.32E-02	6.07E-01	3.35E-01	1.00E+00	2.99E-02	1.00E+00	5.77E-01	1.00E+00	1.35E-01	1.00E+00	2.34E-02	8.38E-01	2.20E-01	1.00E+00	septin complex	C
GO:0031109	31	4.93E-02	1.00E+00	5.61E-02	1.00E+00	1.23E-01	1.00E+00	1.27E-01	1.00E+00	2.29E-01	1.00E+00	7.69E-02	1.00E+00	1.64E-02	4.88E-01	6.11E-02	1.00E+00	microtubule polymerization or depolymeriza	P
GO:0031110	28	4.39E-02	1.00E+00	8.77E-02	1.00E+00	7.89E-02	1.00E+00	1.18E-01	1.00E+00	2.96E-01	1.00E+00	2.12E-01	1.00E+00	1.20E-02	3.39E-01	4.36E-02	1.00E+00	regulation of microtubule polymerization or	P
GO:0031111	18	3.20E-03	2.12E-01	5.87E-03	3.08E-01	6.59E-03	4.69E-01	2.65E-02	1.00E+00	6.58E-02	1.00E+00	2.36E-02	1.00E+00	4.05E-03	2.23E-01	2.14E-02	9.99E-01	negative regulation of microtubule polymeri	P
GO:0031112	11	7.92E-01	1.00E+00	6.18E-01	1.00E+00	9.95E-01	1.00E+00	6.76E-01	1.00E+00	9.64E-01	1.00E+00	7.75E-01	1.00E+00	1.54E-01	1.00E+00	2.09E-01	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031113	12	6.59E-01	1.00E+00	3.27E-01	1.00E+00	8.54E-01	1.00E+00	3.83E-01	1.00E+00	9.90E-01	1.00E+00	6.18E-01	1.00E+00	5.95E-02	1.00E+00	9.99E-02	1.00E+00	regulation of microtubule polymerization	P
GO:0031114	16	4.91E-03	2.72E-01	2.70E-02	1.00E+00	1.37E-02	6.53E-01	6.15E-02	1.00E+00	1.86E-02	7.90E-01	3.35E-02	1.00E+00	1.61E-02	4.88E-01	6.48E-02	1.00E+00	regulation of microtubule depolymerization	P
GO:0031116	10	8.06E-01	1.00E+00	6.17E-01	1.00E+00	9.93E-01	1.00E+00	6.10E-01	1.00E+00	9.39E-01	1.00E+00	7.33E-01	1.00E+00	2.64E-01	1.00E+00	2.93E-01	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031123	16	1.79E-01	1.00E+00	3.32E-02	1.00E+00	1.05E-02	6.53E-01	3.93E-02	1.00E+00	2.76E-01	1.00E+00	1.69E-01	1.00E+00	8.91E-01	1.00E+00	1.39E-01	1.00E+00	RNA 3'-end processing	P
GO:0031124	12	2.58E-01	1.00E+00	1.24E-01	1.00E+00	6.32E-02	1.00E+00	1.15E-01	1.00E+00	2.03E-01	1.00E+00	2.43E-01	1.00E+00	9.22E-01	1.00E+00	6.92E-01	1.00E+00	mRNA 3'-end processing	P
GO:0031128	15	8.05E-01	1.00E+00	8.91E-01	1.00E+00	9.22E-01	1.00E+00	5.97E-01	1.00E+00	6.10E-01	1.00E+00	9.82E-01	1.00E+00	7.18E-01	1.00E+00	8.57E-01	1.00E+00	induction	P
GO:0031175	231	3.27E-01	1.00E+00	2.93E-01	1.00E+00	7.36E-01	1.00E+00	6.91E-01	1.00E+00	2.20E-01	1.00E+00	4.48E-01	1.00E+00	2.91E-01	1.00E+00	4.92E-02	1.00E+00	neurite development	P
GO:0031177	20	3.92E-02	1.00E+00	3.73E-02	1.00E+00	1.18E-01	1.00E+00	2.83E-02	1.00E+00	1.08E-01	1.00E+00	3.39E-01	1.00E+00	6.04E-02	1.00E+00	1.34E-01	1.00E+00	phosphopantetheine binding	F
GO:0031202	13	1.29E-04	1.43E-02	9.62E-03	4.69E-01	2.23E-03	1.03E-01	9.76E-03	5.72E-01	7.04E-04	1.20E-01	5.17E-02	1.00E+00	5.15E-03	2.23E-01	1.66E-01	1.00E+00	RNA splicing factor activity, transesterificati	F
GO:0031214	151	3.86E-02	1.00E+00	2.68E-01	1.00E+00	4.61E-01	1.00E+00	2.99E-01	1.00E+00	2.56E-02	1.00E+00	3.57E-01	1.00E+00	5.45E-02	1.00E+00	3.30E-01	1.00E+00	biomineral formation	P
GO:0031224	6242	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	intrinsic to membrane	C
GO:0031225	125	6.45E-01	1.00E+00	8.57E-01	1.00E+00	6.37E-01	1.00E+00	8.92E-01	1.00E+00	9.90E-01	1.00E+00	8.25E-01	1.00E+00	8.54E-02	1.00E+00	4.82E-01	1.00E+00	anchored to membrane	C
GO:0031226	523	9.45E-01	1.00E+00	2.30E-01	1.00E+00	9.59E-01	1.00E+00	7.50E-01	1.00E+00	9.91E-01	1.00E+00	3.02E-01	1.00E+00	2.40E-01	1.00E+00	4.57E-03	2.01E-01	intrinsic to plasma membrane	C
GO:0031227	44	1.04E-01	1.00E+00	2.80E-02	1.00E+00	1.74E-01	1.00E+00	1.14E-01	1.00E+00	1.46E-01	1.00E+00	2.23E-02	1.00E+00	1.10E-01	1.00E+00	7.88E-02	1.00E+00	intrinsic to endoplasmic reticulum membran	C
GO:0031228	32	1.63E-01	1.00E+00	1.95E-01	1.00E+00	2.50E-01	1.00E+00	5.44E-01	1.00E+00	2.27E-01	1.00E+00	1.69E-01	1.00E+00	5.30E-02	1.00E+00	1.49E-01	1.00E+00	intrinsic to Golgi membrane	C
GO:0031252	93	1.41E-04	1.43E-02	5.04E-05	7.00E-03	2.05E-03	9.50E-02	1.38E-03	9.40E-02	6.75E-03	6.92E-01	1.19E-03	9.00E-02	2.29E-03	8.40E-02	1.30E-03	6.00E-02	leading edge	C
GO:0031253	18	3.82E-01	1.00E+00	5.18E-02	1.00E+00	7.89E-01	1.00E+00	3.41E-01	1.00E+00	5.26E-01	1.00E+00	4.89E-02	1.00E+00	1.21E-01	1.00E+00	1.07E-02	4.76E-01	cell projection membrane	C

GO:0031267	62	5.14E-02	1.00E+00	1.98E-04	2.40E-02	2.37E-01	1.00E+00	4.72E-03	2.88E-01	1.86E-01	1.00E+00	3.40E-03	1.51E-01	3.13E-02	8.38E-01	9.37E-04	6.00E-02	small GTPase binding	F
GO:0031279	23	6.25E-01	1.00E+00	2.51E-01	1.00E+00	7.51E-01	1.00E+00	5.51E-01	1.00E+00	3.89E-01	1.00E+00	2.08E-01	1.00E+00	5.39E-01	1.00E+00	1.22E-01	1.00E+00	regulation of cyclase activity	P
GO:0031281	17	9.79E-01	1.00E+00	4.00E-01	1.00E+00	9.99E-01	1.00E+00	8.16E-01	1.00E+00	6.46E-01	1.00E+00	3.99E-01	1.00E+00	8.87E-01	1.00E+00	9.54E-02	1.00E+00	positive regulation of cyclase activity	P
GO:0031290	11	9.98E-01	1.00E+00	6.97E-01	1.00E+00	9.97E-01	1.00E+00	6.44E-01	1.00E+00	8.82E-01	1.00E+00	6.62E-01	1.00E+00	1.00E+00	1.00E+00	7.48E-01	1.00E+00	retinal ganglion cell axon guidance	P
GO:0031300	94	3.97E-03	2.12E-01	4.79E-04	4.74E-02	7.98E-02	1.00E+00	7.91E-03	4.92E-01	2.55E-02	1.00E+00	1.63E-03	1.22E-01	2.01E-04	1.20E-02	9.07E-03	4.28E-01	intrinsic to organelle membrane	C
GO:0031301	80	2.04E-03	2.12E-01	1.61E-05	4.51E-03	2.98E-02	1.00E+00	1.19E-03	9.40E-02	2.04E-02	7.90E-01	3.54E-04	2.33E-02	2.17E-04	1.20E-02	2.17E-03	7.90E-02	integral to organelle membrane	C
GO:0031323	2816	7.00E-29	0.00E+00	3.01E-39	0.00E+00	4.82E-28	0.00E+00	5.98E-37	0.00E+00	9.15E-20	0.00E+00	5.18E-27	0.00E+00	5.29E-08	0.00E+00	1.41E-12	0.00E+00	regulation of cellular metabolism	P
GO:0031324	424	1.24E-13	0.00E+00	1.28E-13	0.00E+00	1.73E-13	7.08E-04	2.58E-11	0.00E+00	1.43E-06	1.69E-03	3.38E-08	9.03E-04	9.01E-08	0.00E+00	9.64E-08	9.38E-04	negative regulation of cellular metabolism	P
GO:0031325	562	4.30E-06	3.02E-03	2.09E-08	9.59E-04	2.00E-05	3.00E-03	7.72E-05	1.30E-02	3.88E-02	1.00E+00	3.21E-05	9.52E-03	7.26E-06	1.00E-03	1.51E-08	0.00E+00	positive regulation of cellular metabolism	P
GO:0031326	182	8.08E-04	8.86E-02	3.88E-06	4.51E-03	1.29E-02	6.53E-01	2.28E-03	1.39E-01	4.90E-02	1.00E+00	7.21E-04	4.48E-02	6.99E-04	3.44E-02	3.87E-05	7.00E-03	regulation of cellular biosynthesis	P
GO:0031327	41	1.60E-04	1.72E-02	5.99E-05	7.00E-03	9.80E-04	5.10E-02	1.24E-02	6.47E-01	1.92E-02	7.90E-01	1.47E-03	9.30E-02	2.61E-03	8.40E-02	3.71E-03	1.27E-01	negative regulation of cellular biosynthesis	P
GO:0031328	70	3.60E-01	1.00E+00	3.38E-02	1.00E+00	8.13E-01	1.00E+00	3.47E-01	1.00E+00	8.50E-01	1.00E+00	3.99E-01	1.00E+00	9.28E-03	2.75E-01	2.33E-04	2.33E-02	positive regulation of cellular biosynthesis	P
GO:0031341	23	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	9.92E-01	1.00E+00	9.80E-01	1.00E+00	9.93E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	regulation of cell killing	P
GO:0031344	10	1.67E-01	1.00E+00	1.78E-01	1.00E+00	4.00E-02	1.00E+00	2.90E-01	1.00E+00	8.74E-01	1.00E+00	1.30E-01	1.00E+00	2.57E-01	1.00E+00	1.17E-01	1.00E+00	regulation of cell projection organization and	P
GO:0031396	16	4.91E-01	1.00E+00	1.30E-01	1.00E+00	5.02E-02	1.00E+00	9.29E-02	1.00E+00	7.66E-01	1.00E+00	7.76E-02	1.00E+00	5.61E-01	1.00E+00	4.64E-01	1.00E+00	regulation of protein ubiquitination	P
GO:0031399	17	5.72E-01	1.00E+00	1.40E-01	1.00E+00	7.59E-02	1.00E+00	6.35E-02	1.00E+00	8.06E-01	1.00E+00	1.13E-01	1.00E+00	5.94E-01	1.00E+00	4.58E-01	1.00E+00	regulation of protein modification	P
GO:0031402	99	8.05E-01	1.00E+00	5.50E-01	1.00E+00	7.97E-01	1.00E+00	2.17E-01	1.00E+00	6.22E-01	1.00E+00	9.14E-01	1.00E+00	8.38E-01	1.00E+00	7.41E-01	1.00E+00	sodium ion binding	F
GO:0031404	62	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	chloride ion binding	F
GO:0031410	437	4.01E-13	0.00E+00	2.04E-22	0.00E+00	2.32E-09	9.80E-04	3.66E-17	0.00E+00	5.28E-08	9.59E-04	6.80E-12	6.20E-04	9.99E-08	0.00E+00	2.23E-12	0.00E+00	cytoplasmic vesicle	C
GO:0031418	18	2.43E-01	1.00E+00	3.33E-01	1.00E+00	3.84E-01	1.00E+00	3.78E-01	1.00E+00	7.63E-01	1.00E+00	6.77E-02	1.00E+00	1.10E-01	1.00E+00	8.28E-01	1.00E+00	L-ascorbic acid binding	F
GO:0031420	194	9.74E-01	1.00E+00	8.28E-01	1.00E+00	9.65E-01	1.00E+00	8.31E-01	1.00E+00	9.82E-01	1.00E+00	7.62E-01	1.00E+00	7.20E-01	1.00E+00	6.11E-01	1.00E+00	alkali metal ion binding	F
GO:0031424	36	9.48E-01	1.00E+00	9.15E-01	1.00E+00	8.88E-01	1.00E+00	7.85E-01	1.00E+00	6.44E-01	1.00E+00	7.20E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	keratinization	P
GO:0031461	13	3.18E-02	1.00E+00	5.39E-03	3.08E-01	2.29E-02	1.00E+00	5.23E-03	2.88E-01	1.03E-01	1.00E+00	2.32E-02	1.00E+00	2.49E-01	1.00E+00	3.11E-01	1.00E+00	cullin-RING ubiquitin ligase complex	C
GO:0031497	188	5.15E-01	1.00E+00	6.50E-01	1.00E+00	1.17E-01	1.00E+00	2.82E-02	1.00E+00	9.54E-01	1.00E+00	9.44E-01	1.00E+00	3.81E-01	1.00E+00	9.62E-01	1.00E+00	chromatin assembly	P
GO:0031507	16	2.33E-03	2.12E-01	2.35E-03	1.71E-01	6.62E-03	4.69E-01	4.14E-03	2.88E-01	1.87E-02	7.90E-01	9.35E-02	1.00E+00	6.57E-03	2.75E-01	1.35E-02	4.76E-01	heterochromatin formation	P
GO:0031513	22	4.52E-01	1.00E+00	1.31E-01	1.00E+00	8.40E-01	1.00E+00	3.11E-01	1.00E+00	2.72E-01	1.00E+00	7.02E-02	1.00E+00	2.83E-01	1.00E+00	1.30E-01	1.00E+00	nonmotile primary cilium	C
GO:0031519	11	1.25E-01	1.00E+00	2.32E-01	1.00E+00	1.45E-01	1.00E+00	1.40E-01	1.00E+00	1.41E-01	1.00E+00	3.65E-01	1.00E+00	2.44E-01	1.00E+00	5.40E-01	1.00E+00	PcG protein complex	C
GO:0031526	13	5.22E-01	1.00E+00	2.62E-01	1.00E+00	9.78E-01	1.00E+00	7.11E-01	1.00E+00	3.88E-01	1.00E+00	3.33E-01	1.00E+00	2.73E-01	1.00E+00	7.52E-02	1.00E+00	brush border membrane	C
GO:0031570	26	9.35E-04	8.86E-02	4.97E-06	4.51E-03	1.04E-02	6.53E-01	1.06E-03	9.40E-02	5.80E-03	3.75E-01	6.47E-03	4.21E-01	2.95E-02	8.38E-01	4.20E-04	3.00E-02	DNA integrity checkpoint	P
GO:0031589	92	4.87E-02	1.00E+00	3.05E-02	1.00E+00	1.06E-01	1.00E+00	3.46E-01	1.00E+00	2.25E-01	1.00E+00	4.04E-02	1.00E+00	9.59E-03	2.75E-01	8.61E-03	4.28E-01	cell-substrate adhesion	P
GO:0031594	20	6.74E-01	1.00E+00	3.53E-02	1.00E+00	7.76E-01	1.00E+00	2.69E-01	1.00E+00	6.93E-01	1.00E+00	6.41E-02	1.00E+00	5.17E-01	1.00E+00	8.09E-02	1.00E+00	neuromuscular junction	C
GO:0031625	13	4.52E-02	1.00E+00	5.70E-02	1.00E+00	7.63E-02	1.00E+00	6.01E-02	1.00E+00	7.78E-02	1.00E+00	1.01E-01	1.00E+00	2.58E-01	1.00E+00	4.85E-01	1.00E+00	ubiquitin protein ligase binding	F
GO:0031644	82	9.47E-01	1.00E+00	5.38E-01	1.00E+00	9.22E-01	1.00E+00	8.88E-01	1.00E+00	9.86E-01	1.00E+00	2.44E-01	1.00E+00	6.56E-01	1.00E+00	2.96E-01	1.00E+00	regulation of neurophysiological process	P
GO:0031645	15	9.99E-01	1.00E+00	8.27E-01	1.00E+00	1.00E+00	1.00E+00	9.25E-01	1.00E+00	9.30E-01	1.00E+00	6.96E-01	1.00E+00	9.52E-01	1.00E+00	4.82E-01	1.00E+00	negative regulation of neurophysiological pr	P
GO:0031646	16	3.13E-01	1.00E+00	1.77E-01	1.00E+00	1.97E-01	1.00E+00	4.23E-01	1.00E+00	7.84E-01	1.00E+00	4.15E-02	1.00E+00	1.74E-02	4.88E-01	3.18E-01	1.00E+00	positive regulation of neurophysiological pro	P
GO:0031647	23	1.14E-01	1.00E+00	1.47E-02	6.07E-01	8.91E-02	1.00E+00	2.77E-02	1.00E+00	2.49E-01	1.00E+00	4.41E-02	1.00E+00	1.91E-01	1.00E+00	2.79E-02	9.99E-01	regulation of protein stability	P
GO:0031663	13	1.26E-02	6.08E-01	4.24E-03	1.88E-01	2.78E-02	1.00E+00	2.94E-02	1.00E+00	4.05E-02	1.00E+00	1.11E-02	5.03E-01	5.94E-02	1.00E+00	1.42E-02	4.76E-01	lipopolysaccharide-mediated signaling path	P
GO:0031667	72	4.23E-03	2.14E-01	4.71E-03	2.61E-01	1.41E-03	7.90E-02	2.89E-03	1.61E-01	4.04E-02	1.00E+00	6.87E-03	4.21E-01	1.76E-01	1.00E+00	2.90E-01	1.00E+00	response to nutrient levels	P
GO:0031668	19	2.81E-01	1.00E+00	4.60E-01	1.00E+00	3.29E-01	1.00E+00	4.20E-01	1.00E+00	3.88E-01	1.00E+00	6.10E-01	1.00E+00	1.76E-01	1.00E+00	4.12E-01	1.00E+00	cellular response to extracellular stimulus	P
GO:0031669	15	3.58E-01	1.00E+00	6.01E-01	1.00E+00	5.46E-01	1.00E+00	4.99E-01	1.00E+00	3.58E-01	1.00E+00	6.05E-01	1.00E+00	2.29E-01	1.00E+00	7.10E-01	1.00E+00	cellular response to nutrient levels	P
GO:0031672	20	9.40E-01	1.00E+00	5.28E-01	1.00E+00	1.00E+00	1.00E+00	5.58E-01	1.00E+00	7.44E-01	1.00E+00	7.20E-01	1.00E+00	7.43E-01	1.00E+00	2.74E-01	1.00E+00	A band	C
GO:0031901	16	4.19E-01	1.00E+00	4.83E-02	1.00E+00	6.21E-01	1.00E+00	1.03E-01	1.00E+00	2.70E-01	1.00E+00	1.05E-01	1.00E+00	3.64E-01	1.00E+00	1.72E-01	1.00E+00	early endosome membrane	C
GO:0031902	32	1.05E-03	8.86E-02	6.72E-04	5.90E-02	2.50E-02	1.00E+00	3.73E-02	1.00E+00	1.53E-02	6.92E-01	1.44E-02	6.68E-01	4.16E-03	2.23E-01	1.52E-02	6.56E-01	late endosome membrane	C
GO:0031903	40	1.67E-03	2.12E-01	1.05E-02	4.69E-01	5.02E-02	1.00E+00	2.61E-02	1.00E+00	1.35E-02	6.92E-01	5.79E-02	1.00E+00	2.82E-03	8.40E-02	1.61E-02	6.56E-01	microbody membrane	C
GO:0031941	17	1.12E-01	1.00E+00	1.69E-01	1.00E+00	2.05E-01	1.00E+00	2.35E-01	1.00E+00	1.06E-01	1.00E+00	2.09E-01	1.00E+00	2.44E-01	1.00E+00	3.94E-01	1.00E+00	filamentous actin	C
GO:0031965	130	2.31E-08	2.57E-03	2.18E-13	0.00E+00	2.52E-07	2.00E-03	8.77E-11	0.00E+00	1.69E-05	5.37E-03	2.44E-08	9.03E-04	4.31E-03	2.23E-01	4.12E-04	3.00E-02	nuclear membrane	C
GO:0031966	403	8.98E-13	0.00E+00	7.32E-12	0.00E+00	2.13E-08	9.80E-04	5.42E-10	0.00E+00	7.75E-11	0.00E+00	6.81E-09	8.78E-04	4.22E-06	1.00E-03	3.62E-04	3.00E-02	mitochondrial membrane	C
GO:0031967	585	1.99E-20	0.00E+00	1.09E-23	0.00E+00	9.98E-14	7.08E-04	1.46E-19	0.00E+00	5.46E-17	0.00E+00	7.64E-17	0.00E+00	5.40E-08	0.00E+00	5.87E-07	2.00E-03	organelle envelope	C
GO:0031968	78	1.31E-03	8.86E-02	1.06E-06	3.92E-03	2.03E-02	1.00E+00	9.50E-05	1.30E-02	7.94E-03	6.92E-01	1.14E-04	1.30E-02	1.78E-03	8.40E-02	3.35E-03	1.27E-01	organelle outer membrane	C
GO:0031970	35	3.80E-02	1.00E+00	6.58E-02	1.00E+00	9.10E-02	1.00E+00	9.44E-02	1.00E+00	3.51E-02	1.00E+00	6.90E-02	1.00E+00	8.54E-02	1.00E+00	3.32E-01	1.00E+00	organelle envelope lumen	C
GO:0031974	948	2.93E-39	0.00E+00	1.37E-36	0.00E+00	1.64E-34	0.00E+00	7.30E-33	0.00E+00	1.74E-23	0.00E+00	2.46E-22	0.00E+00	2.08E-13	0.00E+00	6.21E-11	0.00E+00	membrane-enclosed lumen	C
GO:0031975	608	7.19E-19	0.00E+00	9.88E-22	0.00E+00	2.21E-12	7.08E-04	4.71E-18	0.00E+00	4.25E-16	0.00E+00	3.13E-15	0.00E+00	2.28E-07	0.00E+00	9.70E-07	2.00E-03	envelope	C
GO:0031980	156	2.60E-06	3.02E-03	8.58E-05	1.50E-02	2.61E-05	3.00E-03	8.57E-03	4.92E-01	4.11E-03	2.13E-01	1.24E-04	1.30E-02	2.59E-03	8.40E-02	2.42E-02	9.99E-01	mitochondrial lumen	C
GO:0031981	689	1.88E-34	0.00E+00	4.30E-33	0.00E+00	1.53E-31	0.00E+00	6.66E-32	0.00E+00	9.57E-21	0.00E+00	4.95E-18	0.00E+00	1.22E-10	0.00E+00	3.40E-10	0.00E+00	nuclear lumen	C
GO:0031982	451	1.59E-12	0.00E+00	2.26E-22	0.00E+00	7.95E-09	9.80E-04	1.84E-17	0.00E+00	8.56E-08	9.59E-04	5.41E-12	6.20E-04	2.08E-07	0.00E+00	4.02E-12	0.00E+00	vesicle	C
GO:0031988	358	3.79E-10	2.57E-03	1.23E-17	0.00E+00	4.12E-07	2.00E-03	8.04E-13	0.00E+00	2.79E-06	1.69E-03	1.35E-10	6.20E-04	6.81E-07	8.23E-04	5.25E-10	0.00E+00	membrane-bound vesicle	C
GO:0032011	17	8.95E-01	1.00E+00	4.24E-01	1.00E+00	8.90E-01	1.00E+00	5.60E-01	1.00E+00	9.76E-01	1.00E+00	3.31E-01	1.00E+00	5.98E-01	1.00E+00	3.76E-01	1.00E+00	ARF protein signal transduction	P
GO:0032012	16	8.57E-01	1.00E+00	3.10E-01	1.00E+00	8.19E-01	1.00E+00	4.46E-01	1.00E+00	9.65E-01	1.00E+00	2.47E-01	1.00E+00	6.03E-01	1.00E+00	2.99E-01	1.00E+00	regulation of ARF protein signal transductio	P
GO:0032039	13	3.34E-02	1.00E+00	2.57E-02	1.00E+00	1.28E-02	6.53E-01	3.37E-02	1.00E+00	2.13E-01	1.00E+00	1.16E-01	1.00E+00	1.05E-01	1.00E+00	5.02E-02	1.00E+00	integrator complex	C
GO:0032094	11	9.16E-01	1.00E+00	5.85E-01	1.00E+00	9.74E-01	1.00E+00	8.87E-01	1.00E+00	9.58E-01	1.00E+00	7.71E-01	1.00E+00	6.39E-01	1.00E+00	1.01E-01	1.00E+00	response to food	P
GO:0032147	51	1.68E-01	1.00E+00	8.25E-02	1.00E+00	2.80E-01	1.00E+00	9.28E-02	1.00E+00	3.89E-01	1.00E+00	3.82E-01	1.00E+00	9.66E-02	1.00E+00	3.40E-02	1.00E+00	activation of protein kinase activity	P
GO:0032156	13	1.44E-01	1.00E+00	1.32E-02	6.07E-01	3.35E-01	1.00E+00	2.99E-02	1.00E+00	5.77E-01	1.00E+00	1.35E-01	1.00E+00	2.34E-02	8.38E-01	2.20E-01	1.00E+00	septin cytoskeleton	C
GO:0032182	10	3.63E-02	1.00E+00	1.45E-01	1.00E+00	2.46E-02	1.00E+00	2.32E-01	1.00E+00	2.16E-01	1.00E+00	8.81E-02	1.00E+00	8.43E-02	1.00E+00	6.57E-01	1.00E+00	small conjugating protein binding	F
GO:0032200	26	8.15E-02	1.00E+00	5.33E-03	3.08E-01	6.01E-02	1.00E+00	2.31E-02	9.37E-01	1.46E-01	1.00E+00	1.09E-02	5.03E-01	1.74E-01	1.00E+00	5.99E-02	1.00E+00	telomere organization and biogenesis	P
GO:0032259	91	4.36E-02	1.00E+00	9.38E-03	4.69E-01	1.89E-02	1.00E+00	1.13E-03	9.40E-02	1.28E-01	1.00E+00	4.91E-02	1.00E+00	2.18E-01	1.00E+00	9.70E-02	1.00E+00	methylation	P
GO:0032312	23	4.86E-02	1.00E+00	5.15E-03	2.79E-01	5.50E-02	1.00E+00	5.68E-02	1.00E+00	1.55E-01	1.00E+00	2.53E-03	1.27E-01	4.58E-02	1.00E+00	1.85E-01	1.00E+00	regulation of ARF GTPase activity	P
GO:0032313	41	9.46E-03	6.08E-01	2.98E-03	1.88E-01	2.44E-02	1.00E+00	1.75E-02	6.47E-01	1.11E-01	1.00E+00	1.49E-03	9.30E-02	1.19E-01	1.00E+00	2.98E-01	1.00E+00	regulation of Rab GTPase activity	P
GO:0032318	72	3.39E-04	3.10E-02	3.27E-05	7.00E-03	1.17E-03	7.90E-02	1.76E-03	1.24E-01	1.58E-02	6.92E-01	2.51E-05	5.87E-03	1.19E-02	3.39E-01	8.38E-02	1.00E+00	regulation of Ras GTPase activity	P
GO:0032392	12	1.02E-02	6.08E-01	4.52E-02	1.00E+00	9.88E-03	6.53E-01	1.62E-02	6.47E-01	1.42E-02	6.92E-01	8.81E-02	1.00E+00	2.18E-01	1.00E+00	8.67E-01	1.00E+00	DNA geometric change	P
GO:0032403	76	2.43E-01	1.00E+00	6.96E-02	1.00E+00	5.79E-01	1.00E+00	2.74E-01	1.00E+00	4.41E-01	1.00E+00	3.98E-01	1.00E+00	3.57E-02	8.38E-01	1.34E-02	4.76E-01	protein complex binding	F
GO:0032432	25	9.86E-05	1.43E-02	6.78E-05	7.00E-03	2.43E-03	1.07E-01	1.65E-02	6.47E-01	3.77E-04	4.90E-02	1.04E-05	5.87E-03	2.62E-03	8.40E-02	4.63E-03	2.01E-01	actin filament bundle	C
GO:0035004	11	6.44E-01	1.00E+00	1.55E-01	1.00E+00	4.57E-01	1.00E+00	9.91E-02	1.00E+00	4.63E-01	1.00E+00	2.95E-01	1.00E+00	9.04E-01	1.00E+00	2.50E-01	1.00E+00	phosphoinositide 3-kinase activity	F
GO:0035014	11	5.83E-01	1.00E+00	7.59E-02	1.00E+00	6.76E-01	1.00E+00	1.32E-01	1.00E+00	8.47E-01	1.00E+00	6.45E-02	1.00E+00	2.66E-01	1.00E+00	2.36E-01	1.00E+00	phosphoinositide 3-kinase regulator activity	F
GO:0035023	73	5.09E-01	1.00E+00	1.97E-03	1.30E-01	6.32E-01	1.00E+00	6.38E-02	1.00E+00	9.52E-01	1.00E+00	1.48E-02	6.68E-01	1.68E-01	1.00E+00	1.93E-03	7.90E-02	regulation of Rho protein signal transductio	P
GO:0035036	22	6.80E-01	1.00E+00	2.19E-01	1.00E+00	7.83E-01	1.00E+00	1.66E-01	1.00E+00	8.64E-01	1.00E+00	3.49E-01	1.00E+00	3.83E-01	1.00E+00	2.90E-01	1.00E+00	sperm-egg recognition	P

GO:0035050	15	4.62E-02	1.00E+00	7.48E-01	1.00E+00	8.14E-02	1.00E+00	3.89E-01	1.00E+00	4.91E-02	1.00E+00	9.81E-01	1.00E+00	3.89E-01	1.00E+00	7.42E-01	1.00E+00	embryonic heart tube development	P
GO:0035051	21	5.89E-01	1.00E+00	8.61E-01	1.00E+00	7.75E-01	1.00E+00	9.84E-01	1.00E+00	6.11E-01	1.00E+00	6.44E-01	1.00E+00	2.91E-01	1.00E+00	6.88E-01	1.00E+00	cardiac cell differentiation	P
GO:0035088	13	1.75E-01	1.00E+00	3.18E-02	1.00E+00	1.12E-01	1.00E+00	1.11E-01	1.00E+00	5.35E-01	1.00E+00	8.34E-02	1.00E+00	3.80E-01	1.00E+00	9.01E-02	1.00E+00	establishment and/or maintenance of apical	P
GO:0035091	77	6.19E-05	1.20E-02	4.62E-08	9.59E-04	4.88E-03	3.08E-01	5.88E-07	2.89E-03	5.73E-04	4.90E-02	6.96E-05	1.10E-02	8.01E-03	2.75E-01	2.44E-04	2.33E-02	phosphoinositide binding	F
GO:0035094	10	8.45E-01	1.00E+00	7.18E-01	1.00E+00	9.54E-01	1.00E+00	9.31E-01	1.00E+00	9.58E-01	1.00E+00	8.60E-01	1.00E+00	1.99E-01	1.00E+00	1.10E-01	1.00E+00	response to nicotine	P
GO:0035107	92	8.62E-01	1.00E+00	9.47E-01	1.00E+00	8.24E-01	1.00E+00	9.83E-01	1.00E+00	9.04E-01	1.00E+00	8.85E-01	1.00E+00	6.89E-01	1.00E+00	6.97E-01	1.00E+00	appendage morphogenesis	P
GO:0035108	92	8.62E-01	1.00E+00	9.47E-01	1.00E+00	8.24E-01	1.00E+00	9.83E-01	1.00E+00	9.04E-01	1.00E+00	8.85E-01	1.00E+00	6.89E-01	1.00E+00	6.97E-01	1.00E+00	limb morphogenesis	P
GO:0035113	85	8.15E-01	1.00E+00	9.71E-01	1.00E+00	8.18E-01	1.00E+00	9.82E-01	1.00E+00	8.46E-01	1.00E+00	9.76E-01	1.00E+00	5.90E-01	1.00E+00	6.58E-01	1.00E+00	embryonic appendage morphogenesis	P
GO:0035115	17	9.99E-01	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.85E-01	1.00E+00	7.63E-01	1.00E+00	8.28E-01	1.00E+00	9.29E-01	1.00E+00	embryonic forelimb morphogenesis	P
GO:0035116	20	2.26E-01	1.00E+00	4.21E-01	1.00E+00	1.56E-01	1.00E+00	4.88E-01	1.00E+00	5.82E-01	1.00E+00	5.81E-01	1.00E+00	2.10E-01	1.00E+00	4.56E-01	1.00E+00	embryonic hindlimb morphogenesis	P
GO:0035136	20	9.68E-01	1.00E+00	8.85E-01	1.00E+00	9.85E-01	1.00E+00	9.54E-01	1.00E+00	9.77E-01	1.00E+00	5.56E-01	1.00E+00	5.47E-01	1.00E+00	9.43E-01	1.00E+00	forelimb morphogenesis	P
GO:0035137	28	3.21E-01	1.00E+00	2.77E-01	1.00E+00	1.69E-01	1.00E+00	4.40E-01	1.00E+00	7.16E-01	1.00E+00	1.45E-01	1.00E+00	3.33E-01	1.00E+00	6.45E-01	1.00E+00	hindlimb morphogenesis	P
GO:0035176	13	1.85E-01	1.00E+00	9.51E-01	1.00E+00	1.33E-01	1.00E+00	8.90E-01	1.00E+00	3.58E-01	1.00E+00	8.42E-01	1.00E+00	1.80E-01	1.00E+00	9.81E-01	1.00E+00	social behavior	P
GO:0035239	118	3.44E-01	1.00E+00	5.76E-01	1.00E+00	6.93E-01	1.00E+00	8.71E-01	1.00E+00	4.94E-01	1.00E+00	8.10E-01	1.00E+00	7.67E-02	1.00E+00	8.00E-02	1.00E+00	tube morphogenesis	P
GO:0035240	62	3.18E-01	1.00E+00	1.11E-01	1.00E+00	1.88E-01	1.00E+00	1.06E-01	1.00E+00	6.76E-01	1.00E+00	3.13E-01	1.00E+00	1.83E-01	1.00E+00	6.36E-02	1.00E+00	dopamine binding	F
GO:0035249	26	9.94E-01	1.00E+00	9.90E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.01E-01	1.00E+00	5.98E-01	1.00E+00	8.49E-01	1.00E+00	synaptic transmission, glutamatergic	P
GO:0035250	24	3.36E-01	1.00E+00	6.76E-01	1.00E+00	5.00E-01	1.00E+00	7.35E-01	1.00E+00	6.95E-02	1.00E+00	1.35E-01	1.00E+00	9.96E-01	1.00E+00	9.92E-01	1.00E+00	UDP-galactosyltransferase activity	F
GO:0035257	45	2.45E-03	2.12E-01	3.30E-04	4.40E-02	1.06E-03	7.90E-02	2.92E-04	4.20E-02	1.70E-02	6.92E-01	3.46E-02	1.00E+00	1.40E-01	1.00E+00	7.88E-02	1.00E+00	nuclear hormone receptor binding	F
GO:0035258	11	1.09E-01	1.00E+00	1.37E-01	1.00E+00	2.37E-01	1.00E+00	1.29E-01	1.00E+00	1.96E-01	1.00E+00	2.85E-01	1.00E+00	2.01E-01	1.00E+00	4.51E-01	1.00E+00	steroid hormone receptor binding	F
GO:0035264	76	7.55E-02	1.00E+00	1.05E-01	1.00E+00	1.54E-01	1.00E+00	2.52E-01	1.00E+00	3.57E-01	1.00E+00	3.25E-01	1.00E+00	3.35E-02	8.38E-01	3.29E-02	1.00E+00	body growth	P
GO:0035265	26	2.88E-01	1.00E+00	4.42E-01	1.00E+00	3.67E-01	1.00E+00	4.15E-01	1.00E+00	3.63E-01	1.00E+00	8.28E-01	1.00E+00	1.49E-01	1.00E+00	9.30E-02	1.00E+00	organ growth	P
GO:0035270	61	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	9.71E-01	1.00E+00	7.64E-01	1.00E+00	9.86E-01	1.00E+00	endocrine system development	P
GO:0035272	17	5.15E-01	1.00E+00	1.99E-01	1.00E+00	4.92E-01	1.00E+00	2.38E-01	1.00E+00	3.18E-01	1.00E+00	4.70E-01	1.00E+00	5.45E-01	1.00E+00	1.73E-01	1.00E+00	exocrine system development	P
GO:0035282	47	8.42E-01	1.00E+00	6.16E-01	1.00E+00	7.29E-01	1.00E+00	3.64E-01	1.00E+00	8.81E-01	1.00E+00	5.17E-01	1.00E+00	6.48E-01	1.00E+00	9.87E-01	1.00E+00	segmentation	P
GO:0035295	201	2.18E-01	1.00E+00	6.37E-01	1.00E+00	3.81E-01	1.00E+00	6.94E-01	1.00E+00	4.25E-01	1.00E+00	8.97E-01	1.00E+00	7.49E-02	1.00E+00	1.22E-01	1.00E+00	tube development	P
GO:0035315	19	9.22E-01	1.00E+00	7.57E-01	1.00E+00	9.72E-01	1.00E+00	9.63E-01	1.00E+00	9.66E-01	1.00E+00	7.27E-01	1.00E+00	4.10E-01	1.00E+00	2.73E-01	1.00E+00	hair cell differentiation	P
GO:0040007	322	2.80E-05	7.00E-03	1.43E-05	4.51E-03	3.14E-03	1.35E-01	1.27E-03	9.40E-02	1.58E-03	1.20E-01	1.18E-02	5.03E-01	2.11E-03	8.40E-02	7.24E-07	2.00E-03	growth	P
GO:0040008	213	1.01E-02	6.08E-01	1.75E-03	9.65E-02	7.19E-02	1.00E+00	1.65E-02	6.47E-01	7.95E-02	1.00E+00	9.62E-02	1.00E+00	2.20E-02	6.36E-01	9.23E-05	1.60E-02	regulation of growth	P
GO:0040011	462	2.53E-01	1.00E+00	8.00E-02	1.00E+00	7.27E-01	1.00E+00	4.06E-01	1.00E+00	4.70E-01	1.00E+00	5.29E-01	1.00E+00	4.48E-02	1.00E+00	3.69E-04	3.00E-02	locomotion	P
GO:0040012	101	4.58E-01	1.00E+00	1.06E-01	1.00E+00	8.00E-01	1.00E+00	1.94E-01	1.00E+00	8.29E-01	1.00E+00	2.71E-01	1.00E+00	9.54E-02	1.00E+00	4.48E-02	1.00E+00	regulation of locomotion	P
GO:0040013	32	2.58E-01	1.00E+00	7.61E-02	1.00E+00	5.84E-01	1.00E+00	3.48E-02	1.00E+00	3.80E-01	1.00E+00	1.47E-01	1.00E+00	2.18E-01	1.00E+00	3.11E-01	1.00E+00	negative regulation of locomotion	P
GO:0040014	61	1.21E-01	1.00E+00	1.45E-01	1.00E+00	1.82E-01	1.00E+00	2.04E-01	1.00E+00	3.78E-01	1.00E+00	6.40E-01	1.00E+00	9.55E-02	1.00E+00	1.93E-02	7.36E-01	regulation of body size	P
GO:0040015	10	1.46E-01	1.00E+00	2.06E-01	1.00E+00	1.59E-01	1.00E+00	2.61E-01	1.00E+00	2.14E-01	1.00E+00	5.66E-01	1.00E+00	3.86E-01	1.00E+00	6.02E-02	1.00E+00	negative regulation of body size	P
GO:0040017	40	7.29E-01	1.00E+00	2.23E-01	1.00E+00	8.95E-01	1.00E+00	3.67E-01	1.00E+00	9.73E-01	1.00E+00	5.55E-01	1.00E+00	2.26E-01	1.00E+00	9.89E-02	1.00E+00	positive regulation of locomotion	P
GO:0040018	26	9.97E-01	1.00E+00	9.80E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	9.20E-01	1.00E+00	3.41E-01	1.00E+00	positive regulation of body size	P
GO:0040029	65	4.93E-02	1.00E+00	1.02E-01	1.00E+00	2.47E-02	1.00E+00	2.49E-02	1.00E+00	2.39E-01	1.00E+00	3.02E-01	1.00E+00	1.20E-01	1.00E+00	2.69E-01	1.00E+00	regulation of gene expression, epigenetic	P
GO:0042035	68	4.17E-01	1.00E+00	1.00E-01	1.00E+00	8.82E-01	1.00E+00	6.38E-01	1.00E+00	7.60E-01	1.00E+00	7.05E-01	1.00E+00	3.14E-02	8.38E-01	2.31E-03	7.90E-02	regulation of cytokine biosynthesis	P
GO:0042036	15	1.17E-01	1.00E+00	1.99E-01	1.00E+00	1.76E-01	1.00E+00	5.80E-01	1.00E+00	3.13E-01	1.00E+00	9.34E-01	1.00E+00	1.11E-01	1.00E+00	4.63E-02	1.00E+00	negative regulation of cytokine biosynthesis	P
GO:0042044	11	4.91E-01	1.00E+00	1.57E-01	1.00E+00	2.94E-01	1.00E+00	2.81E-02	1.00E+00	4.79E-01	1.00E+00	3.93E-01	1.00E+00	8.32E-01	1.00E+00	5.17E-01	1.00E+00	fluid transport	P
GO:0042054	33	4.27E-06	3.02E-03	2.67E-09	8.90E-04	1.27E-06	2.00E-03	8.78E-08	2.89E-03	3.33E-04	4.90E-02	9.24E-06	5.87E-03	4.33E-02	1.00E+00	1.20E-04	1.60E-02	histone methyltransferase activity	F
GO:0042060	169	1.85E-01	1.00E+00	2.60E-01	1.00E+00	4.95E-01	1.00E+00	4.44E-01	1.00E+00	3.63E-01	1.00E+00	2.05E-01	1.00E+00	1.27E-01	1.00E+00	2.21E-01	1.00E+00	wound healing	P
GO:0042063	51	4.64E-01	1.00E+00	8.52E-01	1.00E+00	3.77E-01	1.00E+00	6.48E-01	1.00E+00	6.11E-01	1.00E+00	7.26E-01	1.00E+00	3.71E-01	1.00E+00	9.01E-01	1.00E+00	gliogenesis	P
GO:0042088	14	8.54E-02	1.00E+00	3.03E-03	1.88E-01	3.80E-01	1.00E+00	1.46E-01	1.00E+00	4.21E-01	1.00E+00	5.16E-01	1.00E+00	2.54E-03	8.40E-02	2.44E-05	7.00E-03	T-helper 1 type immune response	P
GO:0042089	80	3.00E-01	1.00E+00	7.24E-02	1.00E+00	8.64E-01	1.00E+00	5.27E-01	1.00E+00	6.63E-01	1.00E+00	6.85E-01	1.00E+00	1.28E-02	4.78E-01	2.31E-03	7.90E-02	cytokine biosynthesis	P
GO:0042093	13	5.99E-02	1.00E+00	7.42E-02	1.00E+00	1.44E-01	1.00E+00	9.56E-02	1.00E+00	4.31E-01	1.00E+00	3.97E-01	1.00E+00	1.36E-02	4.78E-01	1.14E-01	1.00E+00	T-helper cell differentiation	P
GO:0042094	17	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.75E-01	1.00E+00	1.57E-01	1.00E+00	interleukin-2 biosynthesis	P
GO:0042095	14	1.85E-01	1.00E+00	3.21E-01	1.00E+00	7.23E-01	1.00E+00	5.96E-01	1.00E+00	7.03E-01	1.00E+00	5.69E-01	1.00E+00	6.62E-03	2.75E-01	8.89E-02	1.00E+00	interferon-gamma biosynthesis	P
GO:0042098	69	4.23E-01	1.00E+00	3.03E-03	1.88E-01	7.16E-01	1.00E+00	4.15E-02	1.00E+00	8.46E-01	1.00E+00	1.21E-02	5.03E-01	3.38E-02	8.38E-01	6.17E-03	4.28E-01	T cell proliferation	P
GO:0042100	37	7.57E-01	1.00E+00	2.90E-01	1.00E+00	9.09E-01	1.00E+00	3.22E-01	1.00E+00	8.34E-01	1.00E+00	6.92E-01	1.00E+00	2.14E-01	1.00E+00	1.79E-01	1.00E+00	B cell proliferation	P
GO:0042101	11	2.54E-01	1.00E+00	6.87E-01	1.00E+00	7.26E-01	1.00E+00	9.54E-01	1.00E+00	1.43E-01	1.00E+00	6.27E-01	1.00E+00	4.43E-02	1.00E+00	3.04E-01	1.00E+00	T cell receptor complex	C
GO:0042102	35	7.11E-01	1.00E+00	1.42E-02	6.07E-01	9.66E-01	1.00E+00	1.24E-01	1.00E+00	7.98E-01	1.00E+00	7.82E-02	1.00E+00	1.30E-01	1.00E+00	9.27E-03	4.28E-01	positive regulation of T cell proliferation	P
GO:0042107	81	2.85E-01	1.00E+00	9.07E-02	1.00E+00	8.70E-01	1.00E+00	5.70E-01	1.00E+00	7.02E-01	1.00E+00	7.23E-01	1.00E+00	7.63E-03	2.75E-01	2.55E-03	7.90E-02	cytokine metabolism	P
GO:0042108	45	2.65E-01	1.00E+00	8.46E-02	1.00E+00	8.63E-01	1.00E+00	3.42E-01	1.00E+00	5.25E-01	1.00E+00	6.05E-01	1.00E+00	9.71E-03	2.75E-01	2.12E-03	7.90E-02	positive regulation of cytokine biosynthesis	P
GO:0042110	150	1.61E-02	1.00E+00	4.91E-06	4.51E-03	1.17E-01	1.00E+00	2.37E-03	1.39E-01	3.46E-01	1.00E+00	1.35E-03	9.00E-02	1.76E-04	8.00E-03	1.43E-05	7.00E-03	T cell activation	P
GO:0042113	115	6.31E-01	1.00E+00	2.33E-01	1.00E+00	9.55E-01	1.00E+00	1.29E-01	1.00E+00	7.41E-01	1.00E+00	9.43E-01	1.00E+00	1.82E-01	1.00E+00	5.14E-02	1.00E+00	B cell activation	P
GO:0042127	478	6.16E-03	3.09E-01	2.65E-02	1.00E+00	1.41E-01	1.00E+00	4.27E-02	1.00E+00	1.03E-01	1.00E+00	2.11E-01	1.00E+00	3.95E-04	2.40E-02	3.79E-02	1.00E+00	regulation of cell proliferation	P
GO:0042129	50	8.63E-01	1.00E+00	4.18E-02	1.00E+00	9.39E-01	1.00E+00	1.79E-01	1.00E+00	9.82E-01	1.00E+00	1.64E-01	1.00E+00	1.52E-01	1.00E+00	1.70E-02	6.56E-01	regulation of T cell proliferation	P
GO:0042130	17	8.49E-01	1.00E+00	1.85E-01	1.00E+00	7.64E-01	1.00E+00	2.61E-01	1.00E+00	9.75E-01	1.00E+00	1.87E-01	1.00E+00	3.25E-01	1.00E+00	1.25E-01	1.00E+00	negative regulation of T cell proliferation	P
GO:0042133	46	5.67E-01	1.00E+00	6.65E-01	1.00E+00	8.98E-01	1.00E+00	9.19E-01	1.00E+00	3.55E-01	1.00E+00	6.63E-01	1.00E+00	3.36E-01	1.00E+00	1.32E-01	1.00E+00	neurotransmitter metabolism	P
GO:0042135	10	3.58E-01	1.00E+00	5.85E-02	1.00E+00	7.21E-01	1.00E+00	3.30E-01	1.00E+00	4.78E-01	1.00E+00	1.72E-01	1.00E+00	1.29E-01	1.00E+00	1.00E-01	1.00E+00	neurotransmitter catabolism	P
GO:0042136	17	9.47E-01	1.00E+00	9.41E-01	1.00E+00	9.94E-01	1.00E+00	9.97E-01	1.00E+00	7.70E-01	1.00E+00	7.30E-01	1.00E+00	7.80E-01	1.00E+00	6.80E-01	1.00E+00	neurotransmitter biosynthesis	P
GO:0042157	77	5.01E-02	1.00E+00	4.23E-02	1.00E+00	2.77E-01	1.00E+00	2.25E-02	9.37E-01	1.39E-02	6.92E-01	1.73E-01	1.00E+00	5.51E-01	1.00E+00	2.42E-01	1.00E+00	lipoprotein metabolism	P
GO:0042158	55	5.09E-02	1.00E+00	3.77E-02	1.00E+00	2.24E-01	1.00E+00	2.63E-02	1.00E+00	3.49E-02	1.00E+00	1.22E-01	1.00E+00	5.21E-01	1.00E+00	2.85E-01	1.00E+00	lipoprotein biosynthesis	P
GO:0042162	10	3.97E-04	3.10E-02	1.06E-01	1.00E+00	1.04E-02	6.53E-01	5.45E-02	1.00E+00	1.64E-03	1.20E-01	3.99E-02	1.00E+00	7.96E-03	2.75E-01	5.79E-01	1.00E+00	telomeric DNA binding	F
GO:0042165	240	8.02E-01	1.00E+00	8.29E-01	1.00E+00	9.85E-01	1.00E+00	9.34E-01	1.00E+00	7.42E-01	1.00E+00	8.84E-01	1.00E+00	1.84E-01	1.00E+00	2.37E-01	1.00E+00	neurotransmitter binding	F
GO:0042166	29	8.39E-01	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.94E-01	1.00E+00	4.08E-01	1.00E+00	7.88E-01	1.00E+00	acetylcholine binding	F
GO:0042168	18	2.33E-02	1.00E+00	1.38E-01	1.00E+00	3.89E-02	1.00E+00	4.85E-02	1.00E+00	2.33E-02	1.00E+00	1.47E-01	1.00E+00	1.78E-01	1.00E+00	4.51E-01	1.00E+00	heme metabolism	P
GO:0042169	16	1.17E-01	1.00E+00	1.12E-02	4.69E-01	2.43E-01	1.00E+00	4.27E-02	1.00E+00	2.66E-01	1.00E+00	5.44E-02	1.00E+00	6.12E-02	1.00E+00	1.03E-01	1.00E+00	SH2 domain binding	F
GO:0042175	479	4.41E-06	3.02E-03	8.40E-07	3.92E-03	4.84E-04	4.90E-02	5.20E-05	1.07E-02	1.90E-04	4.90E-02	2.41E-05	5.87E-03	5.41E-04	3.44E-02	1.45E-03	6.00E-02	nuclear envelope-endoplasmic reticulum ne	C
GO:0042176	24	8.89E-02	1.00E+00	3.66E-03	1.88E-01	7.44E-02	1.00E+00	2.21E-03	1.39E-01	1.40E-01	1.00E+00	1.39E-01	1.00E+00	6.73E-01	1.00E+00	1.91E-02	7.36E-01	regulation of protein catabolism	P
GO:0042219	18	4.43E-01	1.00E+00	3.60E-01	1.00E+00	7.17E-01	1.00E+00	5.76E-01	1.00E+00	4.91E-01	1.00E+00	5.34E-01	1.00E+00	3.24E-01	1.00E+00	3.39E-01	1.00E+00	amino acid derivative catabolism	P
GO:0042220	10	5.72E-01	1.00E+00	7.20E-01	1.00E+00	8.02E-01	1.00E+00	7.54E-01	1.00E+00	5.36E-01	1.00E+00	7.24E-01	1.00E+00	1.44E-01	1.00E+00	3.77E-01	1.00E+00	response to cocaine	P
GO:0042221	676	3.42E-02	1.00E+00	6.59E-03	3.12E-01	3.59E-01	1.00E+00	7.98E-02	1.00E+00	2.85E-01	1.00E+00	4.72E-03	2.66E-01	3.20E-04	2.29E-02	2.63E-02	9.99E-01	response to chemical stimulus	P
GO:0042226	15	9.70E-01	1.00E+00	8.15E-01	1.00E+00	9.48E-01	1.00E+00	8.91E-01	1.00E+00	1.00E+00	1.00E+00	8.88E-01	1.00E+00	6.46E-01	1.00E+00	1.56E-01	1.00E+00	interleukin-6 biosynthesis	P
GO:0042228	10	2.57E-02	1.00E+00	3.24E-01	1.00E+00	1.35E-01	1.00E+00	5.64E-01	1.00E+00	1.64E-01	1.00E+00	5.19E-01	1.00E+00	2.73E-03	8.40E-02	1.14E-01	1.00E+00	interleukin-8 biosynthesis	P

GO:0042246	22	5.53E-02	1.00E+00	9.48E-02	1.00E+00	3.47E-01	1.00E+00	1.51E-01	1.00E+00	3.78E-02	1.00E+00	1.39E-01	1.00E+00	2.39E-01	1.00E+00	5.75E-02	1.00E+00	tissue regeneration	P
GO:0042254	118	2.10E-08	2.57E-03	3.47E-04	4.40E-02	6.75E-09	9.80E-04	5.91E-04	4.20E-02	1.35E-06	1.69E-03	5.93E-03	4.21E-01	1.13E-02	3.39E-01	1.27E-01	1.00E+00	ribosome biogenesis and assembly	P
GO:0042267	20	8.25E-01	1.00E+00	5.35E-01	1.00E+00	6.33E-01	1.00E+00	4.52E-01	1.00E+00	6.64E-01	1.00E+00	3.17E-01	1.00E+00	9.47E-01	1.00E+00	8.61E-01	1.00E+00	natural killer cell mediated cytotoxicity	P
GO:0042269	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	regulation of natural killer cell mediated cyto	P
GO:0042277	764	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	peptide binding	F
GO:0042287	15	1.05E-02	6.08E-01	3.13E-02	1.00E+00	3.09E-01	1.00E+00	1.08E-01	1.00E+00	5.02E-04	4.90E-02	2.13E-03	1.27E-01	4.29E-01	1.00E+00	6.25E-01	1.00E+00	MHC protein binding	F
GO:0042288	13	4.22E-02	1.00E+00	9.46E-02	1.00E+00	5.86E-01	1.00E+00	2.04E-01	1.00E+00	5.31E-03	3.75E-01	1.44E-02	6.68E-01	4.08E-01	1.00E+00	5.76E-01	1.00E+00	MHC class I protein binding	F
GO:0042303	45	3.01E-01	1.00E+00	2.95E-01	1.00E+00	8.52E-01	1.00E+00	4.60E-01	1.00E+00	3.16E-01	1.00E+00	3.23E-01	1.00E+00	3.02E-02	8.38E-01	1.15E-01	1.00E+00	molting cycle	P
GO:0042306	23	1.58E-02	1.00E+00	8.66E-04	8.70E-02	4.78E-02	1.00E+00	4.09E-03	2.88E-01	4.30E-02	1.00E+00	1.52E-02	6.68E-01	1.44E-01	1.00E+00	1.42E-02	4.76E-01	regulation of protein import into nucleus	P
GO:0042307	11	3.68E-01	1.00E+00	5.71E-02	1.00E+00	5.68E-01	1.00E+00	1.17E-01	1.00E+00	4.23E-01	1.00E+00	1.37E-01	1.00E+00	1.95E-01	1.00E+00	8.95E-02	1.00E+00	positive regulation of protein import into nuc	P
GO:0042309	192	1.62E-01	1.00E+00	2.13E-01	1.00E+00	9.98E-02	1.00E+00	1.50E-01	1.00E+00	4.31E-01	1.00E+00	3.61E-01	1.00E+00	1.31E-01	1.00E+00	2.74E-01	1.00E+00	homoiothermy	P
GO:0042310	22	8.67E-01	1.00E+00	7.49E-01	1.00E+00	9.90E-01	1.00E+00	9.70E-01	1.00E+00	9.31E-01	1.00E+00	7.63E-01	1.00E+00	2.88E-01	1.00E+00	1.73E-01	1.00E+00	vasoconstriction	P
GO:0042311	24	6.38E-01	1.00E+00	8.49E-01	1.00E+00	6.05E-01	1.00E+00	7.63E-01	1.00E+00	9.04E-01	1.00E+00	9.75E-01	1.00E+00	1.40E-01	1.00E+00	3.86E-01	1.00E+00	vasodilation	P
GO:0042325	120	6.05E-01	1.00E+00	1.56E-01	1.00E+00	6.90E-01	1.00E+00	3.60E-01	1.00E+00	9.72E-01	1.00E+00	4.28E-01	1.00E+00	4.61E-02	1.00E+00	3.44E-02	1.00E+00	regulation of phosphorylation	P
GO:0042326	15	3.96E-01	1.00E+00	3.28E-02	1.00E+00	2.55E-01	1.00E+00	7.41E-02	1.00E+00	8.04E-01	1.00E+00	8.73E-02	1.00E+00	2.12E-01	1.00E+00	7.71E-02	1.00E+00	negative regulation of phosphorylation	P
GO:0042327	36	9.63E-01	1.00E+00	3.65E-01	1.00E+00	9.85E-01	1.00E+00	5.84E-01	1.00E+00	9.49E-01	1.00E+00	6.47E-01	1.00E+00	5.65E-01	1.00E+00	4.51E-02	1.00E+00	positive regulation of phosphorylation	P
GO:0042330	173	7.39E-01	1.00E+00	2.29E-01	1.00E+00	9.99E-01	1.00E+00	8.64E-01	1.00E+00	8.76E-01	1.00E+00	1.15E-01	1.00E+00	4.95E-03	2.23E-01	2.02E-02	7.36E-01	taxis	P
GO:0042345	10	2.49E-02	1.00E+00	5.47E-03	3.08E-01	4.70E-02	1.00E+00	2.56E-02	1.00E+00	1.04E-01	1.00E+00	7.35E-02	1.00E+00	4.31E-02	1.00E+00	2.81E-02	9.99E-01	regulation of NF-kappaB import into nucleus	P
GO:0042348	10	2.49E-02	1.00E+00	5.47E-03	3.08E-01	4.70E-02	1.00E+00	2.56E-02	1.00E+00	1.04E-01	1.00E+00	7.35E-02	1.00E+00	4.31E-02	1.00E+00	2.81E-02	9.99E-01	NF-kappaB import into nucleus	P
GO:0042364	23	1.44E-02	8.50E-01	1.84E-01	1.00E+00	5.14E-02	1.00E+00	4.04E-01	1.00E+00	3.00E-02	1.00E+00	3.78E-01	1.00E+00	3.30E-01	1.00E+00	1.28E-01	1.00E+00	water-soluble vitamin biosynthesis	P
GO:0042375	12	4.77E-03	2.72E-01	9.24E-02	1.00E+00	6.66E-03	4.69E-01	9.57E-02	1.00E+00	1.11E-02	6.92E-01	2.23E-01	1.00E+00	3.63E-02	8.38E-01	1.19E-01	1.00E+00	quinone cofactor metabolism	P
GO:0042379	52	3.16E-01	1.00E+00	7.26E-01	1.00E+00	2.69E-01	1.00E+00	9.45E-01	1.00E+00	4.48E-01	1.00E+00	4.84E-01	1.00E+00	1.79E-01	1.00E+00	2.62E-01	1.00E+00	chemokine receptor binding	F
GO:0042383	25	1.97E-01	1.00E+00	2.02E-01	1.00E+00	4.98E-01	1.00E+00	4.14E-01	1.00E+00	1.52E-01	1.00E+00	3.29E-01	1.00E+00	1.20E-01	1.00E+00	2.79E-02	9.99E-01	sarcolemma	C
GO:0042384	20	4.15E-01	1.00E+00	2.31E-01	1.00E+00	6.81E-01	1.00E+00	7.27E-01	1.00E+00	1.69E-01	1.00E+00	2.43E-01	1.00E+00	8.21E-01	1.00E+00	1.38E-01	1.00E+00	cilium biogenesis	P
GO:0042391	54	1.91E-01	1.00E+00	1.96E-01	1.00E+00	5.97E-01	1.00E+00	5.35E-01	1.00E+00	5.81E-01	1.00E+00	2.98E-01	1.00E+00	4.10E-03	2.23E-01	1.01E-01	1.00E+00	regulation of membrane potential	P
GO:0042393	12	4.95E-03	2.72E-01	2.98E-02	1.00E+00	1.86E-03	9.50E-02	3.72E-02	1.00E+00	3.34E-02	1.00E+00	1.45E-02	6.68E-01	7.78E-02	1.00E+00	3.84E-01	1.00E+00	histone binding	F
GO:0042398	36	1.80E-01	1.00E+00	2.64E-01	1.00E+00	3.01E-01	1.00E+00	2.37E-01	1.00E+00	2.43E-01	1.00E+00	5.42E-01	1.00E+00	1.81E-01	1.00E+00	2.60E-01	1.00E+00	amino acid derivative biosynthesis	P
GO:0042401	31	5.98E-01	1.00E+00	3.18E-01	1.00E+00	6.51E-01	1.00E+00	3.32E-01	1.00E+00	7.65E-01	1.00E+00	4.61E-01	1.00E+00	2.47E-01	1.00E+00	2.71E-01	1.00E+00	biogenic amine biosynthesis	P
GO:0042402	16	6.95E-01	1.00E+00	6.60E-01	1.00E+00	8.05E-01	1.00E+00	7.93E-01	1.00E+00	6.32E-01	1.00E+00	6.56E-01	1.00E+00	4.61E-01	1.00E+00	6.04E-01	1.00E+00	biogenic amine catabolism	P
GO:0042403	13	6.60E-01	1.00E+00	7.43E-01	1.00E+00	6.59E-01	1.00E+00	8.15E-01	1.00E+00	7.09E-01	1.00E+00	6.22E-01	1.00E+00	4.44E-01	1.00E+00	5.13E-01	1.00E+00	thyroid hormone metabolism	P
GO:0042417	25	4.46E-01	1.00E+00	4.34E-01	1.00E+00	6.78E-01	1.00E+00	6.91E-01	1.00E+00	2.94E-01	1.00E+00	3.48E-01	1.00E+00	3.80E-01	1.00E+00	2.37E-01	1.00E+00	dopamine metabolism	P
GO:0042423	12	9.57E-01	1.00E+00	6.20E-01	1.00E+00	9.05E-01	1.00E+00	8.52E-01	1.00E+00	9.88E-01	1.00E+00	5.38E-01	1.00E+00	6.91E-01	1.00E+00	2.58E-01	1.00E+00	catecholamine biosynthesis	P
GO:0042430	11	7.31E-01	1.00E+00	4.41E-01	1.00E+00	9.97E-01	1.00E+00	6.60E-01	1.00E+00	4.27E-01	1.00E+00	5.43E-01	1.00E+00	3.25E-01	1.00E+00	2.10E-01	1.00E+00	indole and derivative metabolism	P
GO:0042434	11	7.31E-01	1.00E+00	4.41E-01	1.00E+00	9.97E-01	1.00E+00	6.60E-01	1.00E+00	4.27E-01	1.00E+00	5.43E-01	1.00E+00	3.25E-01	1.00E+00	2.10E-01	1.00E+00	indole derivative metabolism	P
GO:0042438	10	7.36E-01	1.00E+00	7.10E-01	1.00E+00	7.15E-01	1.00E+00	7.28E-01	1.00E+00	9.25E-01	1.00E+00	9.91E-01	1.00E+00	2.45E-01	1.00E+00	1.03E-01	1.00E+00	melanin biosynthesis	P
GO:0042440	40	4.21E-02	1.00E+00	2.14E-01	1.00E+00	2.04E-02	1.00E+00	2.07E-01	1.00E+00	1.66E-01	1.00E+00	4.50E-01	1.00E+00	2.50E-01	1.00E+00	1.48E-01	1.00E+00	pigment metabolism	P
GO:0042445	113	9.98E-01	1.00E+00	9.69E-01	1.00E+00	9.99E-01	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	6.72E-01	1.00E+00	5.84E-01	1.00E+00	hormone metabolism	P
GO:0042446	42	9.77E-01	1.00E+00	9.18E-01	1.00E+00	9.91E-01	1.00E+00	9.96E-01	1.00E+00	9.92E-01	1.00E+00	8.95E-01	1.00E+00	7.24E-01	1.00E+00	5.41E-01	1.00E+00	hormone biosynthesis	P
GO:0042461	18	3.14E-01	1.00E+00	2.30E-01	1.00E+00	3.67E-01	1.00E+00	4.93E-01	1.00E+00	4.66E-01	1.00E+00	2.74E-01	1.00E+00	1.88E-01	1.00E+00	8.38E-02	1.00E+00	photoreceptor cell development	P
GO:0042462	13	3.62E-01	1.00E+00	1.48E-01	1.00E+00	2.71E-01	1.00E+00	3.04E-01	1.00E+00	4.42E-01	1.00E+00	1.71E-01	1.00E+00	3.91E-01	1.00E+00	1.27E-01	1.00E+00	eye photoreceptor cell development	P
GO:0042470	75	8.03E-10	2.57E-03	4.33E-12	0.00E+00	9.73E-07	2.00E-03	4.60E-08	2.89E-03	2.39E-06	1.69E-03	2.84E-06	2.90E-03	1.49E-06	8.23E-04	1.01E-07	9.38E-04	melanosome	C
GO:0042471	62	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.61E-01	1.00E+00	9.91E-01	1.00E+00	8.47E-01	1.00E+00	9.64E-01	1.00E+00	ear morphogenesis	P
GO:0042472	54	9.94E-01	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	8.43E-01	1.00E+00	9.61E-01	1.00E+00	8.97E-01	1.00E+00	9.34E-01	1.00E+00	inner ear morphogenesis	P
GO:0042474	11	8.11E-01	1.00E+00	9.99E-01	1.00E+00	8.61E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	8.95E-01	1.00E+00	1.49E-01	1.00E+00	9.94E-01	1.00E+00	middle ear morphogenesis	P
GO:0042475	42	6.83E-01	1.00E+00	7.68E-01	1.00E+00	7.50E-01	1.00E+00	9.58E-01	1.00E+00	7.42E-01	1.00E+00	5.04E-01	1.00E+00	4.32E-01	1.00E+00	5.90E-01	1.00E+00	odontogenesis (sensu Vertebrata)	P
GO:0042476	45	7.14E-01	1.00E+00	8.37E-01	1.00E+00	8.10E-01	1.00E+00	9.75E-01	1.00E+00	7.93E-01	1.00E+00	5.73E-01	1.00E+00	3.81E-01	1.00E+00	6.55E-01	1.00E+00	odontogenesis	P
GO:0042490	22	9.90E-01	1.00E+00	9.05E-01	1.00E+00	9.88E-01	1.00E+00	9.66E-01	1.00E+00	9.95E-01	1.00E+00	9.62E-01	1.00E+00	8.27E-01	1.00E+00	2.73E-01	1.00E+00	mechanoreceptor differentiation	P
GO:0042491	16	1.00E+00	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	7.32E-01	1.00E+00	2.64E-01	1.00E+00	auditory receptor cell differentiation	P
GO:0042493	128	5.63E-01	1.00E+00	4.16E-01	1.00E+00	9.27E-01	1.00E+00	4.86E-01	1.00E+00	6.81E-01	1.00E+00	6.77E-01	1.00E+00	7.33E-02	1.00E+00	8.34E-02	1.00E+00	response to drug	P
GO:0042509	15	9.74E-01	1.00E+00	5.91E-01	1.00E+00	9.94E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	5.86E-01	1.00E+00	2.41E-01	1.00E+00	1.93E-01	1.00E+00	regulation of tyrosine phosphorylation of ST	P
GO:0042533	10	5.39E-01	1.00E+00	3.77E-01	1.00E+00	6.43E-01	1.00E+00	4.60E-01	1.00E+00	6.40E-01	1.00E+00	7.27E-01	1.00E+00	2.90E-01	1.00E+00	8.32E-02	1.00E+00	tumor necrosis factor-alpha biosynthesis	P
GO:0042534	10	5.39E-01	1.00E+00	3.77E-01	1.00E+00	6.43E-01	1.00E+00	4.60E-01	1.00E+00	6.40E-01	1.00E+00	7.27E-01	1.00E+00	2.90E-01	1.00E+00	8.32E-02	1.00E+00	regulation of tumor necrosis factor-alpha bi	P
GO:0042542	23	2.19E-03	2.12E-01	1.43E-03	9.65E-02	1.16E-02	6.53E-01	1.63E-03	9.60E-02	2.06E-02	7.90E-01	1.57E-04	2.33E-02	1.99E-03	8.40E-02	1.99E-01	1.00E+00	response to hydrogen peroxide	P
GO:0042551	16	8.31E-01	1.00E+00	4.52E-01	1.00E+00	7.79E-01	1.00E+00	9.68E-01	1.00E+00	8.88E-01	1.00E+00	4.54E-01	1.00E+00	3.94E-01	1.00E+00	1.69E-01	1.00E+00	neuron maturation	P
GO:0042552	40	6.27E-01	1.00E+00	2.73E-01	1.00E+00	3.85E-01	1.00E+00	1.95E-01	1.00E+00	6.71E-01	1.00E+00	4.85E-01	1.00E+00	6.75E-01	1.00E+00	1.89E-01	1.00E+00	myelination	P
GO:0042558	15	2.92E-01	1.00E+00	3.73E-02	1.00E+00	4.91E-01	1.00E+00	1.73E-01	1.00E+00	1.12E-01	1.00E+00	6.16E-02	1.00E+00	7.17E-01	1.00E+00	2.14E-01	1.00E+00	pteridine and derivative metabolism	P
GO:0042559	12	3.76E-01	1.00E+00	9.32E-02	1.00E+00	8.58E-01	1.00E+00	4.86E-01	1.00E+00	1.40E-01	1.00E+00	5.48E-02	1.00E+00	6.65E-01	1.00E+00	1.71E-01	1.00E+00	pteridine and derivative biosynthesis	P
GO:0042562	26	9.82E-01	1.00E+00	9.08E-01	1.00E+00	8.95E-01	1.00E+00	9.11E-01	1.00E+00	9.96E-01	1.00E+00	9.94E-01	1.00E+00	8.34E-01	1.00E+00	1.32E-01	1.00E+00	hormone binding	F
GO:0042573	12	1.00E+00	1.00E+00	9.46E-01	1.00E+00	9.98E-01	1.00E+00	9.54E-01	1.00E+00	9.98E-01	1.00E+00	9.22E-01	1.00E+00	9.75E-01	1.00E+00	7.33E-01	1.00E+00	retinoic acid metabolism	P
GO:0042577	11	1.33E-01	1.00E+00	3.61E-01	1.00E+00	8.77E-02	1.00E+00	1.98E-01	1.00E+00	1.31E-01	1.00E+00	3.81E-01	1.00E+00	2.36E-01	1.00E+00	6.44E-01	1.00E+00	lipid phosphatase activity	F
GO:0042578	325	1.46E-05	7.00E-03	2.15E-08	9.59E-04	2.12E-04	2.10E-02	4.59E-06	2.89E-03	1.67E-03	1.20E-01	1.68E-04	2.33E-02	3.54E-04	2.29E-02	8.07E-06	7.00E-03	phosphoric ester hydrolase activity	F
GO:0042579	99	7.41E-03	3.15E-01	1.60E-03	9.65E-02	7.21E-02	1.00E+00	1.60E-02	6.47E-01	9.66E-03	6.92E-01	3.42E-03	1.51E-01	4.98E-02	1.00E+00	4.62E-02	1.00E+00	microbody	C
GO:0042592	601	6.46E-04	8.86E-02	3.90E-05	7.00E-03	4.63E-03	3.08E-01	1.26E-03	9.40E-02	1.11E-01	1.00E+00	1.96E-03	1.27E-01	8.30E-05	8.00E-03	1.49E-04	1.60E-02	homeostasis	P
GO:0042593	39	5.62E-03	3.09E-01	1.41E-02	6.07E-01	8.96E-02	1.00E+00	7.13E-02	1.00E+00	2.83E-02	1.00E+00	2.55E-01	1.00E+00	7.53E-04	3.44E-02	1.40E-03	6.00E-02	glucose homeostasis	P
GO:0042594	18	2.75E-01	1.00E+00	5.55E-01	1.00E+00	7.02E-01	1.00E+00	5.16E-01	1.00E+00	1.05E-01	1.00E+00	5.91E-01	1.00E+00	3.31E-01	1.00E+00	6.67E-01	1.00E+00	response to starvation	P
GO:0042596	17	6.16E-01	1.00E+00	4.96E-01	1.00E+00	9.59E-01	1.00E+00	8.71E-01	1.00E+00	3.31E-01	1.00E+00	2.30E-01	1.00E+00	3.65E-01	1.00E+00	4.57E-01	1.00E+00	fear response	P
GO:0042597	22	9.64E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	9.92E-01	1.00E+00	8.53E-01	1.00E+00	1.00E+00	1.00E+00	8.08E-01	1.00E+00	6.73E-01	1.00E+00	periplasmic space	C
GO:0042598	183	8.07E-01	1.00E+00	3.65E-01	1.00E+00	8.10E-01	1.00E+00	7.88E-01	1.00E+00	4.79E-01	1.00E+00	1.35E-01	1.00E+00	9.17E-01	1.00E+00	1.77E-01	1.00E+00	vesicular fraction	C
GO:0042611	49	7.94E-01	1.00E+00	9.68E-01	1.00E+00	2.02E-01	1.00E+00	8.23E-01	1.00E+00	6.72E-01	1.00E+00	3.76E-01	1.00E+00	9.43E-01	1.00E+00	1.00E+00	1.00E+00	MHC protein complex	C
GO:0042612	39	8.52E-01	1.00E+00	9.88E-01	1.00E+00	1.56E-01	1.00E+00	8.61E-01	1.00E+00	7.06E-01	1.00E+00	6.00E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	MHC class I protein complex	C
GO:0042613	10	2.94E-01	1.00E+00	1.46E-01	1.00E+00	6.18E-01	1.00E+00	4.73E-01	1.00E+00	4.43E-01	1.00E+00	3.49E-02	1.00E+00	2.22E-01	1.00E+00	7.50E-01	1.00E+00	MHC class II protein complex	C
GO:0042623	274	4.61E-06	3.02E-03	7.09E-08	3.92E-03	1.10E-05	2.91E-03	4.26E-06	2.89E-03	7.34E-04	1.20E-01	8.47E-07	2.00E-03	7.42E-02	1.00E+00	7.56E-03	4.28E-01	ATPase activity, coupled	F
GO:0042625	97	1.04E-01	1.00E+00	5.65E-02	1.00E+00	1.36E-01	1.00E+00	1.29E-01	1.00E+00	2.26E-01	1.00E+00	5.10E-02	1.00E+00	3.28E-01	1.00E+00	2.47E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042626	136	2.14E-01	1.00E+00	4.59E-02	1.00E+00	2.53E-01	1.00E+00	2.47E-01	1.00E+00	4.87E-01	1.00E+00	1.79E-02	6.68E-01	3.66E-01	1.00E+00	2.41E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042627	10	4.14E-03	2.14E-01	1.21E-02	6.07E-01	6.11E-03	4.69E-01	6.09E-02	1.00E+00	1.55E-03	1.20E-01	3.98E-01	1.00E+00	1.75E-01	1.00E+00	1.30E-18	0.00E+00	chylomicron	C

GO:0042632	25	3.54E-02	1.00E+00	6.13E-02	1.00E+00	9.00E-02	1.00E+00	4.99E-02	1.00E+00	1.11E-01	1.00E+00	1.72E-01	1.00E+00	7.54E-02	1.00E+00	1.00E-01	1.00E+00	cholesterol homeostasis	P
GO:0042633	45	3.01E-01	1.00E+00	2.95E-01	1.00E+00	8.52E-01	1.00E+00	4.60E-01	1.00E+00	3.16E-01	1.00E+00	3.23E-01	1.00E+00	3.02E-02	8.38E-01	1.15E-01	1.00E+00	hair cycle	P
GO:0042640	10	5.52E-01	1.00E+00	1.11E-01	1.00E+00	8.27E-01	1.00E+00	2.82E-01	1.00E+00	7.52E-01	1.00E+00	8.57E-02	1.00E+00	2.27E-01	1.00E+00	1.76E-01	1.00E+00	anagen	P
GO:0042692	86	9.60E-01	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	7.82E-01	1.00E+00	9.34E-01	1.00E+00	9.43E-01	1.00E+00	5.20E-01	1.00E+00	9.76E-01	1.00E+00	muscle cell differentiation	P
GO:0042698	40	6.57E-02	1.00E+00	2.61E-01	1.00E+00	1.59E-01	1.00E+00	4.13E-01	1.00E+00	6.63E-02	1.00E+00	1.57E-01	1.00E+00	2.21E-01	1.00E+00	3.84E-01	1.00E+00	menstrual cycle	P
GO:0042733	18	1.00E+00	1.00E+00	6.24E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	9.99E-01	1.00E+00	7.44E-01	1.00E+00	9.41E-01	1.00E+00	1.48E-01	1.00E+00	embryonic digit morphogenesis	P
GO:0042734	24	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	6.35E-01	1.00E+00	5.17E-01	1.00E+00	presynaptic membrane	C
GO:0042742	85	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	6.08E-01	1.00E+00	8.68E-01	1.00E+00	defense response to bacterium	P
GO:0042743	19	8.96E-03	6.08E-01	4.70E-03	2.61E-01	7.91E-02	1.00E+00	1.75E-02	6.47E-01	2.46E-02	1.00E+00	7.68E-03	4.21E-01	1.06E-02	2.75E-01	1.87E-02	7.36E-01	hydrogen peroxide metabolism	P
GO:0042744	12	2.36E-02	1.00E+00	8.92E-03	4.69E-01	5.88E-02	1.00E+00	1.15E-02	6.47E-01	1.14E-01	1.00E+00	1.68E-02	6.68E-01	4.61E-03	2.23E-01	3.28E-02	1.00E+00	hydrogen peroxide catabolism	P
GO:0042755	13	4.98E-01	1.00E+00	2.39E-01	1.00E+00	5.48E-01	1.00E+00	6.73E-01	1.00E+00	5.17E-01	1.00E+00	2.64E-01	1.00E+00	2.78E-01	1.00E+00	8.09E-02	1.00E+00	eating behavior	P
GO:0042770	49	1.12E-03	8.86E-02	3.62E-07	3.92E-03	3.56E-03	2.03E-01	1.79E-05	9.57E-03	9.92E-03	6.92E-01	2.14E-03	1.27E-01	4.95E-02	1.00E+00	2.20E-05	7.00E-03	DNA damage response, signal transduction	P
GO:0042771	11	9.79E-02	1.00E+00	2.24E-02	1.00E+00	4.71E-02	1.00E+00	9.63E-02	1.00E+00	1.55E-01	1.00E+00	5.03E-02	1.00E+00	3.66E-01	1.00E+00	9.66E-02	1.00E+00	DNA damage response, signal transduction	P
GO:0042773	35	2.00E-01	1.00E+00	3.98E-01	1.00E+00	2.32E-01	1.00E+00	3.26E-01	1.00E+00	3.46E-01	1.00E+00	3.79E-01	1.00E+00	3.35E-01	1.00E+00	5.71E-01	1.00E+00	ATP synthesis coupled electron transport	P
GO:0042775	26	1.16E-01	1.00E+00	3.33E-01	1.00E+00	1.55E-01	1.00E+00	2.29E-01	1.00E+00	3.03E-01	1.00E+00	4.36E-01	1.00E+00	1.47E-01	1.00E+00	3.43E-01	1.00E+00	ATP synthesis coupled electron transport (s	P
GO:0042802	396	3.25E-08	2.57E-03	3.19E-10	0.00E+00	6.96E-07	2.00E-03	1.09E-07	2.89E-03	2.60E-04	4.90E-02	1.73E-06	2.00E-03	4.62E-05	8.00E-03	2.85E-05	7.00E-03	identical protein binding	F
GO:0042803	191	1.79E-04	1.72E-02	1.23E-06	3.92E-03	1.42E-02	6.53E-01	4.50E-04	4.20E-02	7.60E-03	6.92E-01	3.26E-04	2.33E-02	2.77E-04	2.29E-02	2.02E-04	1.60E-02	protein homodimerization activity	F
GO:0042809	11	6.63E-01	1.00E+00	4.72E-01	1.00E+00	1.02E-01	1.00E+00	1.75E-01	1.00E+00	3.30E-01	1.00E+00	4.09E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	vitamin D receptor binding	F
GO:0042826	10	2.14E-01	1.00E+00	3.55E-01	1.00E+00	1.82E-01	1.00E+00	2.25E-01	1.00E+00	2.30E-01	1.00E+00	4.73E-01	1.00E+00	4.60E-01	1.00E+00	6.41E-01	1.00E+00	histone deacetylase binding	F
GO:0042895	26	7.35E-01	1.00E+00	3.12E-01	1.00E+00	9.59E-01	1.00E+00	7.76E-01	1.00E+00	6.24E-01	1.00E+00	2.94E-01	1.00E+00	6.60E-01	1.00E+00	1.47E-01	1.00E+00	antibiotic transporter activity	F
GO:0042923	143	7.76E-01	1.00E+00	9.26E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	6.47E-01	1.00E+00	8.97E-01	1.00E+00	9.83E-02	1.00E+00	2.87E-01	1.00E+00	neuropeptide binding	F
GO:0042974	17	2.66E-01	1.00E+00	1.93E-01	1.00E+00	8.71E-02	1.00E+00	8.85E-02	1.00E+00	7.50E-02	1.00E+00	4.67E-01	1.00E+00	9.86E-01	1.00E+00	6.94E-01	1.00E+00	retinoic acid receptor binding	F
GO:0042981	540	2.10E-07	2.57E-03	2.11E-08	9.59E-04	1.11E-04	1.16E-02	2.67E-06	2.89E-03	1.90E-04	4.90E-02	3.95E-06	2.90E-03	3.36E-05	4.00E-03	1.25E-04	1.60E-02	regulation of apoptosis	P
GO:0042990	17	1.28E-02	6.08E-01	1.14E-05	4.51E-03	4.36E-02	1.00E+00	2.95E-03	1.61E-01	5.33E-02	1.00E+00	1.76E-03	1.27E-01	1.02E-01	1.00E+00	1.24E-03	6.00E-02	regulation of transcription factor import into	P
GO:0042991	17	1.28E-02	6.08E-01	1.14E-05	4.51E-03	4.36E-02	1.00E+00	2.95E-03	1.61E-01	5.33E-02	1.00E+00	1.76E-03	1.27E-01	1.02E-01	1.00E+00	1.24E-03	6.00E-02	transcription factor import into nucleus	P
GO:0042995	539	3.46E-02	1.00E+00	2.96E-05	7.00E-03	3.24E-01	1.00E+00	1.39E-02	6.47E-01	9.45E-02	1.00E+00	1.34E-03	9.00E-02	1.61E-02	4.88E-01	1.04E-05	7.00E-03	cell projection	C
GO:0043005	176	4.65E-01	1.00E+00	2.24E-01	1.00E+00	5.53E-01	1.00E+00	6.65E-01	1.00E+00	7.96E-01	1.00E+00	1.50E-01	1.00E+00	2.40E-01	1.00E+00	8.59E-02	1.00E+00	neuron projection	C
GO:0043009	243	5.67E-03	3.09E-01	4.19E-02	1.00E+00	6.33E-03	4.69E-01	2.66E-02	1.00E+00	2.51E-02	1.00E+00	1.66E-01	1.00E+00	9.40E-02	1.00E+00	3.04E-01	1.00E+00	embryonic development (sensu Vertebrata)	P
GO:0043010	73	5.19E-02	1.00E+00	6.64E-01	1.00E+00	5.44E-02	1.00E+00	5.17E-01	1.00E+00	1.44E-01	1.00E+00	7.23E-01	1.00E+00	1.49E-01	1.00E+00	6.94E-01	1.00E+00	eye development (sensu Vertebrata)	P
GO:0043015	10	3.56E-03	2.12E-01	3.82E-04	4.40E-02	1.39E-02	6.53E-01	4.88E-02	1.00E+00	3.87E-02	1.00E+00	2.12E-02	7.56E-01	6.56E-02	1.00E+00	2.31E-03	7.90E-02	gamma-tubulin binding	F
GO:0043021	25	1.08E-07	2.57E-03	3.43E-09	8.90E-04	7.14E-06	2.91E-03	1.60E-05	9.57E-03	2.84E-06	1.69E-03	1.42E-06	2.00E-03	4.22E-02	1.00E+00	3.89E-02	1.00E+00	ribonucleoprotein binding	F
GO:0043025	100	1.75E-01	1.00E+00	1.02E-01	1.00E+00	4.78E-01	1.00E+00	2.37E-01	1.00E+00	3.87E-01	1.00E+00	1.37E-01	1.00E+00	9.71E-02	1.00E+00	1.25E-01	1.00E+00	cell soma	C
GO:0043028	12	2.00E-02	1.00E+00	2.52E-02	1.00E+00	3.95E-01	1.00E+00	5.15E-02	1.00E+00	1.97E-03	1.20E-01	4.67E-02	1.00E+00	3.96E-02	1.00E+00	6.24E-02	1.00E+00	caspase regulator activity	F
GO:0043029	18	5.18E-02	1.00E+00	2.30E-03	1.71E-01	1.21E-01	1.00E+00	9.54E-02	1.00E+00	6.43E-01	1.00E+00	1.30E-03	9.00E-02	8.04E-04	3.44E-02	2.56E-02	9.99E-01	T cell homeostasis	P
GO:0043037	165	7.15E-10	2.57E-03	7.14E-12	0.00E+00	4.40E-11	7.08E-04	5.24E-11	0.00E+00	5.65E-08	9.59E-04	8.94E-10	6.20E-04	1.92E-02	6.36E-01	2.09E-03	7.90E-02	translation	P
GO:0043038	68	1.05E-05	7.00E-03	1.16E-04	1.50E-02	2.35E-04	2.10E-02	1.24E-04	1.30E-02	6.40E-05	2.40E-02	2.27E-04	2.33E-02	2.83E-02	8.38E-01	1.63E-01	1.00E+00	amino acid activation	P
GO:0043039	68	1.05E-05	7.00E-03	1.16E-04	1.50E-02	2.35E-04	2.10E-02	1.24E-04	1.30E-02	6.40E-05	2.40E-02	2.27E-04	2.33E-02	2.83E-02	8.38E-01	1.63E-01	1.00E+00	tRNA aminoacylation	P
GO:0043062	83	7.32E-01	1.00E+00	2.39E-01	1.00E+00	9.21E-01	1.00E+00	7.81E-01	1.00E+00	9.62E-01	1.00E+00	4.43E-01	1.00E+00	1.76E-01	1.00E+00	1.28E-02	4.76E-01	extracellular structure organization and bioc	P
GO:0043064	15	5.15E-02	1.00E+00	6.99E-05	7.00E-03	4.69E-02	1.00E+00	1.51E-02	6.47E-01	3.29E-01	1.00E+00	6.17E-04	3.20E-02	9.16E-02	1.00E+00	2.43E-02	9.99E-01	flagellum organization and biogenesis	P
GO:0043065	253	1.15E-04	1.43E-02	1.72E-06	3.92E-03	1.54E-03	9.50E-02	4.70E-05	1.07E-02	3.42E-03	2.13E-01	1.55E-05	5.87E-03	1.95E-03	8.40E-02	2.11E-03	7.90E-02	positive regulation of apoptosis	P
GO:0043066	226	1.29E-04	1.43E-02	2.96E-03	1.88E-01	5.13E-03	3.08E-01	5.40E-03	2.88E-01	9.67E-03	6.92E-01	5.36E-02	1.00E+00	2.74E-04	2.29E-02	1.92E-02	7.36E-01	negative regulation of apoptosis	P
GO:0043067	546	2.67E-07	2.57E-03	2.98E-08	9.59E-04	1.25E-04	1.16E-02	2.91E-06	2.89E-03	2.93E-04	4.90E-02	6.92E-06	5.87E-03	2.63E-05	4.00E-03	9.84E-05	1.60E-02	regulation of programmed cell death	P
GO:0043068	255	8.37E-05	1.43E-02	9.06E-07	3.92E-03	1.25E-03	7.90E-02	3.59E-05	9.57E-03	2.15E-03	1.20E-01	1.38E-05	5.87E-03	1.98E-03	8.40E-02	8.87E-04	6.00E-02	positive regulation of programmed cell deat	P
GO:0043069	230	1.33E-04	1.43E-02	3.09E-03	1.88E-01	5.13E-03	3.08E-01	5.08E-03	2.88E-01	1.19E-02	6.92E-01	6.68E-02	1.00E+00	2.02E-04	1.20E-02	1.44E-02	4.76E-01	negative regulation of programmed cell dea	P
GO:0043085	221	3.60E-04	3.10E-02	2.53E-05	7.00E-03	3.63E-02	1.00E+00	1.80E-03	1.24E-01	2.08E-03	1.20E-01	9.55E-04	9.00E-02	8.49E-04	3.44E-02	6.37E-05	7.00E-03	positive regulation of enzyme activity	P
GO:0043086	77	1.95E-03	2.12E-01	4.86E-06	4.51E-03	3.07E-03	1.35E-01	8.98E-05	1.30E-02	2.59E-02	1.00E+00	7.09E-05	1.10E-02	4.06E-02	1.00E+00	6.02E-04	3.00E-02	negative regulation of enzyme activity	P
GO:0043087	90	2.46E-03	2.12E-01	7.68E-05	1.50E-02	6.29E-03	4.69E-01	3.91E-03	2.88E-01	6.43E-02	1.00E+00	1.09E-04	1.30E-02	2.84E-02	8.38E-01	3.54E-02	1.00E+00	regulation of GTPase activity	P
GO:0043112	28	2.70E-01	1.00E+00	1.01E-01	1.00E+00	4.19E-01	1.00E+00	2.33E-01	1.00E+00	2.34E-01	1.00E+00	3.14E-01	1.00E+00	3.23E-01	1.00E+00	1.15E-01	1.00E+00	receptor metabolism	P
GO:0043113	11	4.66E-01	1.00E+00	1.83E-01	1.00E+00	7.05E-01	1.00E+00	3.04E-01	1.00E+00	8.08E-01	1.00E+00	4.81E-01	1.00E+00	1.50E-01	1.00E+00	1.54E-01	1.00E+00	receptor clustering	P
GO:0043118	1035	3.22E-19	0.00E+00	1.78E-20	0.00E+00	5.45E-15	7.08E-04	9.61E-17	0.00E+00	2.20E-08	9.59E-04	3.12E-11	6.20E-04	1.25E-13	0.00E+00	3.87E-13	0.00E+00	negative regulation of physiological process	P
GO:0043119	1122	1.38E-08	2.57E-03	7.11E-12	0.00E+00	6.83E-07	2.00E-03	4.58E-07	2.89E-03	1.22E-02	6.92E-01	1.96E-07	1.65E-03	9.68E-09	0.00E+00	1.23E-09	0.00E+00	positive regulation of physiological process	P
GO:0043122	80	3.61E-02	1.00E+00	1.27E-04	1.50E-02	1.93E-01	1.00E+00	4.67E-03	2.88E-01	3.24E-01	1.00E+00	1.49E-02	6.68E-01	7.14E-03	2.75E-01	1.91E-03	7.90E-02	regulation of I-kappaB kinase/NF-kappaB c	P
GO:0043123	74	1.52E-02	1.00E+00	8.33E-05	1.50E-02	1.43E-01	1.00E+00	5.07E-03	2.88E-01	2.57E-01	1.00E+00	9.34E-03	5.03E-01	4.07E-03	2.23E-01	2.00E-03	7.90E-02	positive regulation of I-kappaB kinase/NF-k	P
GO:0043154	12	2.85E-02	1.00E+00	2.82E-02	1.00E+00	3.06E-02	1.00E+00	1.26E-02	6.47E-01	9.33E-02	1.00E+00	1.86E-01	1.00E+00	1.69E-01	1.00E+00	1.43E-01	1.00E+00	negative regulation of caspase activity	P
GO:0043161	29	1.19E-01	1.00E+00	4.59E-03	2.61E-01	8.06E-02	1.00E+00	4.29E-03	2.88E-01	2.00E-01	1.00E+00	2.70E-02	1.00E+00	4.28E-01	1.00E+00	3.22E-01	1.00E+00	proteasomal ubiquitin-dependent protein ca	P
GO:0043167	4242	7.74E-15	0.00E+00	8.36E-33	0.00E+00	5.99E-15	7.08E-04	7.31E-26	0.00E+00	4.00E-10	0.00E+00	3.60E-23	0.00E+00	9.10E-04	3.44E-02	1.90E-13	0.00E+00	ion binding	F
GO:0043168	62	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	anion binding	F
GO:0043169	3872	4.74E-13	0.00E+00	1.91E-27	0.00E+00	6.43E-13	7.08E-04	1.64E-23	0.00E+00	1.24E-08	0.00E+00	3.03E-18	0.00E+00	8.87E-04	3.44E-02	3.31E-11	0.00E+00	cation binding	F
GO:0043170	5092	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.58E-23	0.00E+00	2.08E-41	0.00E+00	macromolecule metabolism	P
GO:0043176	48	9.76E-01	1.00E+00	1.00E+00	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	7.71E-01	1.00E+00	6.71E-01	1.00E+00	amine binding	F
GO:0043193	12	9.48E-03	6.08E-01	3.07E-02	1.00E+00	3.50E-02	1.00E+00	6.73E-02	1.00E+00	2.78E-01	1.00E+00	2.28E-02	1.00E+00	9.38E-03	2.75E-01	5.19E-02	1.00E+00	positive regulation of gene-specific transcrip	P
GO:0043197	15	8.06E-01	1.00E+00	6.17E-01	1.00E+00	8.91E-01	1.00E+00	5.59E-01	1.00E+00	6.56E-01	1.00E+00	4.65E-01	1.00E+00	6.09E-01	1.00E+00	7.76E-01	1.00E+00	dendritic spine	C
GO:0043198	13	8.23E-01	1.00E+00	3.34E-01	1.00E+00	9.99E-01	1.00E+00	2.64E-01	1.00E+00	4.63E-01	1.00E+00	2.79E-01	1.00E+00	6.32E-01	1.00E+00	6.85E-01	1.00E+00	dendritic shaft	C
GO:0043226	8400	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.80E-45	0.00E+00	0.00E+00	0.00E+00	organelle	C
GO:0043227	7231	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.39E-39	0.00E+00	0.00E+00	0.00E+00	membrane-bound organelle	C
GO:0043228	2204	2.33E-28	0.00E+00	4.53E-25	0.00E+00	1.14E-26	0.00E+00	3.52E-23	0.00E+00	6.45E-19	0.00E+00	5.85E-14	6.20E-04	1.84E-09	0.00E+00	3.41E-11	0.00E+00	non-membrane-bound organelle	C
GO:0043229	8397	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.80E-45	0.00E+00	0.00E+00	0.00E+00	intracellular organelle	C
GO:0043231	7227	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.52E-39	0.00E+00	0.00E+00	0.00E+00	intracellular membrane-bound organelle	C
GO:0043232	2204	2.33E-28	0.00E+00	4.53E-25	0.00E+00	1.14E-26	0.00E+00	3.52E-23	0.00E+00	6.45E-19	0.00E+00	5.85E-14	6.20E-04	1.84E-09	0.00E+00	3.41E-11	0.00E+00	intracellular non-membrane-bound organell	C
GO:0043233	948	2.93E-39	0.00E+00	1.37E-36	0.00E+00	1.64E-34	0.00E+00	7.30E-33	0.00E+00	1.74E-23	0.00E+00	2.46E-22	0.00E+00	2.08E-13	0.00E+00	6.21E-11	0.00E+00	organelle lumen	C
GO:0043234	2635	0.00E+00	0.00E+00	1.40E-45	0.00E+00	0.00E+00	0.00E+00	1.61E-41	0.00E+00	2.86E-31	0.00E+00	8.16E-28	0.00E+00	1.32E-20	0.00E+00	1.55E-15	0.00E+00	protein complex	C
GO:0043235	83	3.55E-01	1.00E+00	1.89E-01	1.00E+00	6.84E-01	1.00E+00	6.26E-01	1.00E+00	6.33E-01	1.00E+00	5.48E-01	1.00E+00	4.68E-02	1.00E+00	1.80E-02	6.56E-01	receptor complex	C
GO:0043269	40	8.41E-01	1.00E+00	6.10E-01	1.00E+00	9.90E-01	1.00E+00	7.77E-01	1.00E+00	4.00E-01	1.00E+00	9.39E-01	1.00E+00	6.03E-01	1.00E+00	1.31E-01	1.00E+00	regulation of ion transport	P
GO:0043270	11	5.16E-01	1.00E+00	1.09E-01	1.00E+00	6.45E-01	1.00E+00	2.38E-01	1.00E+00	3.47E-01	1.00E+00	3.89E-01	1.00E+00	7.45E-01	1.00E+00	4.61E-02	1.00E+00	positive regulation of ion transport	P
GO:0043279	14	6.38E-01	1.00E+00	8.90E-01	1.00E+00	8.35E-01	1.00E+00	8.97E-01	1.00E+00	8.45E-01	1.00E+00	8.30E-01	1.00E+00	2.29E-02	8.38E-01	7.15E-01	1.00E+00	response to alkaloid	P

GO:0043280	40	8.54E-06	3.62E-03	4.75E-04	4.74E-02	1.86E-03	9.50E-02	8.79E-03	4.92E-01	3.21E-04	4.90E-02	1.59E-03	1.22E-01	2.77E-03	8.40E-02	7.83E-03	4.28E-01	positive regulation of caspase activity	P
GO:0043281	55	2.15E-06	3.00E-03	6.88E-05	7.00E-03	1.97E-04	2.10E-02	9.18E-04	9.40E-02	1.15E-04	2.70E-02	1.08E-03	9.00E-02	1.36E-03	6.14E-02	3.56E-03	1.27E-01	regulation of caspase activity	P
GO:0043283	3098	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.75E-41	0.00E+00	0.00E+00	0.00E+00	5.48E-15	0.00E+00	9.71E-34	0.00E+00	biopolymer metabolism	P
GO:0043284	42	6.00E-01	1.00E+00	2.30E-02	1.00E+00	8.34E-01	1.00E+00	1.69E-01	1.00E+00	2.75E-01	1.00E+00	2.39E-02	1.00E+00	6.75E-01	1.00E+00	1.88E-02	7.36E-01	biopolymer biosynthesis	P
GO:0043285	293	3.64E-12	0.00E+00	1.43E-12	0.00E+00	3.19E-11	7.08E-04	4.05E-13	0.00E+00	3.21E-08	9.59E-04	7.74E-07	2.00E-03	3.14E-03	8.78E-02	8.96E-06	7.00E-03	biopolymer catabolism	P
GO:0043292	86	2.49E-01	1.00E+00	3.00E-02	1.00E+00	6.15E-01	1.00E+00	1.72E-01	1.00E+00	1.81E-01	1.00E+00	1.33E-01	1.00E+00	4.58E-01	1.00E+00	8.73E-03	4.28E-01	contractile fiber	C
GO:0043296	121	2.90E-02	1.00E+00	4.84E-02	1.00E+00	3.46E-01	1.00E+00	3.56E-01	1.00E+00	2.72E-01	1.00E+00	4.12E-01	1.00E+00	2.14E-03	8.40E-02	5.77E-04	3.00E-02	apical junction complex	C
GO:0043299	12	1.54E-02	1.00E+00	5.52E-02	1.00E+00	4.87E-02	1.00E+00	1.06E-01	1.00E+00	1.23E-01	1.00E+00	1.65E-01	1.00E+00	3.53E-02	8.38E-01	6.03E-02	1.00E+00	leukocyte degranulation	P
GO:0043330	10	1.13E-01	1.00E+00	1.64E-01	1.00E+00	2.22E-01	1.00E+00	3.24E-01	1.00E+00	1.57E-01	1.00E+00	3.41E-01	1.00E+00	8.94E-02	1.00E+00	1.22E-01	1.00E+00	response to exogenous dsRNA	P
GO:0043331	13	2.02E-02	1.00E+00	3.13E-02	1.00E+00	7.66E-02	1.00E+00	6.60E-02	1.00E+00	4.10E-02	1.00E+00	4.87E-02	1.00E+00	5.11E-02	1.00E+00	1.43E-01	1.00E+00	response to dsRNA	P
GO:0043367	18	1.14E-01	1.00E+00	2.77E-01	1.00E+00	2.33E-01	1.00E+00	3.18E-01	1.00E+00	5.93E-01	1.00E+00	6.27E-01	1.00E+00	1.79E-02	5.17E-01	1.98E-01	1.00E+00	CD4-positive, alpha beta T cell differentiatic	P
GO:0043393	11	6.62E-02	1.00E+00	1.12E-01	1.00E+00	3.15E-01	1.00E+00	7.02E-01	1.00E+00	5.79E-01	1.00E+00	2.58E-01	1.00E+00	3.52E-02	8.38E-01	2.31E-02	9.99E-01	regulation of protein binding	P
GO:0043405	93	1.30E-02	6.08E-01	3.63E-03	1.88E-01	9.01E-02	1.00E+00	4.44E-02	1.00E+00	4.63E-02	1.00E+00	1.19E-02	5.03E-01	1.41E-02	4.78E-01	7.61E-03	4.28E-01	regulation of MAPK activity	P
GO:0043406	67	2.32E-02	1.00E+00	3.83E-02	1.00E+00	1.44E-01	1.00E+00	1.62E-01	1.00E+00	3.36E-02	1.00E+00	4.66E-02	1.00E+00	4.32E-02	1.00E+00	3.80E-02	1.00E+00	positive regulation of MAPK activity	P
GO:0043407	21	2.55E-01	1.00E+00	1.63E-02	7.63E-01	2.80E-01	1.00E+00	3.03E-02	1.00E+00	5.48E-01	1.00E+00	1.14E-01	1.00E+00	1.24E-01	1.00E+00	3.72E-02	1.00E+00	negative regulation of MAPK activity	P
GO:0043408	31	7.29E-01	1.00E+00	5.73E-02	1.00E+00	8.03E-01	1.00E+00	1.08E-01	1.00E+00	6.14E-01	1.00E+00	1.54E-01	1.00E+00	6.19E-01	1.00E+00	2.81E-02	9.99E-01	regulation of MAPKKK cascade	P
GO:0043410	20	7.30E-01	1.00E+00	2.71E-01	1.00E+00	7.69E-01	1.00E+00	3.00E-01	1.00E+00	6.65E-01	1.00E+00	5.74E-01	1.00E+00	5.51E-01	1.00E+00	1.27E-01	1.00E+00	positive regulation of MAPKKK cascade	P
GO:0043412	1882	1.17E-25	0.00E+00	0.00E+00	0.00E+00	1.58E-24	0.00E+00	1.09E-40	0.00E+00	4.86E-16	0.00E+00	4.83E-31	0.00E+00	1.78E-07	0.00E+00	4.43E-24	0.00E+00	biopolymer modification	P
GO:0043413	94	6.79E-02	1.00E+00	1.92E-02	1.00E+00	1.06E-01	1.00E+00	8.90E-02	1.00E+00	3.40E-01	1.00E+00	4.73E-02	1.00E+00	1.65E-02	4.88E-01	1.23E-02	4.76E-01	biopolymer glycosylation	P
GO:0043414	74	1.59E-02	1.00E+00	3.92E-03	1.88E-01	4.60E-03	3.08E-01	6.63E-04	4.20E-02	1.49E-01	1.00E+00	2.80E-02	1.00E+00	9.60E-02	1.00E+00	5.83E-02	1.00E+00	biopolymer methylation	P
GO:0043433	21	1.07E-03	8.86E-02	1.30E-05	4.51E-03	4.53E-04	4.90E-02	1.25E-05	2.89E-03	1.73E-01	1.00E+00	4.18E-03	2.66E-01	3.20E-02	8.38E-01	2.40E-04	2.33E-02	negative regulation of transcription factor ac	P
GO:0043434	21	6.24E-01	1.00E+00	5.68E-01	1.00E+00	6.25E-01	1.00E+00	9.48E-01	1.00E+00	8.85E-01	1.00E+00	2.35E-01	1.00E+00	8.14E-02	1.00E+00	3.56E-01	1.00E+00	response to peptide hormone stimulus	P
GO:0043449	29	6.83E-01	1.00E+00	5.78E-01	1.00E+00	7.60E-01	1.00E+00	7.83E-01	1.00E+00	3.72E-01	1.00E+00	2.35E-01	1.00E+00	8.21E-01	1.00E+00	7.13E-01	1.00E+00	alkene metabolism	P
GO:0043450	19	5.70E-01	1.00E+00	4.37E-01	1.00E+00	7.30E-01	1.00E+00	5.79E-01	1.00E+00	1.98E-01	1.00E+00	2.57E-01	1.00E+00	7.48E-01	1.00E+00	5.95E-01	1.00E+00	alkene biosynthesis	P
GO:0043473	43	1.49E-01	1.00E+00	2.13E-01	1.00E+00	2.04E-01	1.00E+00	3.15E-01	1.00E+00	2.96E-01	1.00E+00	1.89E-01	1.00E+00	8.73E-02	1.00E+00	2.64E-01	1.00E+00	pigmentation	P
GO:0043487	18	2.26E-02	1.00E+00	3.41E-04	4.40E-02	1.44E-02	6.53E-01	1.68E-02	6.47E-01	8.98E-02	1.00E+00	3.79E-02	1.00E+00	1.23E-01	1.00E+00	3.53E-03	1.27E-01	regulation of RNA stability	P
GO:0043488	16	1.67E-02	1.00E+00	1.75E-03	9.65E-02	9.38E-03	6.53E-01	1.72E-02	6.47E-01	6.90E-02	1.00E+00	4.99E-02	1.00E+00	1.14E-01	1.00E+00	1.94E-02	7.36E-01	regulation of mRNA stability	P
GO:0043491	12	3.21E-01	1.00E+00	2.19E-01	1.00E+00	1.86E-01	1.00E+00	1.22E-01	1.00E+00	5.77E-01	1.00E+00	1.56E-01	1.00E+00	7.22E-01	1.00E+00	4.98E-01	1.00E+00	protein kinase B signaling cascade	P
GO:0043492	139	1.72E-01	1.00E+00	2.24E-02	1.00E+00	2.29E-01	1.00E+00	1.84E-01	1.00E+00	3.62E-01	1.00E+00	9.35E-03	5.03E-01	4.32E-01	1.00E+00	1.57E-01	1.00E+00	ATPase activity, coupled to movement of su	F
GO:0043498	12	3.25E-01	1.00E+00	1.55E-01	1.00E+00	5.80E-01	1.00E+00	2.70E-01	1.00E+00	1.81E-01	1.00E+00	2.79E-01	1.00E+00	7.61E-01	1.00E+00	1.19E-01	1.00E+00	cell surface binding	F
GO:0043506	21	1.57E-01	1.00E+00	4.52E-01	1.00E+00	3.91E-01	1.00E+00	9.47E-01	1.00E+00	3.81E-01	1.00E+00	6.16E-01	1.00E+00	1.38E-02	4.78E-01	6.69E-02	1.00E+00	regulation of JNK activity	P
GO:0043507	16	3.00E-01	1.00E+00	5.71E-01	1.00E+00	6.43E-01	1.00E+00	8.48E-01	1.00E+00	4.19E-01	1.00E+00	8.74E-01	1.00E+00	4.89E-02	1.00E+00	1.48E-01	1.00E+00	positive regulation of JNK activity	P
GO:0043523	61	9.36E-03	6.08E-01	5.61E-03	3.08E-01	1.18E-01	1.00E+00	1.80E-02	9.37E-01	1.02E-02	6.92E-01	9.52E-03	5.03E-01	2.19E-02	6.36E-01	5.22E-02	1.00E+00	regulation of neuron apoptosis	P
GO:0043524	34	1.28E-01	1.00E+00	1.43E-01	1.00E+00	4.31E-01	1.00E+00	3.35E-01	1.00E+00	1.80E-01	1.00E+00	1.79E-01	1.00E+00	8.75E-02	1.00E+00	1.44E-01	1.00E+00	negative regulation of neuron apoptosis	P
GO:0043525	16	7.29E-03	3.15E-01	1.26E-03	9.65E-02	1.67E-02	1.00E+00	6.30E-04	4.20E-02	1.71E-03	1.20E-01	3.38E-03	1.51E-01	3.30E-02	8.38E-01	1.78E-01	1.00E+00	positive regulation of neuron apoptosis	P
GO:0043534	10	1.37E-01	1.00E+00	7.23E-02	1.00E+00	1.09E-01	1.00E+00	1.33E-01	1.00E+00	1.85E-01	1.00E+00	1.10E-01	1.00E+00	4.02E-01	1.00E+00	9.59E-02	1.00E+00	blood vessel endothelial cell migration	P
GO:0043542	17	1.97E-01	1.00E+00	4.41E-02	1.00E+00	1.16E-01	1.00E+00	8.57E-02	1.00E+00	1.47E-01	1.00E+00	4.50E-02	1.00E+00	8.41E-01	1.00E+00	1.55E-01	1.00E+00	endothelial cell migration	P
GO:0043543	27	3.31E-03	2.12E-01	1.08E-03	9.65E-02	3.07E-02	1.00E+00	7.24E-03	4.92E-01	5.88E-02	1.00E+00	1.23E-02	5.03E-01	1.97E-01	1.00E+00	7.88E-03	4.28E-01	protein amino acid acylation	P
GO:0043549	196	7.80E-04	8.86E-02	1.78E-06	3.92E-03	2.59E-03	1.07E-01	9.60E-05	1.30E-02	4.24E-02	1.00E+00	1.89E-04	2.33E-02	2.27E-03	8.40E-02	5.40E-05	7.00E-03	regulation of kinase activity	P
GO:0043550	10	6.03E-01	1.00E+00	1.45E-02	6.07E-01	5.17E-01	1.00E+00	7.60E-03	4.92E-01	6.20E-01	1.00E+00	6.19E-02	1.00E+00	4.87E-01	1.00E+00	2.14E-02	9.99E-01	regulation of lipid kinase activity	P
GO:0043565	621	2.69E-01	1.00E+00	9.90E-01	1.00E+00	6.36E-01	1.00E+00	9.38E-01	1.00E+00	5.26E-01	1.00E+00	9.96E-01	1.00E+00	3.30E-02	8.38E-01	9.23E-01	1.00E+00	sequence-specific DNA binding	F
GO:0043566	83	5.70E-04	8.86E-02	2.01E-03	1.30E-01	2.60E-04	4.00E-02	8.34E-03	4.92E-01	3.84E-02	1.00E+00	3.42E-02	1.00E+00	5.29E-02	1.00E+00	3.83E-02	1.00E+00	structure-specific DNA binding	F
GO:0043574	10	7.33E-02	1.00E+00	1.37E-01	1.00E+00	2.06E-01	1.00E+00	1.49E-01	1.00E+00	1.06E-01	1.00E+00	3.02E-01	1.00E+00	1.31E-01	1.00E+00	7.62E-02	1.00E+00	peroxisomal transport	P
GO:0043583	76	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.85E-01	1.00E+00	8.06E-01	1.00E+00	9.86E-01	1.00E+00	ear development	P
GO:0043588	17	2.21E-01	1.00E+00	3.56E-01	1.00E+00	7.19E-01	1.00E+00	7.42E-01	1.00E+00	2.45E-01	1.00E+00	2.88E-01	1.00E+00	3.03E-02	8.38E-01	2.85E-02	9.99E-01	skin development	P
GO:0043596	12	9.51E-04	8.86E-02	2.43E-04	2.40E-02	6.24E-04	4.90E-02	1.65E-04	1.30E-02	2.91E-03	2.13E-01	1.29E-01	1.00E+00	4.09E-02	1.00E+00	1.47E-01	1.00E+00	replication fork (sensu Eukaryota)	C
GO:0043601	10	3.12E-03	2.12E-01	4.01E-03	1.88E-01	4.16E-03	2.20E-01	3.29E-03	1.76E-01	6.70E-04	1.20E-01	1.18E-01	1.00E+00	9.51E-02	1.00E+00	2.28E-01	1.00E+00	replisome (sensu Eukaryota)	C
GO:0043616	11	7.87E-01	1.00E+00	8.16E-01	1.00E+00	9.19E-01	1.00E+00	9.95E-01	1.00E+00	4.80E-01	1.00E+00	1.00E+00	1.00E+00	7.08E-01	1.00E+00	2.33E-02	9.99E-01	keratinocyte proliferation	P
GO:0043621	11	3.46E-01	1.00E+00	5.74E-01	1.00E+00	9.12E-01	1.00E+00	5.96E-01	1.00E+00	6.34E-01	1.00E+00	3.77E-01	1.00E+00	8.70E-03	2.75E-01	5.44E-01	1.00E+00	protein self-association	F
GO:0043627	38	7.01E-01	1.00E+00	8.38E-01	1.00E+00	9.44E-01	1.00E+00	8.16E-01	1.00E+00	7.94E-01	1.00E+00	6.66E-01	1.00E+00	1.03E-01	1.00E+00	9.50E-01	1.00E+00	response to estrogen stimulus	P
GO:0043631	13	2.04E-01	1.00E+00	1.02E-01	1.00E+00	1.24E-02	6.53E-01	1.10E-01	1.00E+00	3.75E-01	1.00E+00	2.34E-01	1.00E+00	9.94E-01	1.00E+00	2.22E-01	1.00E+00	RNA polyadenylation	P
GO:0043632	162	3.22E-05	7.00E-03	6.72E-10	8.90E-04	6.13E-07	2.00E-03	2.31E-10	0.00E+00	5.45E-03	3.75E-01	3.59E-06	2.90E-03	1.69E-01	1.00E+00	3.72E-04	3.00E-02	modification-dependent macromolecule cata	P
GO:0043648	11	8.47E-01	1.00E+00	3.04E-01	1.00E+00	9.95E-01	1.00E+00	6.62E-01	1.00E+00	8.89E-01	1.00E+00	1.92E-01	1.00E+00	4.72E-01	1.00E+00	2.88E-01	1.00E+00	dicarboxylic acid metabolism	P
GO:0043681	11	4.92E-02	1.00E+00	8.69E-02	1.00E+00	1.66E-01	1.00E+00	2.72E-01	1.00E+00	7.65E-02	1.00E+00	2.99E-01	1.00E+00	1.29E-02	4.78E-01	7.91E-02	1.00E+00	protein import into mitochondrion	P
GO:0044237	8026	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.64E-28	0.00E+00	0.00E+00	0.00E+00	cellular metabolism	P
GO:0044238	8011	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.93E-25	0.00E+00	0.00E+00	0.00E+00	primary metabolism	P
GO:0044242	43	7.14E-04	8.86E-02	3.89E-03	1.88E-01	2.01E-02	1.00E+00	2.01E-02	9.37E-01	1.77E-04	4.90E-02	2.77E-03	1.44E-01	5.42E-02	1.00E+00	2.10E-01	1.00E+00	cellular lipid catabolism	P
GO:0044247	14	4.72E-01	1.00E+00	9.20E-01	1.00E+00	6.55E-01	1.00E+00	8.89E-01	1.00E+00	1.85E-01	1.00E+00	9.52E-01	1.00E+00	6.45E-01	1.00E+00	7.76E-01	1.00E+00	cellular polysaccharide catabolism	P
GO:0044248	560	6.92E-14	0.00E+00	6.06E-18	0.00E+00	4.64E-12	7.08E-04	3.82E-13	0.00E+00	7.72E-11	0.00E+00	4.11E-14	6.20E-04	2.39E-03	8.40E-02	7.04E-07	2.00E-03	cellular catabolism	P
GO:0044249	1545	7.03E-21	0.00E+00	5.77E-20	0.00E+00	9.43E-17	0.00E+00	3.57E-13	0.00E+00	2.39E-15	0.00E+00	1.02E-13	6.20E-04	2.35E-08	0.00E+00	5.81E-11	0.00E+00	cellular biosynthesis	P
GO:0044255	632	2.03E-08	2.57E-03	5.03E-13	0.00E+00	3.32E-06	2.91E-03	6.97E-08	2.89E-03	8.18E-06	2.00E-03	1.45E-07	1.65E-03	3.06E-05	4.00E-03	2.13E-10	0.00E+00	cellular lipid metabolism	P
GO:0044257	185	1.14E-05	7.00E-03	1.67E-08	9.59E-04	4.86E-07	2.00E-03	8.03E-09	8.93E-04	4.45E-03	2.13E-01	4.38E-05	9.66E-03	8.23E-02	1.00E+00	3.49E-04	3.00E-02	cellular protein catabolism	P
GO:0044260	3520	9.66E-42	0.00E+00	0.00E+00	0.00E+00	2.68E-36	0.00E+00	0.00E+00	0.00E+00	6.93E-27	0.00E+00	4.37E-35	0.00E+00	5.51E-15	0.00E+00	4.95E-32	0.00E+00	cellular macromolecule metabolism	P
GO:0044262	381	1.94E-03	2.12E-01	2.19E-05	7.00E-03	1.14E-02	6.53E-01	6.76E-03	3.33E-01	1.93E-02	7.90E-01	7.00E-07	2.00E-03	4.23E-02	1.00E+00	1.89E-02	7.36E-01	cellular carbohydrate metabolism	P
GO:0044264	75	5.26E-01	1.00E+00	2.00E-01	1.00E+00	7.50E-01	1.00E+00	3.58E-01	1.00E+00	2.64E-01	1.00E+00	3.03E-01	1.00E+00	7.02E-01	1.00E+00	5.37E-02	1.00E+00	cellular polysaccharide metabolism	P
GO:0044265	319	8.95E-10	2.57E-03	5.76E-12	0.00E+00	7.40E-11	7.08E-04	7.26E-09	8.93E-04	3.45E-06	1.69E-03	6.59E-10	6.20E-04	1.44E-02	4.78E-01	5.37E-05	7.00E-03	cellular macromolecule catabolism	P
GO:0044267	3467	2.88E-42	0.00E+00	0.00E+00	0.00E+00	5.84E-37	0.00E+00	0.00E+00	0.00E+00	1.73E-26	0.00E+00	2.14E-35	0.00E+00	1.19E-15	0.00E+00	6.85E-32	0.00E+00	cellular protein metabolism	P
GO:0044270	66	2.15E-01	1.00E+00	7.35E-03	3.12E-01	4.47E-01	1.00E+00	3.47E-02	1.00E+00	1.59E-01	1.00E+00	3.46E-02	1.00E+00	3.51E-01	1.00E+00	3.94E-02	1.00E+00	nitrogen compound catabolism	P
GO:0044271	126	3.49E-02	1.00E+00	8.62E-03	4.69E-01	1.37E-01	1.00E+00	1.28E-01	1.00E+00	1.79E-01	1.00E+00	4.17E-03	2.66E-01	8.26E-03	2.75E-01	4.52E-02	1.00E+00	nitrogen compound biosynthesis	P
GO:0044272	39	1.20E-01	1.00E+00	9.24E-02	1.00E+00	4.03E-01	1.00E+00	2.00E-02	9.37E-01	2.96E-01	1.00E+00	1.61E-01	1.00E+00	3.48E-02	8.38E-01	6.94E-01	1.00E+00	sulfur compound biosynthesis	P
GO:0044275	99	2.41E-03	2.12E-01	2.27E-03	1.71E-01	1.12E-03	7.90E-02	1.95E-01	1.00E+00	4.15E-03	2.13E-01	3.37E-05	9.52E-03	2.47E-01	1.00E+00	9.56E-02	1.00E+00	cellular carbohydrate catabolism	P
GO:0044403	48	5.31E-01	1.00E+00	3.81E-01	1.00E+00	3.61E-01	1.00E+00	2.68E-01	1.00E+00	9.32E-01	1.00E+00	9.31E-01	1.00E+00	3.18E-01	1.00E+00	1.80E-01	1.00E+00	symbiosis, encompassing mutualism throug	P
GO:0044419	59	2.27E-01	1.00E+00	2.54E-01	1.00E+00	1.35E-01	1.00E+00	2.22E-01	1.00E+00	6.85E-01	1.00E+00	7.69E-01	1.00E+00	1.43E-01	1.00E+00	1.49E-01	1.00E+00	interspecies interaction between organisms	P
GO:0044420	97	9.39E-01	1.00E+00	7.24E-01	1.00E+00	9.97E-01	1.00E+00	8.66E-01	1.00E+00	9.22E-01	1.00E+00	7.91E-01	1.00E+00	4.31E-01	1.00E+00	1.60E-01	1.00E+00	extracellular matrix part	C
GO:0044421	1985	2.58E-01	1.00E+00	3.84E-01	1.00E+00	9.23E-01	1.00E+00	9.48E-01	1.00E+00	5.60E-01	1.00E+00	7.16E-01	1.00E+00	2.12E-04	1.20E-02	5.35E-04	3.00E-02	extracellular region part	C

GO:0044422	3604	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.42E-30	0.00E+00	7.07E-29	0.00E+00	organelle part	C
GO:0044423	18	2.90E-01	1.00E+00	9.58E-02	1.00E+00	2.03E-01	1.00E+00	5.07E-02	1.00E+00	3.48E-01	1.00E+00	9.68E-02	1.00E+00	3.01E-01	1.00E+00	6.22E-01	1.00E+00	virion part	C
GO:0044424	9928	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	intracellular part	C
GO:0044425	6939	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.58E-01	1.00E+00	membrane part	C
GO:0044427	445	2.95E-08	2.57E-03	4.78E-08	9.59E-04	2.46E-10	7.95E-04	1.18E-12	0.00E+00	1.96E-04	4.90E-02	1.19E-03	9.00E-02	3.34E-03	2.23E-01	6.31E-03	4.28E-01	chromosomal part	C
GO:0044428	1060	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.54E-34	0.00E+00	9.94E-33	0.00E+00	1.28E-15	0.00E+00	1.29E-15	0.00E+00	nuclear part	C
GO:0044429	544	5.78E-18	0.00E+00	3.47E-15	0.00E+00	1.66E-12	7.08E-04	9.82E-12	0.00E+00	1.06E-13	0.00E+00	1.55E-12	6.20E-04	1.19E-07	0.00E+00	1.12E-04	1.60E-02	mitochondrial part	C
GO:0044430	732	4.12E-06	3.02E-03	7.00E-06	4.51E-03	5.90E-04	4.90E-02	2.76E-04	4.20E-02	4.63E-04	4.90E-02	1.35E-03	9.00E-02	5.00E-05	8.00E-03	7.31E-05	7.00E-03	cytoskeletal part	C
GO:0044431	379	4.59E-09	2.57E-03	3.51E-11	0.00E+00	8.05E-06	2.91E-03	6.89E-08	2.89E-03	1.18E-06	1.69E-03	2.05E-06	2.00E-03	1.24E-04	8.00E-03	1.49E-06	2.00E-03	Golgi apparatus part	C
GO:0044432	536	2.95E-07	2.57E-03	1.02E-07	3.92E-03	2.76E-04	4.00E-02	7.17E-06	2.89E-03	7.88E-06	2.00E-03	1.17E-06	2.00E-03	1.13E-04	8.00E-03	1.69E-03	7.90E-02	endoplasmic reticulum part	C
GO:0044433	108	1.07E-03	8.86E-02	8.26E-05	1.50E-02	3.83E-03	2.20E-01	4.69E-04	4.20E-02	1.97E-02	7.90E-01	7.39E-04	4.48E-02	1.34E-02	4.78E-01	1.11E-02	4.76E-01	cytoplasmic vesicle part	C
GO:0044437	70	7.09E-04	8.86E-02	3.59E-05	7.00E-03	3.97E-02	1.00E+00	6.08E-03	2.88E-01	1.46E-02	6.92E-01	1.27E-03	9.00E-02	1.32E-02	4.78E-01	6.35E-03	4.28E-01	vacuolar part	C
GO:0044438	43	1.71E-03	2.12E-01	1.60E-02	7.63E-01	5.31E-02	1.00E+00	2.67E-02	1.00E+00	1.52E-02	6.92E-01	1.02E-01	1.00E+00	3.77E-03	2.23E-01	2.30E-02	9.99E-01	microbody part	C
GO:0044439	43	1.71E-03	2.12E-01	1.60E-02	7.63E-01	5.31E-02	1.00E+00	2.67E-02	1.00E+00	1.52E-02	6.92E-01	1.02E-01	1.00E+00	3.77E-03	2.23E-01	2.30E-02	9.99E-01	peroxisomal part	C
GO:0044440	93	5.75E-05	1.20E-02	1.81E-07	3.92E-03	1.34E-02	6.53E-01	1.57E-04	1.30E-02	1.79E-03	1.20E-01	6.35E-05	9.66E-03	1.43E-03	6.14E-02	1.08E-03	6.00E-02	endosomal part	C
GO:0044441	12	1.26E-01	1.00E+00	2.12E-01	1.00E+00	2.58E-01	1.00E+00	4.02E-01	1.00E+00	3.56E-01	1.00E+00	1.10E-01	1.00E+00	1.06E-01	1.00E+00	7.52E-01	1.00E+00	cilium part	C
GO:0044444	3965	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.23E-30	0.00E+00	1.14E-28	0.00E+00	cytoplasmic part	C
GO:0044445	71	1.48E-01	1.00E+00	1.86E-04	1.80E-02	4.58E-02	1.00E+00	4.37E-04	4.20E-02	3.90E-01	1.00E+00	3.62E-04	2.33E-02	5.11E-01	1.00E+00	1.40E-01	1.00E+00	cytosolic part	C
GO:0044446	3604	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.42E-30	0.00E+00	7.07E-29	0.00E+00	intracellular organelle part	C
GO:0044448	59	5.09E-03	2.72E-01	6.27E-08	3.92E-03	4.61E-03	3.08E-01	8.00E-06	2.89E-03	8.70E-02	1.00E+00	8.61E-04	4.48E-02	9.73E-02	1.00E+00	5.79E-04	3.00E-02	cell cortex part	C
GO:0044449	78	3.37E-01	1.00E+00	4.98E-02	1.00E+00	6.20E-01	1.00E+00	1.42E-01	1.00E+00	2.18E-01	1.00E+00	2.28E-01	1.00E+00	6.66E-01	1.00E+00	1.71E-02	6.56E-01	contractile fiber part	C
GO:0044450	25	6.16E-03	3.09E-01	1.27E-02	6.07E-01	9.30E-03	6.53E-01	3.39E-02	1.00E+00	4.15E-03	2.13E-01	3.15E-02	1.00E+00	1.01E-01	1.00E+00	4.68E-02	1.00E+00	microtubule organizing center part	C
GO:0044451	485	3.92E-21	0.00E+00	1.30E-22	0.00E+00	7.17E-18	0.00E+00	1.56E-20	0.00E+00	2.21E-13	0.00E+00	9.81E-14	6.20E-04	6.43E-08	0.00E+00	1.82E-08	0.00E+00	nucleoplasm part	C
GO:0044452	40	1.61E-04	1.72E-02	3.92E-02	1.00E+00	2.72E-04	4.00E-02	3.80E-02	1.00E+00	3.86E-04	4.90E-02	2.77E-01	1.00E+00	3.71E-02	8.38E-01	4.51E-02	1.00E+00	nucleolar part	C
GO:0044453	91	1.97E-08	2.57E-03	7.92E-13	0.00E+00	3.24E-08	9.80E-04	4.86E-12	0.00E+00	2.47E-05	6.00E-03	2.17E-06	2.00E-03	8.69E-03	2.75E-01	1.08E-04	1.60E-02	nuclear membrane part	C
GO:0044454	92	1.67E-08	2.57E-03	1.02E-06	3.92E-03	4.43E-08	9.80E-04	1.07E-06	2.89E-03	2.91E-05	6.33E-03	1.00E-04	1.10E-02	9.09E-04	3.44E-02	4.01E-02	1.00E+00	nuclear chromosome part	C
GO:0044455	98	2.43E-05	7.00E-03	2.58E-05	7.00E-03	2.94E-03	1.35E-01	9.83E-05	1.30E-02	4.15E-04	4.90E-02	1.28E-04	1.30E-02	3.55E-04	2.29E-02	1.91E-02	7.36E-01	mitochondrial membrane part	C
GO:0044456	146	9.99E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.92E-01	1.00E+00	9.45E-01	1.00E+00	9.10E-01	1.00E+00	8.02E-02	1.00E+00	synapse part	C
GO:0044459	1391	2.90E-01	1.00E+00	4.80E-05	7.00E-03	8.05E-01	1.00E+00	1.23E-01	1.00E+00	7.54E-01	1.00E+00	2.07E-03	1.27E-01	2.24E-03	8.40E-02	1.75E-09	0.00E+00	plasma membrane part	C
GO:0044460	13	4.74E-01	1.00E+00	7.18E-01	1.00E+00	3.68E-01	1.00E+00	7.31E-01	1.00E+00	6.14E-01	1.00E+00	6.57E-01	1.00E+00	3.11E-01	1.00E+00	4.77E-01	1.00E+00	flagellar part	C
GO:0044462	24	9.68E-01	1.00E+00	9.88E-01	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	8.44E-01	1.00E+00	9.99E-01	1.00E+00	8.42E-01	1.00E+00	4.08E-01	1.00E+00	external encapsulating structure part	C
GO:0044463	97	5.07E-01	1.00E+00	7.69E-02	1.00E+00	6.89E-01	1.00E+00	3.16E-01	1.00E+00	5.68E-01	1.00E+00	6.90E-02	1.00E+00	2.09E-01	1.00E+00	7.74E-02	1.00E+00	cell projection part	C
GO:0044464	15412	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.20E-45	0.00E+00	0.00E+00	0.00E+00	1.04E-09	0.00E+00	8.07E-43	0.00E+00	cell part	C
GO:0045005	15	3.11E-01	1.00E+00	4.30E-02	1.00E+00	2.03E-01	1.00E+00	2.67E-01	1.00E+00	6.19E-01	1.00E+00	2.34E-02	1.00E+00	5.62E-01	1.00E+00	2.60E-02	9.99E-01	maintenance of fidelity during DNA-dependi	P
GO:0045017	11	3.62E-01	1.00E+00	4.73E-01	1.00E+00	2.64E-01	1.00E+00	2.40E-01	1.00E+00	4.44E-01	1.00E+00	6.35E-01	1.00E+00	3.06E-01	1.00E+00	4.55E-01	1.00E+00	glycerolipid biosynthesis	P
GO:0045028	138	9.70E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.09E-01	1.00E+00	9.66E-01	1.00E+00	4.18E-01	1.00E+00	4.72E-01	1.00E+00	purinergic nucleotide receptor activity, G-pr	F
GO:0045045	226	2.61E-03	2.12E-01	1.54E-03	9.65E-02	5.87E-02	1.00E+00	2.07E-02	9.37E-01	2.33E-02	1.00E+00	1.08E-02	5.03E-01	7.92E-03	2.75E-01	2.68E-03	8.32E-02	secretory pathway	P
GO:0045047	22	7.71E-03	6.08E-01	4.53E-02	1.00E+00	8.35E-02	1.00E+00	3.25E-02	1.00E+00	7.25E-03	6.92E-01	1.13E-01	1.00E+00	7.15E-02	1.00E+00	3.48E-01	1.00E+00	protein targeting to ER	P
GO:0045055	83	9.81E-01	1.00E+00	7.73E-01	1.00E+00	9.87E-01	1.00E+00	9.58E-01	1.00E+00	9.76E-01	1.00E+00	4.92E-01	1.00E+00	8.14E-01	1.00E+00	4.66E-01	1.00E+00	regulated secretory pathway	P
GO:0045058	19	4.16E-01	1.00E+00	1.34E-01	1.00E+00	5.15E-01	1.00E+00	5.82E-01	1.00E+00	5.22E-01	1.00E+00	5.12E-02	1.00E+00	1.09E-01	1.00E+00	2.31E-01	1.00E+00	T cell selection	P
GO:0045061	15	4.15E-01	1.00E+00	1.07E-01	1.00E+00	4.82E-01	1.00E+00	3.09E-01	1.00E+00	3.32E-01	1.00E+00	8.48E-02	1.00E+00	2.70E-01	1.00E+00	2.41E-01	1.00E+00	thymic T cell selection	P
GO:0045072	12	2.07E-01	1.00E+00	4.83E-01	1.00E+00	5.28E-01	1.00E+00	6.70E-01	1.00E+00	6.94E-01	1.00E+00	5.89E-01	1.00E+00	2.77E-02	8.38E-01	2.60E-01	1.00E+00	regulation of interferon-gamma biosynthesis	P
GO:0045076	15	1.00E+00	1.00E+00	8.27E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	6.57E-01	1.00E+00	1.54E-01	1.00E+00	regulation of interleukin-2 biosynthesis	P
GO:0045078	10	9.94E-02	1.00E+00	3.86E-01	1.00E+00	3.06E-01	1.00E+00	4.81E-01	1.00E+00	3.90E-01	1.00E+00	5.00E-01	1.00E+00	3.02E-02	8.38E-01	2.68E-01	1.00E+00	positive regulation of interferon-gamma bios	P
GO:0045087	108	5.81E-01	1.00E+00	9.35E-01	1.00E+00	7.20E-01	1.00E+00	7.49E-01	1.00E+00	9.16E-01	1.00E+00	9.90E-01	1.00E+00	1.18E-01	1.00E+00	6.63E-01	1.00E+00	innate immune response	P
GO:0045088	12	7.08E-01	1.00E+00	7.70E-01	1.00E+00	9.46E-01	1.00E+00	9.83E-01	1.00E+00	7.99E-01	1.00E+00	9.97E-01	1.00E+00	4.23E-01	1.00E+00	1.84E-01	1.00E+00	regulation of innate immune response	P
GO:0045089	11	8.96E-01	1.00E+00	8.50E-01	1.00E+00	9.98E-01	1.00E+00	9.85E-01	1.00E+00	8.80E-01	1.00E+00	9.97E-01	1.00E+00	7.00E-01	1.00E+00	3.20E-01	1.00E+00	positive regulation of innate immune respor	P
GO:0045095	56	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.99E-01	1.00E+00	keratin filament	C
GO:0045103	19	3.51E-01	1.00E+00	4.97E-01	1.00E+00	2.29E-01	1.00E+00	3.38E-01	1.00E+00	4.57E-01	1.00E+00	5.25E-01	1.00E+00	6.36E-01	1.00E+00	5.78E-01	1.00E+00	intermediate filament-based process	P
GO:0045104	16	4.65E-01	1.00E+00	6.92E-01	1.00E+00	3.28E-01	1.00E+00	6.67E-01	1.00E+00	6.60E-01	1.00E+00	5.51E-01	1.00E+00	5.61E-01	1.00E+00	8.10E-01	1.00E+00	intermediate filament cytoskeleton organiza	P
GO:0045109	12	6.02E-01	1.00E+00	7.92E-01	1.00E+00	5.37E-01	1.00E+00	6.34E-01	1.00E+00	8.21E-01	1.00E+00	7.46E-01	1.00E+00	5.64E-01	1.00E+00	8.86E-01	1.00E+00	intermediate filament organization	P
GO:0045111	165	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	intermediate filament cytoskeleton	C
GO:0045120	17	4.19E-05	9.52E-03	1.15E-07	3.92E-03	1.24E-05	3.00E-03	1.76E-07	2.89E-03	1.40E-03	1.20E-01	1.20E-04	1.30E-02	2.35E-02	8.38E-01	4.48E-02	1.00E+00	pronucleus	C
GO:0045121	60	4.62E-01	1.00E+00	2.12E-02	1.00E+00	7.90E-01	1.00E+00	7.72E-02	1.00E+00	2.34E-01	1.00E+00	4.27E-02	1.00E+00	3.21E-01	1.00E+00	1.55E-02	6.56E-01	lipid raft	C
GO:0045125	28	2.59E-01	1.00E+00	2.71E-01	1.00E+00	2.25E-01	1.00E+00	2.18E-01	1.00E+00	6.26E-01	1.00E+00	8.35E-01	1.00E+00	9.48E-02	1.00E+00	7.07E-02	1.00E+00	bioactive lipid receptor activity	F
GO:0045132	10	8.87E-02	1.00E+00	2.70E-01	1.00E+00	1.93E-02	1.00E+00	3.71E-01	1.00E+00	5.53E-01	1.00E+00	2.49E-01	1.00E+00	2.11E-01	1.00E+00	1.10E-01	1.00E+00	meiotic chromosome segregation	P
GO:0045137	69	7.52E-02	1.00E+00	6.79E-01	1.00E+00	6.92E-02	1.00E+00	8.04E-01	1.00E+00	1.79E-01	1.00E+00	3.94E-01	1.00E+00	1.74E-01	1.00E+00	7.83E-01	1.00E+00	development of primary sexual characteristi	P
GO:0045165	133	8.85E-01	1.00E+00	9.92E-01	1.00E+00	7.80E-01	1.00E+00	9.87E-01	1.00E+00	9.25E-01	1.00E+00	9.61E-01	1.00E+00	5.65E-01	1.00E+00	9.64E-01	1.00E+00	cell fate commitment	P
GO:0045168	15	8.05E-01	1.00E+00	8.91E-01	1.00E+00	9.22E-01	1.00E+00	5.97E-01	1.00E+00	6.10E-01	1.00E+00	9.82E-01	1.00E+00	7.18E-01	1.00E+00	8.57E-01	1.00E+00	cell-cell signaling during cell fate commitme	P
GO:0045177	134	7.70E-01	1.00E+00	1.11E-01	1.00E+00	8.78E-01	1.00E+00	2.59E-01	1.00E+00	9.36E-01	1.00E+00	6.67E-01	1.00E+00	1.61E-01	1.00E+00	1.29E-02	4.76E-01	apical part of cell	C
GO:0045178	31	8.06E-01	1.00E+00	6.52E-01	1.00E+00	3.91E-01	1.00E+00	5.15E-01	1.00E+00	9.76E-01	1.00E+00	4.45E-01	1.00E+00	3.75E-01	1.00E+00	9.58E-01	1.00E+00	basal part of cell	C
GO:0045182	146	1.30E-07	2.57E-03	2.12E-12	0.00E+00	5.80E-11	7.08E-04	4.73E-09	8.93E-04	3.05E-05	6.33E-03	1.80E-10	6.20E-04	4.48E-02	1.00E+00	1.70E-04	1.60E-02	translation regulator activity	F
GO:0045184	888	3.82E-25	0.00E+00	3.46E-37	0.00E+00	6.87E-19	0.00E+00	1.85E-29	0.00E+00	8.00E-22	0.00E+00	3.22E-25	0.00E+00	1.30E-07	0.00E+00	2.45E-13	0.00E+00	establishment of protein localization	P
GO:0045185	20	1.24E-01	1.00E+00	3.63E-01	1.00E+00	1.36E-01	1.00E+00	4.90E-01	1.00E+00	1.92E-01	1.00E+00	1.96E-01	1.00E+00	2.31E-01	1.00E+00	4.87E-01	1.00E+00	maintenance of protein localization	P
GO:0045190	25	2.54E-01	1.00E+00	6.07E-03	3.08E-01	4.19E-01	1.00E+00	2.87E-03	1.61E-01	2.75E-01	1.00E+00	4.16E-01	1.00E+00	2.69E-01	1.00E+00	4.13E-02	1.00E+00	isotype switching	P
GO:0045191	13	2.65E-01	1.00E+00	1.51E-01	1.00E+00	3.46E-01	1.00E+00	1.63E-01	1.00E+00	3.07E-01	1.00E+00	8.44E-01	1.00E+00	2.91E-01	1.00E+00	6.79E-02	1.00E+00	regulation of isotype switching	P
GO:0045202	274	9.65E-01	1.00E+00	2.16E-01	1.00E+00	9.97E-01	1.00E+00	8.78E-01	1.00E+00	8.95E-01	1.00E+00	3.54E-01	1.00E+00	6.20E-01	1.00E+00	1.37E-03	6.00E-02	synapse	C
GO:0045211	129	9.99E-01	1.00E+00	8.89E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.87E-01	1.00E+00	9.48E-01	1.00E+00	9.63E-01	1.00E+00	1.09E-01	1.00E+00	postsynaptic membrane	C
GO:0045214	12	3.13E-01	1.00E+00	3.15E-01	1.00E+00	4.40E-01	1.00E+00	3.13E-01	1.00E+00	6.47E-01	1.00E+00	3.02E-01	1.00E+00	1.59E-01	1.00E+00	4.17E-01	1.00E+00	sarcomere organization	P
GO:0045216	12	4.99E-05	9.52E-03	2.36E-03	1.71E-01	9.26E-04	4.90E-02	1.02E-04	1.30E-02	6.63E-03	6.92E-01	1.60E-02	6.68E-01	2.45E-02	8.38E-01	1.72E-01	1.00E+00	intercellular junction assembly and mainten	P
GO:0045259	18	1.34E-02	6.08E-01	5.68E-02	1.00E+00	2.88E-02	1.00E+00	8.45E-02	1.00E+00	4.58E-02	1.00E+00	1.15E-01	1.00E+00	4.24E-02	1.00E+00	7.39E-02	1.00E+00	proton-transporting ATP synthase complex	C
GO:0045263	12	8.85E-02	1.00E+00	1.92E-01	1.00E+00	1.04E-01	1.00E+00	1.65E-01	1.00E+00	1.77E-01	1.00E+00	2.31E-01	1.00E+00	8.14E-02	1.00E+00	3.00E-01	1.00E+00	proton-transporting ATP synthase complex,	C
GO:0045271	15	2.39E-02	1.00E+00	3.52E-02	1.00E+00	4.42E-02	1.00E+00	1.49E-01	1.00E+00	2.25E-01	1.00E+00	1.09E-01	1.00E+00	5.82E-02	1.00E+00	6.71E-02	1.00E+00	respiratory chain complex I	C
GO:0045296	12	6.91E-01	1.00E+00	2.34E-01	1.00E+00	8.33E-01	1.00E+00	4.66E-01	1.00E+00	5.92E-01	1.00E+00	8.37E-02	1.00E+00	7.38E-01	1.00E+00	7.03E-01	1.00E+00	cadherin binding	F
GO:0045309	10	5.68E-02	1.00E+00	3.02E-01	1.00E+00	4.59E-02	1.00E+00	1.02E-01	1.00E+00	6.25E-02	1.00E+00	5.01E-01	1.00E+00	1.73E-01	1.00E+00	4.43E-01	1.00E+00	protein phosphorylated amino acid binding	F

GO:0045321	267	4.76E-02	1.00E+00	2.05E-04	2.40E-02	2.83E-01	1.00E+00	3.31E-03	1.76E-01	5.27E-01	1.00E+00	7.59E-02	1.00E+00	6.74E-04	3.44E-02	3.56E-05	7.00E-03	leukocyte activation	P
GO:0045333	36	5.37E-03	3.09E-01	2.60E-02	1.00E+00	6.20E-02	1.00E+00	5.53E-02	1.00E+00	2.28E-02	1.00E+00	6.62E-02	1.00E+00	7.87E-02	1.00E+00	5.18E-02	1.00E+00	cellular respiration	P
GO:0045351	10	4.95E-03	2.72E-01	3.55E-02	1.00E+00	2.01E-01	1.00E+00	2.00E-01	1.00E+00	6.92E-02	1.00E+00	4.90E-02	1.00E+00	1.63E-02	4.88E-01	1.11E-01	1.00E+00	interferon type I biosynthesis	P
GO:0045408	14	9.44E-01	1.00E+00	8.08E-01	1.00E+00	9.17E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	8.52E-01	1.00E+00	5.63E-01	1.00E+00	1.52E-01	1.00E+00	regulation of interleukin-6 biosynthesis	P
GO:0045426	10	1.02E-02	6.08E-01	1.45E-01	1.00E+00	1.36E-02	6.53E-01	1.48E-01	1.00E+00	3.23E-02	1.00E+00	2.41E-01	1.00E+00	8.06E-02	1.00E+00	3.17E-01	1.00E+00	quinone cofactor biosynthesis	P
GO:0045428	13	3.95E-01	1.00E+00	6.77E-03	3.12E-01	6.55E-01	1.00E+00	1.84E-01	1.00E+00	4.28E-01	1.00E+00	7.30E-03	4.21E-01	2.12E-01	1.00E+00	8.41E-02	1.00E+00	regulation of nitric oxide biosynthesis	P
GO:0045429	10	6.27E-01	1.00E+00	2.08E-02	1.00E+00	8.22E-01	1.00E+00	2.12E-01	1.00E+00	6.18E-01	1.00E+00	2.95E-02	1.00E+00	3.53E-01	1.00E+00	8.25E-02	1.00E+00	positive regulation of nitric oxide biosynthes	P
GO:0045444	36	1.73E-02	1.00E+00	9.15E-03	4.69E-01	1.82E-01	1.00E+00	2.18E-01	1.00E+00	2.04E-02	7.90E-01	1.68E-02	6.68E-01	5.12E-02	1.00E+00	1.09E-02	4.76E-01	fat cell differentiation	P
GO:0045445	45	7.07E-01	1.00E+00	5.33E-01	1.00E+00	8.42E-01	1.00E+00	4.83E-01	1.00E+00	9.39E-01	1.00E+00	5.54E-01	1.00E+00	2.55E-01	1.00E+00	7.51E-01	1.00E+00	myoblast differentiation	P
GO:0045446	11	4.64E-02	1.00E+00	2.23E-01	1.00E+00	9.74E-02	1.00E+00	1.56E-01	1.00E+00	8.28E-02	1.00E+00	1.85E-01	1.00E+00	1.05E-01	1.00E+00	4.67E-01	1.00E+00	endothelial cell differentiation	P
GO:0045449	2504	3.49E-24	0.00E+00	1.48E-32	0.00E+00	5.93E-25	0.00E+00	2.15E-33	0.00E+00	2.96E-17	0.00E+00	3.72E-23	0.00E+00	1.36E-05	3.63E-03	8.67E-09	0.00E+00	regulation of transcription	P
GO:0045453	19	5.23E-01	1.00E+00	5.86E-01	1.00E+00	7.11E-01	1.00E+00	9.00E-01	1.00E+00	6.34E-01	1.00E+00	5.74E-01	1.00E+00	2.74E-01	1.00E+00	7.66E-02	1.00E+00	bone resorption	P
GO:0045454	57	2.31E-02	1.00E+00	3.06E-03	1.88E-01	3.55E-03	2.03E-01	2.68E-03	1.61E-01	1.56E-01	1.00E+00	8.97E-03	5.03E-01	2.60E-01	1.00E+00	1.23E-01	1.00E+00	cell redox homeostasis	P
GO:0045471	20	4.55E-01	1.00E+00	5.98E-01	1.00E+00	9.57E-01	1.00E+00	5.78E-01	1.00E+00	3.65E-01	1.00E+00	5.77E-01	1.00E+00	1.89E-01	1.00E+00	5.15E-01	1.00E+00	response to ethanol	P
GO:0045494	13	8.63E-01	1.00E+00	9.15E-01	1.00E+00	8.04E-01	1.00E+00	9.31E-01	1.00E+00	9.15E-01	1.00E+00	8.15E-01	1.00E+00	6.43E-01	1.00E+00	7.94E-01	1.00E+00	photoreceptor maintenance	P
GO:0045576	13	4.83E-01	1.00E+00	6.09E-01	1.00E+00	5.83E-01	1.00E+00	5.44E-01	1.00E+00	5.45E-01	1.00E+00	6.38E-01	1.00E+00	2.90E-01	1.00E+00	6.30E-01	1.00E+00	mast cell activation	P
GO:0045577	13	2.43E-01	1.00E+00	7.25E-02	1.00E+00	6.42E-01	1.00E+00	1.22E-01	1.00E+00	6.18E-01	1.00E+00	6.05E-01	1.00E+00	1.98E-02	6.36E-01	3.40E-02	1.00E+00	regulation of B cell differentiation	P
GO:0045580	21	2.87E-01	1.00E+00	2.28E-02	1.00E+00	3.73E-01	1.00E+00	2.93E-01	1.00E+00	3.67E-01	1.00E+00	6.41E-02	1.00E+00	2.21E-01	1.00E+00	3.47E-02	1.00E+00	regulation of T cell differentiation	P
GO:0045582	16	1.02E-01	1.00E+00	2.57E-02	1.00E+00	2.03E-01	1.00E+00	2.57E-01	1.00E+00	1.56E-01	1.00E+00	1.09E-02	5.03E-01	1.38E-01	1.00E+00	7.95E-02	1.00E+00	positive regulation of T cell differentiation	P
GO:0045595	216	3.82E-01	1.00E+00	6.66E-01	1.00E+00	2.85E-01	1.00E+00	7.53E-01	1.00E+00	8.41E-01	1.00E+00	8.41E-01	1.00E+00	8.12E-02	1.00E+00	2.22E-01	1.00E+00	regulation of cell differentiation	P
GO:0045596	116	5.62E-01	1.00E+00	9.43E-01	1.00E+00	4.84E-01	1.00E+00	6.53E-01	1.00E+00	7.71E-01	1.00E+00	1.00E+00	1.00E+00	2.28E-01	1.00E+00	6.40E-01	1.00E+00	negative regulation of cell differentiation	P
GO:0045597	87	7.32E-01	1.00E+00	8.87E-01	1.00E+00	6.08E-01	1.00E+00	9.75E-01	1.00E+00	9.34E-01	1.00E+00	6.06E-01	1.00E+00	1.97E-01	1.00E+00	6.82E-01	1.00E+00	positive regulation of cell differentiation	P
GO:0045619	30	2.93E-01	1.00E+00	1.56E-02	7.63E-01	3.56E-01	1.00E+00	1.09E-01	1.00E+00	6.50E-01	1.00E+00	1.43E-01	1.00E+00	1.33E-01	1.00E+00	1.72E-02	6.56E-01	regulation of lymphocyte differentiation	P
GO:0045621	20	7.04E-02	1.00E+00	5.59E-02	1.00E+00	1.46E-01	1.00E+00	2.85E-01	1.00E+00	2.73E-01	1.00E+00	6.02E-02	1.00E+00	8.30E-02	1.00E+00	1.24E-01	1.00E+00	positive regulation of lymphocyte differentia	P
GO:0045637	52	2.37E-01	1.00E+00	8.51E-01	1.00E+00	1.69E-01	1.00E+00	6.68E-01	1.00E+00	8.40E-01	1.00E+00	8.84E-01	1.00E+00	2.08E-02	6.36E-01	8.84E-01	1.00E+00	regulation of myeloid cell differentiation	P
GO:0045638	24	2.26E-01	1.00E+00	7.13E-01	1.00E+00	9.82E-02	1.00E+00	4.57E-01	1.00E+00	6.65E-01	1.00E+00	8.68E-01	1.00E+00	1.30E-01	1.00E+00	7.25E-01	1.00E+00	negative regulation of myeloid cell differenti	P
GO:0045639	22	6.07E-01	1.00E+00	9.82E-01	1.00E+00	6.78E-01	1.00E+00	9.61E-01	1.00E+00	8.68E-01	1.00E+00	9.35E-01	1.00E+00	2.29E-01	1.00E+00	9.86E-01	1.00E+00	positive regulation of myeloid cell differentia	P
GO:0045646	15	5.71E-01	1.00E+00	9.40E-01	1.00E+00	5.47E-01	1.00E+00	8.61E-01	1.00E+00	9.96E-01	1.00E+00	9.80E-01	1.00E+00	6.19E-02	1.00E+00	4.70E-01	1.00E+00	regulation of erythrocyte differentiation	P
GO:0045661	11	6.81E-01	1.00E+00	9.51E-01	1.00E+00	7.06E-01	1.00E+00	9.03E-01	1.00E+00	9.49E-01	1.00E+00	9.95E-01	1.00E+00	3.05E-01	1.00E+00	7.34E-01	1.00E+00	regulation of myoblast differentiation	P
GO:0045664	43	9.47E-01	1.00E+00	7.57E-01	1.00E+00	9.83E-01	1.00E+00	6.87E-01	1.00E+00	9.82E-01	1.00E+00	9.37E-01	1.00E+00	3.67E-01	1.00E+00	3.43E-01	1.00E+00	regulation of neuron differentiation	P
GO:0045665	29	8.99E-01	1.00E+00	8.27E-01	1.00E+00	9.12E-01	1.00E+00	5.21E-01	1.00E+00	8.57E-01	1.00E+00	9.77E-01	1.00E+00	4.31E-01	1.00E+00	6.35E-01	1.00E+00	negative regulation of neuron differentiation	P
GO:0045666	12	9.08E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	7.82E-01	1.00E+00	9.99E-01	1.00E+00	5.50E-01	1.00E+00	5.19E-01	1.00E+00	positive regulation of neuron differentiation	P
GO:0045667	29	8.17E-01	1.00E+00	2.85E-01	1.00E+00	4.73E-01	1.00E+00	7.84E-01	1.00E+00	9.67E-01	1.00E+00	3.69E-01	1.00E+00	4.41E-01	1.00E+00	3.93E-02	1.00E+00	regulation of osteoblast differentiation	P
GO:0045669	21	6.53E-01	1.00E+00	2.90E-01	1.00E+00	3.97E-01	1.00E+00	7.34E-01	1.00E+00	8.68E-01	1.00E+00	2.68E-01	1.00E+00	3.41E-01	1.00E+00	6.11E-02	1.00E+00	positive regulation of osteoblast differentiati	P
GO:0045670	16	4.90E-01	1.00E+00	5.87E-01	1.00E+00	2.34E-01	1.00E+00	6.06E-01	1.00E+00	8.06E-01	1.00E+00	4.44E-01	1.00E+00	5.97E-01	1.00E+00	8.58E-01	1.00E+00	regulation of osteoclast differentiation	P
GO:0045685	12	9.22E-01	1.00E+00	9.62E-01	1.00E+00	9.43E-01	1.00E+00	9.54E-01	1.00E+00	6.48E-01	1.00E+00	8.82E-01	1.00E+00	9.37E-01	1.00E+00	9.40E-01	1.00E+00	regulation of glial cell differentiation	P
GO:0045727	56	5.54E-01	1.00E+00	1.36E-01	1.00E+00	9.15E-01	1.00E+00	4.72E-01	1.00E+00	8.66E-01	1.00E+00	7.41E-01	1.00E+00	3.35E-02	8.38E-01	2.02E-03	7.90E-02	positive regulation of protein biosynthesis	P
GO:0045735	77	5.44E-01	1.00E+00	1.60E-01	1.00E+00	4.66E-01	1.00E+00	8.00E-02	1.00E+00	7.30E-01	1.00E+00	3.69E-01	1.00E+00	4.62E-01	1.00E+00	2.35E-01	1.00E+00	nutrient reservoir activity	F
GO:0045736	11	1.26E-02	6.08E-01	2.47E-07	3.92E-03	1.93E-03	9.50E-02	2.47E-05	9.57E-03	2.83E-02	1.00E+00	1.03E-05	5.87E-03	2.94E-01	1.00E+00	5.19E-05	7.00E-03	negative regulation of cyclin-dependent pro	P
GO:0045740	10	1.46E-01	1.00E+00	2.12E-01	1.00E+00	5.41E-01	1.00E+00	7.76E-01	1.00E+00	1.41E-01	1.00E+00	2.71E-01	1.00E+00	6.55E-02	1.00E+00	9.70E-02	1.00E+00	positive regulation of DNA replication	P
GO:0045761	21	8.41E-01	1.00E+00	3.11E-01	1.00E+00	9.19E-01	1.00E+00	7.06E-01	1.00E+00	4.59E-01	1.00E+00	2.56E-01	1.00E+00	7.40E-01	1.00E+00	8.59E-02	1.00E+00	regulation of adenylate cyclase activity	P
GO:0045762	17	9.79E-01	1.00E+00	4.00E-01	1.00E+00	9.99E-01	1.00E+00	8.16E-01	1.00E+00	6.46E-01	1.00E+00	3.99E-01	1.00E+00	8.87E-01	1.00E+00	9.54E-02	1.00E+00	positive regulation of adenylate cyclase acti	P
GO:0045763	15	9.36E-01	1.00E+00	5.20E-01	1.00E+00	8.63E-01	1.00E+00	5.21E-01	1.00E+00	8.63E-01	1.00E+00	3.97E-01	1.00E+00	9.52E-01	1.00E+00	6.15E-01	1.00E+00	negative regulation of amino acid metabolis	P
GO:0045764	47	6.26E-01	1.00E+00	3.08E-01	1.00E+00	8.70E-01	1.00E+00	4.82E-01	1.00E+00	9.10E-01	1.00E+00	2.77E-01	1.00E+00	6.92E-02	1.00E+00	1.66E-01	1.00E+00	positive regulation of amino acid metabolisr	P
GO:0045765	41	6.33E-01	1.00E+00	2.52E-01	1.00E+00	8.00E-01	1.00E+00	3.06E-01	1.00E+00	7.58E-01	1.00E+00	4.56E-01	1.00E+00	2.69E-01	1.00E+00	8.75E-02	1.00E+00	regulation of angiogenesis	P
GO:0045766	13	9.93E-01	1.00E+00	6.13E-01	1.00E+00	9.96E-01	1.00E+00	6.07E-01	1.00E+00	9.92E-01	1.00E+00	8.01E-01	1.00E+00	5.86E-01	1.00E+00	3.41E-01	1.00E+00	positive regulation of angiogenesis	P
GO:0045767	12	1.55E-01	1.00E+00	1.21E-01	1.00E+00	1.52E-01	1.00E+00	5.24E-02	1.00E+00	1.16E-01	1.00E+00	1.12E-01	1.00E+00	6.60E-01	1.00E+00	3.96E-01	1.00E+00	regulation of anti-apoptosis	P
GO:0045778	17	8.39E-01	1.00E+00	5.46E-01	1.00E+00	5.08E-01	1.00E+00	9.68E-01	1.00E+00	9.66E-01	1.00E+00	3.05E-01	1.00E+00	4.39E-01	1.00E+00	3.67E-01	1.00E+00	positive regulation of ossification	P
GO:0045785	12	5.57E-01	1.00E+00	4.44E-01	1.00E+00	6.85E-01	1.00E+00	6.42E-01	1.00E+00	6.92E-01	1.00E+00	7.85E-01	1.00E+00	3.24E-01	1.00E+00	1.78E-01	1.00E+00	positive regulation of cell adhesion	P
GO:0045786	161	9.98E-03	6.08E-01	1.53E-05	4.51E-03	5.71E-03	4.69E-01	7.90E-05	1.30E-02	2.09E-01	1.00E+00	4.35E-04	2.33E-02	2.12E-02	6.36E-01	1.56E-03	6.00E-02	negative regulation of progression through	P
GO:0045787	32	4.76E-02	1.00E+00	2.52E-01	1.00E+00	1.09E-01	1.00E+00	6.67E-01	1.00E+00	8.21E-02	1.00E+00	1.55E-01	1.00E+00	6.10E-02	1.00E+00	2.41E-01	1.00E+00	positive regulation of progression through c	P
GO:0045792	54	1.21E-02	6.08E-01	5.64E-03	3.08E-01	5.96E-03	4.69E-01	1.61E-02	6.47E-01	3.72E-01	1.00E+00	1.15E-01	1.00E+00	3.85E-02	8.54E-01	3.61E-03	1.27E-01	negative regulation of cell size	P
GO:0045793	12	3.77E-01	1.00E+00	2.17E-01	1.00E+00	7.79E-01	1.00E+00	3.01E-01	1.00E+00	3.22E-01	1.00E+00	4.50E-01	1.00E+00	3.49E-01	1.00E+00	1.77E-01	1.00E+00	positive regulation of cell size	P
GO:0045807	29	9.98E-01	1.00E+00	6.03E-01	1.00E+00	9.32E-01	1.00E+00	7.03E-01	1.00E+00	9.99E-01	1.00E+00	6.96E-01	1.00E+00	9.95E-01	1.00E+00	4.08E-01	1.00E+00	positive regulation of endocytosis	P
GO:0045814	18	5.70E-03	3.09E-01	5.79E-03	3.08E-01	1.24E-02	6.53E-01	4.17E-03	2.88E-01	2.90E-02	1.00E+00	1.20E-01	1.00E+00	1.48E-02	4.78E-01	3.68E-02	1.00E+00	negative regulation of gene expression, epi	P
GO:0045830	10	3.31E-01	1.00E+00	1.42E-01	1.00E+00	2.88E-01	1.00E+00	1.11E-01	1.00E+00	3.29E-01	1.00E+00	6.95E-01	1.00E+00	5.30E-01	1.00E+00	1.75E-01	1.00E+00	positive regulation of isotype switching	P
GO:0045834	13	1.47E-01	1.00E+00	3.86E-02	1.00E+00	3.08E-01	1.00E+00	1.37E-01	1.00E+00	1.95E-01	1.00E+00	4.28E-02	1.00E+00	1.84E-01	1.00E+00	4.12E-02	1.00E+00	positive regulation of lipid metabolism	P
GO:0045840	15	1.93E-01	1.00E+00	2.68E-01	1.00E+00	1.48E-01	1.00E+00	3.06E-01	1.00E+00	2.27E-01	1.00E+00	2.12E-01	1.00E+00	2.94E-01	1.00E+00	3.25E-01	1.00E+00	positive regulation of mitosis	P
GO:0045859	188	6.33E-04	8.86E-02	9.43E-06	4.51E-03	2.92E-03	1.35E-01	5.30E-04	4.20E-02	3.14E-02	1.00E+00	3.47E-04	2.33E-02	2.30E-03	8.40E-02	3.71E-04	3.00E-02	regulation of protein kinase activity	P
GO:0045860	128	8.25E-03	6.08E-01	3.37E-02	1.00E+00	1.27E-01	1.00E+00	1.22E-01	1.00E+00	2.58E-02	1.00E+00	9.06E-02	1.00E+00	4.39E-03	2.23E-01	2.98E-02	9.99E-01	positive regulation of protein kinase activity	P
GO:0045884	15	8.49E-01	1.00E+00	8.55E-01	1.00E+00	9.74E-01	1.00E+00	9.41E-01	1.00E+00	9.88E-01	1.00E+00	8.11E-01	1.00E+00	4.87E-01	1.00E+00	4.93E-01	1.00E+00	regulation of survival gene product activity	P
GO:0045892	260	2.20E-08	2.57E-03	4.52E-08	9.59E-04	1.06E-08	9.80E-04	1.19E-06	2.89E-03	1.51E-03	1.20E-01	1.61E-04	2.33E-02	9.58E-06	2.94E-03	8.75E-06	7.00E-03	negative regulation of transcription, DNA-de	P
GO:0045893	372	2.22E-04	1.72E-02	8.81E-06	4.51E-03	7.13E-05	1.07E-02	1.19E-04	1.30E-02	1.08E-01	1.00E+00	3.04E-03	1.44E-01	9.63E-04	3.62E-02	1.83E-05	7.00E-03	positive regulation of transcription, DNA-de	P
GO:0045926	65	3.36E-03	2.12E-01	3.74E-03	1.88E-01	2.08E-03	9.50E-02	7.40E-03	4.92E-01	1.22E-01	1.00E+00	1.18E-01	1.00E+00	4.28E-02	1.00E+00	1.39E-03	6.00E-02	negative regulation of growth	P
GO:0045927	42	9.76E-01	1.00E+00	8.91E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	5.97E-01	1.00E+00	2.50E-02	9.99E-01	positive regulation of growth	P
GO:0045930	16	8.74E-01	1.00E+00	2.48E-01	1.00E+00	4.86E-01	1.00E+00	6.51E-01	1.00E+00	1.00E+00	1.00E+00	2.04E-01	1.00E+00	2.42E-01	1.00E+00	1.37E-01	1.00E+00	negative regulation of progression through	P
GO:0045934	357	2.47E-12	0.00E+00	1.71E-11	0.00E+00	2.75E-12	7.08E-04	3.46E-10	0.00E+00	5.85E-06	1.69E-03	8.00E-07	2.00E-03	4.38E-07	8.23E-04	8.06E-07	2.00E-03	negative regulation of nucleobase, nucleosi	P
GO:0045935	465	1.08E-06	2.76E-03	1.06E-08	8.90E-04	1.58E-06	2.00E-03	1.12E-05	2.89E-03	1.08E-02	6.92E-01	1.49E-05	5.87E-03	5.38E-05	8.00E-03	1.43E-07	9.38E-04	positive regulation of nucleobase, nucleosid	P
GO:0045936	17	2.10E-01	1.00E+00	1.96E-02	1.00E+00	1.14E-01	1.00E+00	2.90E-02	1.00E+00	4.17E-01	1.00E+00	6.48E-02	1.00E+00	1.78E-01	1.00E+00	1.10E-01	1.00E+00	negative regulation of phosphate metabolisi	P
GO:0045937	39	9.30E-01	1.00E+00	3.65E-01	1.00E+00	9.56E-01	1.00E+00	4.54E-01	1.00E+00	9.57E-01	1.00E+00	7.31E-01	1.00E+00	5.81E-01	1.00E+00	5.30E-02	1.00E+00	positive regulation of phosphate metabolism	P
GO:0045941	444	4.03E-06	3.02E-03	6.53E-08	3.92E-03	2.38E-06	2.00E-03	1.46E-05	2.89E-03	3.02E-02	1.00E+00	3.70E-05	9.66E-03	1.13E-04	8.00E-03	2.26E-06	2.00E-03	positive regulation of transcription	P
GO:0045944	307	1.83E-02	1.00E+00	8.93E-03	4.69E-01	2.82E-03	1.35E-01	7.96E-03	4.92E-01	4.50E-01	1.00E+00	1.12E-01	1.00E+00	1.75E-02	4.88E-01	1.37E-02	4.76E-01	positive regulation of transcription from RN/	P
GO:0045954	12	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.65E-01	1.00E+00	positive regulation of natural killer cell medi	P
GO:0046006	10	2.89E-01	1.00E+00	1.32E-02	6.07E-01	7.84E-01	1.00E+00	5.21E-02	1.00E+00	7.00E-01	1.00E+00	4.92E-02	1.00E+00	1.75E-02	4.88E-01	1.75E-02	6.56E-01	regulation of activated T cell proliferation	P
GO:0046034	53	8.07E-02	1.00E+00	2.41E-01	1.00E+00	6.84E-02	1.00E+00	2.51E-01	1.00E+00	4.26E-02	1.00E+00	1.97E-01	1.00E+00	7.85E-01	1.00E+00	4.38E-01	1.00E+00	ATP metabolism	P

GO:0046036	13	6.96E-02	1.00E+00	1.59E-03	9.65E-02	1.08E-01	1.00E+00	1.55E-02	6.47E-01	2.36E-02	1.00E+00	1.14E-02	5.03E-01	5.54E-01	1.00E+00	5.21E-02	1.00E+00	CTP metabolism	P
GO:0046039	13	4.09E-02	1.00E+00	8.53E-04	8.70E-02	1.10E-01	1.00E+00	1.71E-02	6.47E-01	7.78E-03	6.92E-01	4.36E-03	2.66E-01	5.05E-01	1.00E+00	5.00E-02	1.00E+00	GTP metabolism	P
GO:0046051	12	6.11E-02	1.00E+00	2.24E-03	1.71E-01	1.03E-01	1.00E+00	3.15E-02	1.00E+00	1.82E-02	7.90E-01	3.47E-03	1.51E-01	5.60E-01	1.00E+00	8.52E-02	1.00E+00	UTP metabolism	P
GO:0046058	27	4.69E-01	1.00E+00	9.38E-02	1.00E+00	8.85E-01	1.00E+00	6.30E-01	1.00E+00	4.41E-01	1.00E+00	1.52E-01	1.00E+00	1.88E-01	1.00E+00	2.73E-02	9.99E-01	cAMP metabolism	P
GO:0046068	17	5.64E-01	1.00E+00	8.04E-01	1.00E+00	9.30E-01	1.00E+00	7.44E-01	1.00E+00	3.39E-01	1.00E+00	8.87E-01	1.00E+00	3.94E-01	1.00E+00	6.45E-01	1.00E+00	cGMP metabolism	P
GO:0046148	34	9.01E-02	1.00E+00	2.91E-01	1.00E+00	3.60E-02	1.00E+00	2.38E-01	1.00E+00	3.13E-01	1.00E+00	6.40E-01	1.00E+00	2.14E-01	1.00E+00	1.18E-01	1.00E+00	pigment biosynthesis	P
GO:0046164	84	1.08E-03	8.86E-02	4.06E-05	7.00E-03	6.12E-04	4.90E-02	2.07E-02	9.37E-01	4.78E-03	3.75E-01	6.79E-06	5.87E-03	2.19E-01	1.00E+00	2.81E-02	9.99E-01	alcohol catabolism	P
GO:0046165	32	2.03E-02	1.00E+00	2.67E-03	1.88E-01	8.96E-02	1.00E+00	1.34E-02	6.47E-01	1.49E-01	1.00E+00	4.86E-02	1.00E+00	1.59E-02	4.88E-01	4.30E-02	1.00E+00	alcohol biosynthesis	P
GO:0046209	22	2.05E-01	1.00E+00	1.98E-02	1.00E+00	3.56E-01	1.00E+00	2.51E-01	1.00E+00	2.46E-01	1.00E+00	2.79E-02	1.00E+00	1.64E-01	1.00E+00	5.42E-02	1.00E+00	nitric oxide metabolism	P
GO:0046323	14	9.84E-03	6.08E-01	7.40E-02	1.00E+00	6.52E-02	1.00E+00	1.02E-01	1.00E+00	5.97E-03	3.75E-01	4.43E-02	1.00E+00	5.30E-02	1.00E+00	4.04E-01	1.00E+00	glucose import	P
GO:0046324	13	2.15E-02	1.00E+00	9.38E-02	1.00E+00	4.97E-02	1.00E+00	1.37E-01	1.00E+00	1.66E-02	6.92E-01	6.71E-02	1.00E+00	8.02E-02	1.00E+00	3.68E-01	1.00E+00	regulation of glucose import	P
GO:0046328	24	3.60E-01	1.00E+00	1.92E-01	1.00E+00	3.42E-01	1.00E+00	2.18E-01	1.00E+00	1.97E-01	1.00E+00	3.08E-01	1.00E+00	7.79E-01	1.00E+00	1.88E-01	1.00E+00	regulation of JNK cascade	P
GO:0046330	15	9.29E-01	1.00E+00	7.07E-01	1.00E+00	7.51E-01	1.00E+00	6.46E-01	1.00E+00	9.41E-01	1.00E+00	6.46E-01	1.00E+00	6.98E-01	1.00E+00	6.95E-01	1.00E+00	positive regulation of JNK cascade	P
GO:0046332	20	5.19E-02	1.00E+00	1.44E-01	1.00E+00	5.61E-02	1.00E+00	3.32E-01	1.00E+00	3.89E-02	1.00E+00	1.86E-01	1.00E+00	3.28E-01	1.00E+00	9.63E-02	1.00E+00	SMAD binding	F
GO:0046348	11	9.00E-01	1.00E+00	7.64E-01	1.00E+00	8.74E-01	1.00E+00	6.72E-01	1.00E+00	5.93E-01	1.00E+00	6.58E-01	1.00E+00	9.88E-01	1.00E+00	8.56E-01	1.00E+00	amino sugar catabolism	P
GO:0046356	24	1.99E-02	1.00E+00	4.72E-02	1.00E+00	4.63E-02	1.00E+00	9.37E-02	1.00E+00	3.64E-02	1.00E+00	5.34E-02	1.00E+00	3.07E-01	1.00E+00	1.63E-01	1.00E+00	acetyl-CoA catabolism	P
GO:0046364	31	2.40E-02	1.00E+00	3.42E-03	1.88E-01	8.65E-02	1.00E+00	2.32E-02	9.37E-01	1.45E-01	1.00E+00	4.95E-02	1.00E+00	2.47E-02	8.38E-01	3.65E-02	1.00E+00	monosaccharide biosynthesis	P
GO:0046365	75	1.21E-03	8.86E-02	5.18E-05	7.00E-03	6.68E-04	4.90E-02	3.65E-02	1.00E+00	5.71E-03	3.75E-01	1.98E-06	2.00E-03	2.99E-01	1.00E+00	3.98E-02	1.00E+00	monosaccharide catabolism	P
GO:0046394	94	4.11E-02	1.00E+00	3.39E-03	1.88E-01	1.03E-01	1.00E+00	1.12E-01	1.00E+00	4.32E-02	1.00E+00	1.47E-02	6.68E-01	7.03E-02	1.00E+00	2.43E-03	7.90E-02	carboxylic acid biosynthesis	P
GO:0046425	21	9.14E-01	1.00E+00	1.44E-01	1.00E+00	9.97E-01	1.00E+00	5.66E-01	1.00E+00	9.89E-01	1.00E+00	1.40E-01	1.00E+00	1.86E-01	1.00E+00	8.93E-02	1.00E+00	regulation of JAK-STAT cascade	P
GO:0046427	12	8.64E-01	1.00E+00	2.29E-01	1.00E+00	9.74E-01	1.00E+00	6.50E-01	1.00E+00	9.97E-01	1.00E+00	5.98E-01	1.00E+00	2.11E-01	1.00E+00	4.47E-02	1.00E+00	positive regulation of JAK-STAT cascade	P
GO:0046456	26	5.11E-01	1.00E+00	8.11E-02	1.00E+00	5.13E-01	1.00E+00	9.88E-02	1.00E+00	2.90E-01	1.00E+00	1.07E-01	1.00E+00	7.40E-01	1.00E+00	2.10E-01	1.00E+00	icosanoid biosynthesis	P
GO:0046460	10	2.66E-01	1.00E+00	3.49E-01	1.00E+00	2.02E-01	1.00E+00	2.18E-01	1.00E+00	3.61E-01	1.00E+00	5.48E-01	1.00E+00	3.28E-01	1.00E+00	3.44E-01	1.00E+00	neutral lipid biosynthesis	P
GO:0046463	10	2.66E-01	1.00E+00	3.49E-01	1.00E+00	2.02E-01	1.00E+00	2.18E-01	1.00E+00	3.61E-01	1.00E+00	5.48E-01	1.00E+00	3.28E-01	1.00E+00	3.44E-01	1.00E+00	acylglycerol biosynthesis	P
GO:0046466	22	2.27E-03	2.12E-01	2.64E-02	1.00E+00	2.02E-02	1.00E+00	9.78E-02	1.00E+00	4.86E-03	3.75E-01	9.44E-03	5.03E-01	1.69E-02	4.88E-01	4.60E-01	1.00E+00	membrane lipid catabolism	P
GO:0046467	96	4.16E-03	2.14E-01	4.21E-05	7.00E-03	1.81E-03	9.50E-02	8.09E-04	6.90E-02	7.25E-02	1.00E+00	9.88E-03	5.03E-01	1.43E-01	1.00E+00	3.98E-02	1.00E+00	membrane lipid biosynthesis	P
GO:0046470	13	1.03E-01	1.00E+00	5.92E-02	1.00E+00	5.02E-02	1.00E+00	2.46E-02	1.00E+00	2.07E-01	1.00E+00	3.53E-01	1.00E+00	3.56E-01	1.00E+00	1.13E-01	1.00E+00	phosphatidylcholine metabolism	P
GO:0046474	39	3.84E-02	1.00E+00	3.80E-03	1.88E-01	5.25E-02	1.00E+00	1.40E-03	9.40E-02	8.84E-02	1.00E+00	6.01E-02	1.00E+00	5.51E-01	1.00E+00	1.63E-01	1.00E+00	glycerophospholipid biosynthesis	P
GO:0046483	92	3.87E-04	3.10E-02	3.34E-02	1.00E+00	5.01E-03	3.08E-01	4.64E-02	1.00E+00	4.08E-04	4.90E-02	1.40E-01	1.00E+00	6.24E-02	1.00E+00	1.32E-01	1.00E+00	heterocycle metabolism	P
GO:0046486	36	5.91E-03	3.09E-01	2.12E-02	1.00E+00	4.32E-02	1.00E+00	1.57E-02	6.47E-01	1.66E-02	6.92E-01	3.35E-01	1.00E+00	1.05E-02	2.75E-01	8.46E-03	4.28E-01	glycerolipid metabolism	P
GO:0046488	14	1.96E-02	1.00E+00	1.83E-02	1.00E+00	4.62E-02	1.00E+00	1.76E-02	6.47E-01	4.36E-02	1.00E+00	3.13E-02	1.00E+00	1.38E-01	1.00E+00	6.29E-02	1.00E+00	phosphatidylinositol metabolism	P
GO:0046489	27	6.56E-02	1.00E+00	1.40E-02	6.07E-01	1.73E-01	1.00E+00	7.57E-03	4.92E-01	8.29E-02	1.00E+00	1.51E-02	6.68E-01	5.43E-01	1.00E+00	5.39E-01	1.00E+00	phosphoinositide biosynthesis	P
GO:0046504	11	3.62E-01	1.00E+00	4.73E-01	1.00E+00	2.64E-01	1.00E+00	2.40E-01	1.00E+00	4.44E-01	1.00E+00	6.35E-01	1.00E+00	3.06E-01	1.00E+00	4.55E-01	1.00E+00	glycerol ether biosynthesis	P
GO:0046519	32	2.67E-06	3.02E-03	6.07E-06	4.51E-03	1.64E-04	1.16E-02	3.41E-03	1.76E-01	1.21E-03	1.20E-01	2.34E-04	2.33E-02	9.09E-04	3.44E-02	2.38E-03	7.90E-02	sphingoid metabolism	P
GO:0046520	10	1.09E-02	6.08E-01	7.37E-02	1.00E+00	6.30E-02	1.00E+00	4.00E-01	1.00E+00	6.95E-02	1.00E+00	3.96E-02	1.00E+00	6.82E-02	1.00E+00	2.76E-01	1.00E+00	sphingoid biosynthesis	P
GO:0046527	11	3.62E-01	1.00E+00	3.73E-01	1.00E+00	6.44E-01	1.00E+00	8.28E-01	1.00E+00	2.05E-01	1.00E+00	4.55E-01	1.00E+00	4.01E-01	1.00E+00	3.58E-01	1.00E+00	glucosyltransferase activity	F
GO:0046530	23	2.89E-01	1.00E+00	1.70E-01	1.00E+00	3.40E-01	1.00E+00	2.70E-01	1.00E+00	3.89E-01	1.00E+00	2.15E-01	1.00E+00	2.94E-01	1.00E+00	9.19E-02	1.00E+00	photoreceptor cell differentiation	P
GO:0046545	46	2.73E-02	1.00E+00	4.42E-01	1.00E+00	8.67E-02	1.00E+00	5.49E-01	1.00E+00	3.51E-02	1.00E+00	2.47E-01	1.00E+00	1.65E-01	1.00E+00	7.34E-01	1.00E+00	development of primary female sexual char	P
GO:0046546	27	3.15E-01	1.00E+00	7.70E-01	1.00E+00	2.07E-01	1.00E+00	6.93E-01	1.00E+00	6.73E-01	1.00E+00	6.55E-01	1.00E+00	2.07E-01	1.00E+00	7.64E-01	1.00E+00	development of primary male sexual charac	P
GO:0046578	13	6.34E-01	1.00E+00	7.85E-02	1.00E+00	9.47E-01	1.00E+00	2.78E-01	1.00E+00	4.42E-01	1.00E+00	5.01E-02	1.00E+00	2.49E-01	1.00E+00	1.08E-01	1.00E+00	regulation of Ras protein signal transductior	P
GO:0046620	16	4.90E-01	1.00E+00	5.87E-01	1.00E+00	5.77E-01	1.00E+00	5.78E-01	1.00E+00	4.82E-01	1.00E+00	9.54E-01	1.00E+00	3.44E-01	1.00E+00	1.91E-01	1.00E+00	regulation of organ size	P
GO:0046631	44	2.01E-01	1.00E+00	1.57E-01	1.00E+00	7.03E-01	1.00E+00	3.48E-01	1.00E+00	2.99E-01	1.00E+00	2.91E-01	1.00E+00	2.42E-02	8.38E-01	1.17E-01	1.00E+00	alpha-beta T cell activation	P
GO:0046632	32	5.43E-02	1.00E+00	1.70E-01	1.00E+00	3.66E-01	1.00E+00	3.32E-01	1.00E+00	2.45E-01	1.00E+00	5.45E-01	1.00E+00	3.70E-03	2.23E-01	3.91E-02	1.00E+00	alpha-beta T cell differentiation	P
GO:0046633	14	7.90E-01	1.00E+00	2.29E-01	1.00E+00	9.79E-01	1.00E+00	5.99E-01	1.00E+00	4.37E-01	1.00E+00	4.22E-02	1.00E+00	4.62E-01	1.00E+00	4.36E-01	1.00E+00	alpha-beta T cell proliferation	P
GO:0046634	14	6.99E-01	1.00E+00	2.19E-01	1.00E+00	9.87E-01	1.00E+00	5.98E-01	1.00E+00	3.43E-01	1.00E+00	1.35E-01	1.00E+00	3.96E-01	1.00E+00	1.29E-01	1.00E+00	regulation of alpha-beta T cell activation	P
GO:0046635	11	3.89E-01	1.00E+00	1.36E-01	1.00E+00	9.16E-01	1.00E+00	4.27E-01	1.00E+00	1.44E-01	1.00E+00	8.63E-02	1.00E+00	2.63E-01	1.00E+00	1.32E-01	1.00E+00	positive regulation of alpha-beta T cell activ	P
GO:0046640	11	6.78E-01	1.00E+00	2.95E-01	1.00E+00	9.47E-01	1.00E+00	5.96E-01	1.00E+00	4.63E-01	1.00E+00	8.73E-02	1.00E+00	3.21E-01	1.00E+00	3.58E-01	1.00E+00	regulation of alpha-beta T cell proliferation	P
GO:0046649	244	3.94E-02	1.00E+00	4.10E-05	7.00E-03	2.60E-01	1.00E+00	1.15E-03	9.40E-02	3.62E-01	1.00E+00	2.51E-02	1.00E+00	1.83E-03	8.40E-02	2.54E-05	7.00E-03	lymphocyte activation	P
GO:0046651	100	2.97E-01	1.00E+00	4.48E-03	2.61E-01	6.71E-01	1.00E+00	2.10E-02	9.37E-01	6.96E-01	1.00E+00	4.87E-02	1.00E+00	2.70E-02	8.38E-01	8.55E-03	4.28E-01	lymphocyte proliferation	P
GO:0046658	13	8.95E-01	1.00E+00	8.47E-01	1.00E+00	8.31E-01	1.00E+00	8.28E-01	1.00E+00	8.46E-01	1.00E+00	5.55E-01	1.00E+00	7.53E-01	1.00E+00	8.98E-01	1.00E+00	anchored to plasma membrane	C
GO:0046660	49	4.00E-02	1.00E+00	4.63E-01	1.00E+00	1.06E-01	1.00E+00	6.08E-01	1.00E+00	5.60E-02	1.00E+00	2.82E-01	1.00E+00	1.55E-01	1.00E+00	6.47E-01	1.00E+00	female sex differentiation	P
GO:0046661	41	3.84E-01	1.00E+00	8.30E-01	1.00E+00	3.05E-01	1.00E+00	7.21E-01	1.00E+00	7.20E-01	1.00E+00	8.25E-01	1.00E+00	1.62E-01	1.00E+00	7.37E-01	1.00E+00	male sex differentiation	P
GO:0046677	36	5.16E-01	1.00E+00	4.03E-01	1.00E+00	8.58E-01	1.00E+00	8.51E-01	1.00E+00	3.83E-01	1.00E+00	3.96E-01	1.00E+00	4.13E-01	1.00E+00	8.68E-02	1.00E+00	response to antibiotic	P
GO:0046777	63	1.19E-01	1.00E+00	1.77E-03	9.65E-02	1.24E-01	1.00E+00	4.38E-02	1.00E+00	9.56E-02	1.00E+00	7.87E-03	4.21E-01	4.25E-01	1.00E+00	7.74E-03	4.28E-01	protein amino acid autophosphorylation	P
GO:0046785	15	6.56E-01	1.00E+00	2.12E-01	1.00E+00	9.26E-01	1.00E+00	3.91E-01	1.00E+00	8.77E-01	1.00E+00	2.54E-01	1.00E+00	1.00E-01	1.00E+00	1.37E-01	1.00E+00	microtubule polymerization	P
GO:0046822	31	3.17E-03	2.12E-01	9.39E-05	1.50E-02	1.03E-02	6.53E-01	1.44E-04	1.30E-02	1.79E-02	7.90E-01	3.43E-03	1.51E-01	7.58E-02	1.00E+00	6.32E-03	4.28E-01	regulation of nucleocytoplasmic transport	P
GO:0046823	10	7.84E-02	1.00E+00	9.38E-02	1.00E+00	1.31E-01	1.00E+00	1.96E-02	9.37E-01	1.35E-01	1.00E+00	2.57E-01	1.00E+00	5.10E-01	1.00E+00	1.66E-01	1.00E+00	negative regulation of nucleocytoplasmic tra	P
GO:0046824	14	1.33E-01	1.00E+00	8.81E-03	4.69E-01	3.00E-01	1.00E+00	1.46E-02	6.47E-01	3.18E-01	1.00E+00	3.18E-02	1.00E+00	1.70E-01	1.00E+00	5.24E-02	1.00E+00	positive regulation of nucleocytoplasmic tra	P
GO:0046834	16	3.41E-02	1.00E+00	1.64E-02	7.63E-01	1.05E-01	1.00E+00	2.87E-02	1.00E+00	1.47E-01	1.00E+00	2.60E-02	1.00E+00	1.70E-02	4.88E-01	7.20E-02	1.00E+00	lipid phosphorylation	P
GO:0046839	14	3.11E-01	1.00E+00	9.34E-02	1.00E+00	5.01E-01	1.00E+00	1.51E-01	1.00E+00	7.09E-02	1.00E+00	2.64E-01	1.00E+00	9.75E-01	1.00E+00	3.46E-02	1.00E+00	phospholipid dephosphorylation	P
GO:0046847	13	1.86E-02	1.00E+00	5.55E-02	1.00E+00	1.91E-01	1.00E+00	1.34E-01	1.00E+00	6.89E-02	1.00E+00	2.38E-01	1.00E+00	2.09E-02	6.36E-01	9.94E-03	4.76E-01	filopodium formation	P
GO:0046849	165	4.83E-02	1.00E+00	3.09E-01	1.00E+00	4.19E-01	1.00E+00	4.22E-01	1.00E+00	3.92E-02	1.00E+00	4.30E-01	1.00E+00	5.73E-02	1.00E+00	1.97E-01	1.00E+00	bone remodeling	P
GO:0046850	46	5.18E-01	1.00E+00	8.89E-01	1.00E+00	8.21E-01	1.00E+00	9.96E-01	1.00E+00	4.92E-01	1.00E+00	5.33E-01	1.00E+00	2.87E-01	1.00E+00	5.68E-01	1.00E+00	regulation of bone remodeling	P
GO:0046851	18	4.91E-01	1.00E+00	8.41E-01	1.00E+00	6.83E-01	1.00E+00	9.88E-01	1.00E+00	9.81E-01	1.00E+00	6.62E-01	1.00E+00	1.57E-01	1.00E+00	1.69E-01	1.00E+00	negative regulation of bone remodeling	P
GO:0046852	20	9.23E-01	1.00E+00	7.23E-01	1.00E+00	6.40E-01	1.00E+00	9.91E-01	1.00E+00	9.85E-01	1.00E+00	4.26E-01	1.00E+00	5.18E-01	1.00E+00	4.42E-01	1.00E+00	positive regulation of bone remodeling	P
GO:0046854	15	1.60E-02	1.00E+00	9.19E-03	4.69E-01	5.50E-02	1.00E+00	1.57E-02	6.47E-01	8.68E-02	1.00E+00	2.78E-02	1.00E+00	1.58E-02	4.88E-01	3.97E-02	1.00E+00	phosphoinositide phosphorylation	P
GO:0046872	4161	1.99E-15	0.00E+00	2.82E-33	0.00E+00	1.10E-15	0.00E+00	1.99E-26	0.00E+00	9.93E-10	0.00E+00	1.33E-23	0.00E+00	2.77E-04	2.29E-02	2.91E-13	0.00E+00	metal ion binding	F
GO:0046873	51	1.79E-01	1.00E+00	5.93E-02	1.00E+00	1.78E-01	1.00E+00	5.12E-02	1.00E+00	2.89E-01	1.00E+00	1.75E-01	1.00E+00	6.17E-01	1.00E+00	4.77E-01	1.00E+00	metal ion transporter activity	F
GO:0046879	73	5.76E-01	1.00E+00	2.64E-01	1.00E+00	8.17E-01	1.00E+00	7.25E-01	1.00E+00	8.41E-01	1.00E+00	6.20E-01	1.00E+00	3.42E-02	8.38E-01	2.10E-02	9.99E-01	hormone secretion	P
GO:0046883	29	2.00E-01	1.00E+00	2.09E-02	1.00E+00	3.83E-01	1.00E+00	1.22E-01	1.00E+00	4.70E-01	1.00E+00	1.97E-01	1.00E+00	2.71E-02	8.38E-01	1.14E-02	4.76E-01	regulation of hormone secretion	P
GO:0046888	15	1.50E-01	1.00E+00	1.06E-02	4.69E-01	2.74E-01	1.00E+00	2.76E-02	1.00E+00	5.51E-01	1.00E+00	2.11E-01	1.00E+00	9.68E-03	2.75E-01	2.40E-02	9.99E-01	negative regulation of hormone secretion	P
GO:0046890	14	2.12E-04	1.72E-02	2.94E-02	1.00E+00	3.58E-02	1.00E+00	3.60E-02	1.00E+00	3.73E-02	1.00E+00	1.68E-02	6.68E-01	2.66E-03	8.40E-02	1.59E-01	1.00E+00	regulation of lipid biosynthesis	P
GO:0046903	345	1.95E-03	2.12E-01	1.75E-04	1.80E-02	5.54E-02	1.00E+00	1.16E-02	6.47E-01	2.87E-02	1.00E+00	4.65E-03	2.66E-01	1.64E-03	8.40E-02	1.84E-04	1.60E-02	secretion	P
GO:0046906	203	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.70E-01	1.00E+00	6.95E-01	1.00E+00	tetrapyrrole binding	F
GO:0046907	799	4.94E-27	0.00E+00	2.18E-37	0.00E+00	1.07E-20	0.00E+00	3.09E-28	0.00E+00	3.03E-21	0.00E+00	1.01E-23	0.00E+00	1.02E-08	0.00E+00	2.57E-15	0.00E+00	intracellular transport	P

GO:0046914	2760	2.94E-20	0.00E+00	2.93E-33	0.00E+00	7.72E-24	0.00E+00	1.90E-32	0.00E+00	2.06E-12	0.00E+00	1.23E-25	0.00E+00	5.78E-04	3.44E-02	1.10E-07	9.38E-04	transition metal ion binding	F
GO:0046915	31	6.45E-02	1.00E+00	8.02E-03	4.16E-01	3.75E-02	1.00E+00	1.31E-02	6.47E-01	2.88E-01	1.00E+00	4.44E-02	1.00E+00	3.86E-01	1.00E+00	2.88E-01	1.00E+00	transition metal ion transporter activity	F
GO:0046916	53	2.97E-01	1.00E+00	2.22E-01	1.00E+00	2.79E-01	1.00E+00	9.15E-02	1.00E+00	3.19E-01	1.00E+00	2.64E-01	1.00E+00	6.02E-01	1.00E+00	7.68E-01	1.00E+00	transition metal ion homeostasis	P
GO:0046928	30	9.90E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	7.51E-01	1.00E+00	6.33E-01	1.00E+00	7.35E-01	1.00E+00	regulation of neurotransmitter secretion	P
GO:0046930	58	9.26E-09	2.57E-03	3.52E-13	0.00E+00	6.83E-08	9.80E-04	2.26E-11	0.00E+00	6.89E-06	2.00E-03	7.63E-06	5.87E-03	5.91E-02	1.00E+00	5.41E-05	7.00E-03	pore complex	C
GO:0046933	41	7.90E-03	6.08E-01	2.76E-02	1.00E+00	7.08E-03	4.69E-01	9.69E-02	1.00E+00	1.63E-02	6.92E-01	6.20E-02	1.00E+00	2.81E-01	1.00E+00	5.47E-02	1.00E+00	hydrogen-transporting ATP synthase activity	F
GO:0046942	149	2.45E-01	1.00E+00	4.51E-02	1.00E+00	2.92E-01	1.00E+00	3.30E-01	1.00E+00	1.55E-01	1.00E+00	4.56E-02	1.00E+00	4.31E-01	1.00E+00	2.71E-02	9.99E-01	carboxylic acid transport	P
GO:0046943	139	6.93E-01	1.00E+00	2.20E-01	1.00E+00	5.58E-01	1.00E+00	4.90E-01	1.00E+00	6.35E-01	1.00E+00	2.08E-01	1.00E+00	8.32E-01	1.00E+00	2.62E-01	1.00E+00	carboxylic acid transporter activity	F
GO:0046961	44	1.04E-02	6.08E-01	4.56E-02	1.00E+00	1.34E-02	6.53E-01	1.63E-01	1.00E+00	1.78E-02	7.90E-01	7.42E-02	1.00E+00	2.62E-01	1.00E+00	7.85E-02	1.00E+00	hydrogen-transporting ATPase activity, rotat	F
GO:0046966	21	2.24E-02	1.00E+00	1.67E-02	7.63E-01	9.46E-04	4.90E-02	7.45E-03	4.92E-01	4.40E-02	1.00E+00	1.92E-01	1.00E+00	4.94E-01	1.00E+00	1.48E-01	1.00E+00	thyroid hormone receptor binding	F
GO:0046982	143	2.10E-02	1.00E+00	7.66E-03	4.16E-01	1.91E-01	1.00E+00	1.38E-02	6.47E-01	7.70E-02	1.00E+00	7.17E-02	1.00E+00	1.94E-02	6.36E-01	9.80E-03	4.76E-01	protein heterodimerization activity	F
GO:0046983	380	3.64E-06	3.02E-03	2.53E-07	3.92E-03	6.20E-04	4.90E-02	1.37E-05	2.89E-03	5.16E-04	4.90E-02	9.56E-04	9.00E-02	2.83E-04	2.29E-02	2.04E-05	7.00E-03	protein dimerization activity	F
GO:0047485	32	3.93E-03	2.12E-01	3.30E-05	7.00E-03	1.12E-03	7.90E-02	1.35E-05	2.89E-03	1.83E-02	7.90E-01	1.61E-02	6.68E-01	7.37E-02	1.00E+00	6.56E-03	4.28E-01	protein N-terminus binding	F
GO:0048002	33	7.98E-02	1.00E+00	5.38E-01	1.00E+00	1.76E-02	1.00E+00	4.57E-01	1.00E+00	2.93E-01	1.00E+00	8.17E-02	1.00E+00	4.40E-01	1.00E+00	9.79E-01	1.00E+00	antigen processing and presentation of pep	P
GO:0048008	10	2.94E-01	1.00E+00	1.05E-01	1.00E+00	4.60E-01	1.00E+00	1.61E-01	1.00E+00	1.06E-01	1.00E+00	6.22E-02	1.00E+00	5.33E-01	1.00E+00	2.14E-01	1.00E+00	platelet-derived growth factor receptor signa	P
GO:0048009	16	8.75E-01	1.00E+00	6.03E-01	1.00E+00	8.61E-01	1.00E+00	9.91E-01	1.00E+00	9.62E-01	1.00E+00	8.84E-01	1.00E+00	8.28E-01	1.00E+00	7.60E-02	1.00E+00	insulin-like growth factor receptor signaling	P
GO:0048010	17	6.51E-01	1.00E+00	5.62E-01	1.00E+00	4.45E-01	1.00E+00	8.34E-01	1.00E+00	8.93E-01	1.00E+00	6.72E-01	1.00E+00	6.38E-01	1.00E+00	4.67E-02	1.00E+00	vascular endothelial growth factor receptor	P
GO:0048011	13	2.98E-03	2.12E-01	4.05E-02	1.00E+00	2.91E-02	1.00E+00	3.78E-02	1.00E+00	2.29E-02	1.00E+00	1.61E-01	1.00E+00	1.12E-02	3.39E-01	8.52E-02	1.00E+00	nerve growth factor receptor signaling path	P
GO:0048015	62	2.28E-01	1.00E+00	1.04E-01	1.00E+00	4.70E-01	1.00E+00	2.03E-01	1.00E+00	2.73E-01	1.00E+00	3.68E-01	1.00E+00	1.01E-01	1.00E+00	1.51E-02	6.56E-01	phosphoinositide-mediated signaling	P
GO:0048029	22	2.65E-01	1.00E+00	1.80E-01	1.00E+00	3.96E-01	1.00E+00	1.63E-01	1.00E+00	2.68E-01	1.00E+00	3.09E-01	1.00E+00	3.01E-01	1.00E+00	2.70E-01	1.00E+00	monosaccharide binding	F
GO:0048037	297	6.79E-04	8.86E-02	4.47E-02	1.00E+00	1.24E-02	6.53E-01	1.20E-01	1.00E+00	1.29E-02	6.92E-01	1.24E-02	5.03E-01	2.43E-03	8.40E-02	3.50E-01	1.00E+00	cofactor binding	F
GO:0048041	15	7.16E-04	8.86E-02	2.59E-03	1.80E-01	4.16E-03	2.20E-01	4.18E-02	1.00E+00	2.73E-02	1.00E+00	4.70E-04	2.33E-02	8.23E-04	3.44E-02	2.29E-02	9.99E-01	focal adhesion formation	P
GO:0048048	11	1.03E-01	1.00E+00	4.28E-01	1.00E+00	2.37E-01	1.00E+00	2.98E-01	1.00E+00	6.17E-02	1.00E+00	8.90E-01	1.00E+00	4.00E-01	1.00E+00	3.27E-01	1.00E+00	embryonic eye morphogenesis	P
GO:0048066	17	2.72E-01	1.00E+00	2.37E-01	1.00E+00	2.80E-01	1.00E+00	3.60E-01	1.00E+00	6.92E-01	1.00E+00	2.19E-01	1.00E+00	1.42E-01	1.00E+00	3.72E-01	1.00E+00	pigmentation during development	P
GO:0048144	19	8.97E-03	6.08E-01	3.92E-02	1.00E+00	4.53E-02	1.00E+00	3.60E-02	1.00E+00	2.05E-02	7.90E-01	4.27E-02	1.00E+00	1.24E-02	4.24E-01	3.46E-01	1.00E+00	fibroblast proliferation	P
GO:0048145	19	8.97E-03	6.08E-01	3.92E-02	1.00E+00	4.53E-02	1.00E+00	3.60E-02	1.00E+00	2.05E-02	7.90E-01	4.27E-02	1.00E+00	1.24E-02	4.24E-01	3.46E-01	1.00E+00	regulation of fibroblast proliferation	P
GO:0048146	14	1.21E-01	1.00E+00	2.92E-01	1.00E+00	4.19E-01	1.00E+00	4.03E-01	1.00E+00	1.84E-01	1.00E+00	2.97E-01	1.00E+00	5.59E-02	1.00E+00	2.99E-01	1.00E+00	positive regulation of fibroblast proliferation	P
GO:0048167	38	7.51E-01	1.00E+00	6.70E-01	1.00E+00	8.68E-01	1.00E+00	7.18E-01	1.00E+00	8.94E-01	1.00E+00	5.84E-01	1.00E+00	4.42E-01	1.00E+00	5.94E-01	1.00E+00	regulation of synaptic plasticity	P
GO:0048168	22	5.51E-01	1.00E+00	8.31E-01	1.00E+00	7.15E-01	1.00E+00	8.62E-01	1.00E+00	2.65E-01	1.00E+00	5.64E-01	1.00E+00	8.01E-01	1.00E+00	7.77E-01	1.00E+00	regulation of neuronal synaptic plasticity	P
GO:0048169	15	8.33E-01	1.00E+00	5.76E-01	1.00E+00	8.64E-01	1.00E+00	5.44E-01	1.00E+00	4.80E-01	1.00E+00	3.07E-01	1.00E+00	9.46E-01	1.00E+00	8.43E-01	1.00E+00	regulation of long-term neuronal synaptic pl	P
GO:0048193	62	5.62E-05	1.20E-02	1.68E-06	3.92E-03	1.24E-03	7.90E-02	6.45E-06	2.89E-03	1.64E-03	1.20E-01	8.42E-04	4.48E-02	2.57E-02	8.38E-01	9.28E-04	6.00E-02	Golgi vesicle transport	P
GO:0048232	233	4.70E-07	2.57E-03	1.41E-05	4.51E-03	4.04E-07	2.00E-03	8.35E-05	1.30E-02	9.49E-04	1.20E-01	1.63E-03	1.22E-01	1.44E-03	6.14E-02	6.90E-03	4.28E-01	male gamete generation	P
GO:0048265	17	9.10E-01	1.00E+00	7.48E-01	1.00E+00	1.00E+00	1.00E+00	8.34E-01	1.00E+00	9.70E-01	1.00E+00	3.65E-01	1.00E+00	8.78E-02	1.00E+00	5.65E-01	1.00E+00	response to pain	P
GO:0048278	19	1.14E-01	1.00E+00	2.10E-01	1.00E+00	2.25E-01	1.00E+00	4.30E-01	1.00E+00	1.44E-01	1.00E+00	1.06E-01	1.00E+00	2.35E-01	1.00E+00	3.74E-01	1.00E+00	vesicle docking	P
GO:0048286	16	4.11E-01	1.00E+00	2.96E-01	1.00E+00	2.93E-01	1.00E+00	4.58E-01	1.00E+00	9.25E-01	1.00E+00	2.93E-01	1.00E+00	2.81E-01	1.00E+00	1.57E-01	1.00E+00	alveolus development	P
GO:0048305	11	5.78E-02	1.00E+00	1.21E-01	1.00E+00	1.51E-01	1.00E+00	4.32E-01	1.00E+00	3.61E-01	1.00E+00	1.21E-01	1.00E+00	4.13E-02	1.00E+00	4.20E-01	1.00E+00	immunoglobulin secretion	P
GO:0048306	17	6.95E-02	1.00E+00	5.28E-01	1.00E+00	1.92E-01	1.00E+00	5.45E-01	1.00E+00	1.43E-01	1.00E+00	3.68E-01	1.00E+00	1.05E-01	1.00E+00	6.98E-01	1.00E+00	calcium-dependent protein binding	F
GO:0048332	37	9.66E-03	6.08E-01	5.64E-04	4.74E-02	2.47E-03	1.07E-01	9.86E-03	5.72E-01	2.25E-01	1.00E+00	4.15E-03	2.66E-01	7.99E-02	1.00E+00	1.48E-02	6.56E-01	mesoderm morphogenesis	P
GO:0048339	13	2.12E-01	1.00E+00	1.67E-01	1.00E+00	9.02E-02	1.00E+00	2.98E-01	1.00E+00	1.68E-01	1.00E+00	4.79E-01	1.00E+00	4.25E-01	1.00E+00	1.06E-01	1.00E+00	paraxial mesoderm development	P
GO:0048384	10	2.63E-01	1.00E+00	5.12E-01	1.00E+00	6.93E-01	1.00E+00	7.54E-01	1.00E+00	8.06E-02	1.00E+00	3.40E-01	1.00E+00	2.15E-01	1.00E+00	5.54E-01	1.00E+00	retinoic acid receptor signaling pathway	P
GO:0048468	652	7.89E-03	6.08E-01	1.37E-02	6.07E-01	5.19E-02	1.00E+00	1.22E-01	1.00E+00	2.16E-01	1.00E+00	1.15E-01	1.00E+00	1.04E-03	3.62E-02	1.98E-03	7.90E-02	cell development	P
GO:0048469	89	1.39E-01	1.00E+00	1.98E-01	1.00E+00	1.27E-01	1.00E+00	8.36E-01	1.00E+00	7.03E-01	1.00E+00	2.76E-01	1.00E+00	6.65E-02	1.00E+00	4.45E-02	1.00E+00	cell maturation	P
GO:0048471	86	6.35E-03	3.09E-01	1.45E-04	1.50E-02	2.82E-02	1.00E+00	3.18E-04	4.20E-02	1.71E-02	6.92E-01	1.91E-03	1.27E-01	4.71E-02	1.00E+00	2.97E-02	9.99E-01	perinuclear region	C
GO:0048475	61	2.62E-06	3.02E-03	3.59E-08	9.59E-04	9.97E-05	1.16E-02	1.12E-08	8.93E-04	2.74E-03	2.13E-01	1.11E-05	5.87E-03	4.86E-04	3.44E-02	1.10E-02	4.76E-01	coated membrane	C
GO:0048477	29	2.54E-02	1.00E+00	2.45E-01	1.00E+00	5.90E-02	1.00E+00	3.23E-01	1.00E+00	2.54E-01	1.00E+00	2.08E-01	1.00E+00	3.11E-02	8.38E-01	6.01E-01	1.00E+00	oogenesis	P
GO:0048483	15	4.19E-01	1.00E+00	8.92E-01	1.00E+00	3.60E-01	1.00E+00	8.22E-01	1.00E+00	2.84E-01	1.00E+00	8.35E-01	1.00E+00	7.00E-01	1.00E+00	8.54E-01	1.00E+00	autonomic nervous system development	P
GO:0048489	27	2.35E-01	1.00E+00	1.29E-01	1.00E+00	1.99E-01	1.00E+00	2.88E-01	1.00E+00	5.93E-01	1.00E+00	1.18E-01	1.00E+00	9.11E-02	1.00E+00	1.59E-01	1.00E+00	synaptic vesicle transport	P
GO:0048500	15	5.17E-03	2.72E-01	5.15E-02	1.00E+00	2.73E-01	1.00E+00	7.33E-02	1.00E+00	3.28E-03	2.13E-01	7.45E-02	1.00E+00	7.83E-02	1.00E+00	1.19E-01	1.00E+00	signal recognition particle	C
GO:0048511	86	8.89E-02	1.00E+00	2.96E-01	1.00E+00	2.75E-01	1.00E+00	4.86E-01	1.00E+00	5.83E-02	1.00E+00	3.50E-01	1.00E+00	1.52E-01	1.00E+00	2.92E-01	1.00E+00	rhythmic process	P
GO:0048513	1460	1.82E-04	1.72E-02	2.85E-02	1.00E+00	3.35E-02	1.00E+00	6.73E-02	1.00E+00	7.25E-02	1.00E+00	5.56E-01	1.00E+00	5.78E-07	8.23E-04	1.16E-03	6.00E-02	organ development	P
GO:0048514	212	3.31E-01	1.00E+00	1.74E-01	1.00E+00	7.90E-01	1.00E+00	7.54E-01	1.00E+00	4.33E-01	1.00E+00	4.92E-01	1.00E+00	1.03E-01	1.00E+00	1.82E-03	7.90E-02	blood vessel morphogenesis	P
GO:0048515	46	1.59E-02	1.00E+00	1.02E-02	4.69E-01	4.91E-03	3.08E-01	1.54E-02	6.47E-01	3.35E-01	1.00E+00	4.60E-02	1.00E+00	7.94E-03	2.75E-01	4.39E-02	1.00E+00	spermatid differentiation	P
GO:0048518	1387	4.67E-11	2.57E-03	9.32E-15	0.00E+00	3.00E-08	9.80E-04	8.65E-09	8.93E-04	8.41E-04	1.20E-01	3.63E-08	9.03E-04	2.16E-10	0.00E+00	1.17E-12	0.00E+00	positive regulation of biological process	P
GO:0048519	1249	6.87E-19	0.00E+00	3.61E-20	0.00E+00	1.75E-13	7.08E-04	1.45E-15	0.00E+00	4.01E-08	9.59E-04	1.15E-10	6.20E-04	1.50E-14	0.00E+00	3.06E-14	0.00E+00	negative regulation of biological process	P
GO:0048522	1134	3.42E-08	2.57E-03	1.17E-12	0.00E+00	1.06E-06	2.00E-03	1.37E-07	2.89E-03	1.55E-02	6.92E-01	1.98E-07	1.65E-03	2.11E-08	0.00E+00	2.72E-10	0.00E+00	positive regulation of cellular process	P
GO:0048523	1134	1.83E-17	0.00E+00	3.39E-18	0.00E+00	2.30E-13	7.08E-04	1.22E-14	0.00E+00	3.08E-07	9.59E-04	2.73E-09	8.78E-04	1.68E-13	0.00E+00	9.81E-13	0.00E+00	negative regulation of cellular process	P
GO:0048534	300	5.17E-04	4.40E-02	1.23E-02	6.07E-01	1.16E-04	1.16E-02	1.51E-02	6.47E-01	4.35E-01	1.00E+00	2.68E-01	1.00E+00	9.94E-05	8.00E-03	2.11E-02	9.99E-01	hemopoietic or lymphoid organ developmer	P
GO:0048535	19	3.98E-02	1.00E+00	4.84E-01	1.00E+00	6.83E-02	1.00E+00	2.69E-01	1.00E+00	8.42E-02	1.00E+00	4.26E-01	1.00E+00	4.25E-02	1.00E+00	7.15E-01	1.00E+00	lymph node development	P
GO:0048536	16	5.28E-01	1.00E+00	6.29E-01	1.00E+00	7.20E-01	1.00E+00	7.11E-01	1.00E+00	3.32E-01	1.00E+00	4.33E-01	1.00E+00	4.74E-01	1.00E+00	6.88E-01	1.00E+00	spleen development	P
GO:0048538	18	2.76E-01	1.00E+00	3.17E-01	1.00E+00	3.42E-01	1.00E+00	3.58E-01	1.00E+00	6.07E-01	1.00E+00	2.64E-01	1.00E+00	1.06E-01	1.00E+00	5.06E-01	1.00E+00	thymus development	P
GO:0048545	65	6.96E-01	1.00E+00	6.38E-01	1.00E+00	8.04E-01	1.00E+00	7.76E-01	1.00E+00	8.15E-01	1.00E+00	3.59E-01	1.00E+00	1.86E-01	1.00E+00	7.57E-01	1.00E+00	response to steroid hormone stimulus	P
GO:0048546	18	5.40E-02	1.00E+00	1.31E-01	1.00E+00	1.14E-01	1.00E+00	2.56E-01	1.00E+00	4.09E-01	1.00E+00	2.35E-01	1.00E+00	1.56E-02	4.88E-01	2.90E-02	9.99E-01	digestive tract morphogenesis	P
GO:0048547	16	4.78E-02	1.00E+00	8.66E-02	1.00E+00	1.27E-01	1.00E+00	1.44E-01	1.00E+00	3.92E-01	1.00E+00	2.28E-01	1.00E+00	1.17E-02	3.39E-01	1.70E-02	6.56E-01	gut morphogenesis	P
GO:0048557	10	2.50E-02	1.00E+00	4.05E-02	1.00E+00	7.39E-02	1.00E+00	4.88E-02	1.00E+00	1.77E-01	1.00E+00	1.44E-01	1.00E+00	5.26E-03	2.23E-01	2.95E-02	9.99E-01	embryonic digestive tract morphogenesis	P
GO:0048562	27	7.37E-02	1.00E+00	2.24E-01	1.00E+00	2.49E-01	1.00E+00	2.52E-01	1.00E+00	8.61E-02	1.00E+00	5.23E-01	1.00E+00	5.52E-02	1.00E+00	6.53E-02	1.00E+00	embryonic organ morphogenesis	P
GO:0048565	27	4.19E-01	1.00E+00	3.48E-01	1.00E+00	3.10E-01	1.00E+00	5.02E-01	1.00E+00	8.08E-01	1.00E+00	7.97E-01	1.00E+00	1.18E-01	1.00E+00	2.16E-02	9.99E-01	gut development	P
GO:0048566	18	3.33E-01	1.00E+00	1.91E-01	1.00E+00	5.78E-01	1.00E+00	3.25E-01	1.00E+00	4.97E-01	1.00E+00	6.06E-01	1.00E+00	1.43E-01	1.00E+00	1.64E-02	6.56E-01	embryonic gut development	P
GO:0048567	10	1.83E-01	1.00E+00	4.11E-02	1.00E+00	5.41E-01	1.00E+00	1.05E-01	1.00E+00	3.52E-01	1.00E+00	1.43E-01	1.00E+00	7.40E-02	1.00E+00	2.78E-03	1.27E-01	ectodermal gut morphogenesis	P
GO:0048568	51	1.10E-01	1.00E+00	2.39E-01	1.00E+00	2.46E-01	1.00E+00	3.40E-01	1.00E+00	2.24E-01	1.00E+00	6.40E-01	1.00E+00	6.58E-02	1.00E+00	3.80E-02	1.00E+00	embryonic organ development	P
GO:0048583	15	9.29E-01	1.00E+00	7.25E-01	1.00E+00	9.02E-01	1.00E+00	6.47E-01	1.00E+00	9.17E-01	1.00E+00	8.13E-01	1.00E+00	7.20E-01	1.00E+00	3.79E-01	1.00E+00	regulation of response to stimulus	P
GO:0048584	10	9.31E-01	1.00E+00	6.29E-01	1.00E+00	8.14E-01	1.00E+00	5.99E-01	1.00E+00	9.87E-01	1.00E+00	6.39E-01	1.00E+00	5.90E-01	1.00E+00	4.42E-01	1.00E+00	positive regulation of response to stimulus	P
GO:0048589	54	2.75E-03	2.12E-01	3.06E-03	1.88E-01	3.00E-02	1.00E+00	2.26E-02	9.37E-01	6.88E-03	6.92E-01	4.11E-02	1.00E+00	7.37E-02	1.00E+00	2.67E-03	8.32E-02	developmental growth	P
GO:0048592	44	1.08E-01	1.00E+00	1.91E-01	1.00E+00	1.87E-01	1.00E+00	1.19E-01	1.00E+00	1.10E-01	1.00E+00	2.59E-01	1.00E+00	2.00E-01	1.00E+00	3.97E-01	1.00E+00	eye morphogenesis	P
GO:0048593	18	1.10E-01	1.00E+00	1.61E-01	1.00E+00	1.21E-01	1.00E+00	1.04E-01	1.00E+00	5.10E-02	1.00E+00	3.95E-01	1.00E+00	7.07E-01	1.00E+00	1.82E-01	1.00E+00	eye morphogenesis (sensu Vertebrata)	P
GO:0048598	249	9.23E-01	1.00E+00	9.98E-01	1.00E+00	9.83E-01	1.00E+00	9.99E-01	1.00E+00	7.75E-01	1.00E+00	9.97E-01	1.00E+00	6.22E-01	1.00E+00	6.43E-01	1.00E+00	embryonic morphogenesis	P

GO:0048599	13	4.97E-02	1.00E+00	2.88E-01	1.00E+00	8.54E-02	1.00E+00	5.96E-01	1.00E+00	1.94E-01	1.00E+00	1.75E-01	1.00E+00	2.00E-01	1.00E+00	6.65E-01	1.00E+00	oocyte development	P
GO:0048609	115	6.31E-01	1.00E+00	8.81E-01	1.00E+00	7.95E-01	1.00E+00	9.64E-01	1.00E+00	3.57E-01	1.00E+00	8.05E-01	1.00E+00	6.25E-01	1.00E+00	5.33E-01	1.00E+00	reproductive organismal physiological proce	P
GO:0048627	26	2.39E-01	1.00E+00	1.53E-01	1.00E+00	2.16E-01	1.00E+00	2.19E-01	1.00E+00	6.95E-01	1.00E+00	1.25E-01	1.00E+00	1.61E-01	1.00E+00	5.04E-01	1.00E+00	myoblast development	P
GO:0048628	25	2.59E-01	1.00E+00	3.02E-01	1.00E+00	3.57E-01	1.00E+00	4.58E-01	1.00E+00	6.41E-01	1.00E+00	2.44E-01	1.00E+00	1.18E-01	1.00E+00	5.54E-01	1.00E+00	myoblast maturation	P
GO:0048637	80	5.68E-01	1.00E+00	2.55E-01	1.00E+00	7.36E-01	1.00E+00	2.73E-01	1.00E+00	8.77E-01	1.00E+00	5.51E-01	1.00E+00	8.64E-02	1.00E+00	1.91E-01	1.00E+00	skeletal muscle development	P
GO:0048644	21	4.36E-01	1.00E+00	9.21E-01	1.00E+00	5.40E-01	1.00E+00	9.46E-01	1.00E+00	7.79E-01	1.00E+00	8.60E-01	1.00E+00	1.14E-01	1.00E+00	9.02E-01	1.00E+00	muscle morphogenesis	P
GO:0048646	86	1.15E-02	6.08E-01	3.81E-03	1.88E-01	3.86E-03	2.20E-01	1.91E-02	9.37E-01	1.13E-01	1.00E+00	6.26E-02	1.00E+00	1.41E-01	1.00E+00	2.09E-03	7.90E-02	anatomical structure formation	P
GO:0048659	30	2.12E-01	1.00E+00	3.55E-01	1.00E+00	1.25E-01	1.00E+00	2.88E-01	1.00E+00	6.88E-01	1.00E+00	2.11E-01	1.00E+00	1.39E-01	1.00E+00	7.24E-01	1.00E+00	smooth muscle cell proliferation	P
GO:0048660	28	2.20E-01	1.00E+00	3.26E-01	1.00E+00	8.54E-02	1.00E+00	2.76E-01	1.00E+00	7.03E-01	1.00E+00	2.57E-01	1.00E+00	1.69E-01	1.00E+00	5.68E-01	1.00E+00	regulation of smooth muscle cell proliferatio	P
GO:0048661	19	1.17E-01	1.00E+00	4.73E-01	1.00E+00	4.41E-02	1.00E+00	2.81E-01	1.00E+00	4.38E-01	1.00E+00	4.36E-01	1.00E+00	1.17E-01	1.00E+00	6.11E-01	1.00E+00	positive regulation of smooth muscle cell pr	P
GO:0048663	35	9.50E-01	1.00E+00	9.65E-01	1.00E+00	9.94E-01	1.00E+00	8.82E-01	1.00E+00	9.79E-01	1.00E+00	9.87E-01	1.00E+00	3.86E-01	1.00E+00	7.96E-01	1.00E+00	neuron fate commitment	P
GO:0048665	13	9.58E-01	1.00E+00	9.92E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.67E-01	1.00E+00	3.32E-01	1.00E+00	9.12E-01	1.00E+00	neuron fate specification	P
GO:0048666	268	3.70E-01	1.00E+00	4.98E-01	1.00E+00	8.23E-01	1.00E+00	8.28E-01	1.00E+00	2.50E-01	1.00E+00	6.61E-01	1.00E+00	2.34E-01	1.00E+00	8.60E-02	1.00E+00	neuron development	P
GO:0048667	196	4.20E-01	1.00E+00	5.00E-01	1.00E+00	8.07E-01	1.00E+00	8.09E-01	1.00E+00	2.23E-01	1.00E+00	6.07E-01	1.00E+00	3.34E-01	1.00E+00	1.11E-01	1.00E+00	neuron morphogenesis during differentiatio	P
GO:0048675	25	7.87E-02	1.00E+00	3.28E-01	1.00E+00	1.97E-01	1.00E+00	2.31E-01	1.00E+00	1.18E-01	1.00E+00	5.97E-01	1.00E+00	3.16E-01	1.00E+00	2.12E-01	1.00E+00	axon extension	P
GO:0048699	407	2.72E-01	1.00E+00	4.05E-01	1.00E+00	8.80E-01	1.00E+00	6.93E-01	1.00E+00	2.32E-01	1.00E+00	7.25E-01	1.00E+00	6.89E-02	1.00E+00	4.22E-02	1.00E+00	generation of neurons	P
GO:0048701	14	3.88E-01	1.00E+00	9.76E-01	1.00E+00	5.09E-01	1.00E+00	9.87E-01	1.00E+00	7.76E-01	1.00E+00	9.09E-01	1.00E+00	1.31E-01	1.00E+00	8.59E-01	1.00E+00	embryonic cranial skeleton morphogenesis	P
GO:0048704	51	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	embryonic skeletal morphogenesis	P
GO:0048705	64	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	skeletal morphogenesis	P
GO:0048706	67	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	embryonic skeletal development	P
GO:0048709	20	5.93E-01	1.00E+00	6.40E-01	1.00E+00	9.82E-02	1.00E+00	6.69E-01	1.00E+00	9.30E-01	1.00E+00	4.25E-01	1.00E+00	7.84E-01	1.00E+00	7.47E-01	1.00E+00	oligodendrocyte differentiation	P
GO:0048729	115	1.28E-01	1.00E+00	1.74E-01	1.00E+00	1.13E-01	1.00E+00	3.70E-01	1.00E+00	4.91E-01	1.00E+00	9.85E-02	1.00E+00	1.19E-01	1.00E+00	2.06E-01	1.00E+00	tissue morphogenesis	P
GO:0048730	78	6.44E-01	1.00E+00	8.28E-01	1.00E+00	7.56E-01	1.00E+00	9.01E-01	1.00E+00	7.29E-01	1.00E+00	6.77E-01	1.00E+00	3.63E-01	1.00E+00	6.14E-01	1.00E+00	epidermis morphogenesis	P
GO:0048731	834	2.16E-01	1.00E+00	3.31E-01	1.00E+00	8.07E-01	1.00E+00	8.14E-01	1.00E+00	4.89E-01	1.00E+00	6.13E-01	1.00E+00	2.03E-03	8.40E-02	1.65E-02	6.56E-01	system development	P
GO:0048732	90	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	9.18E-01	1.00E+00	9.83E-01	1.00E+00	gland development	P
GO:0048736	92	8.62E-01	1.00E+00	9.47E-01	1.00E+00	8.24E-01	1.00E+00	9.83E-01	1.00E+00	9.04E-01	1.00E+00	8.85E-01	1.00E+00	6.89E-01	1.00E+00	6.97E-01	1.00E+00	appendage development	P
GO:0048738	14	4.63E-01	1.00E+00	1.09E-01	1.00E+00	6.91E-01	1.00E+00	2.80E-01	1.00E+00	9.21E-01	1.00E+00	6.93E-02	1.00E+00	1.10E-01	1.00E+00	1.74E-01	1.00E+00	cardiac muscle development	P
GO:0048741	76	5.53E-01	1.00E+00	2.08E-01	1.00E+00	6.81E-01	1.00E+00	2.26E-01	1.00E+00	9.08E-01	1.00E+00	5.00E-01	1.00E+00	7.14E-02	1.00E+00	1.59E-01	1.00E+00	skeletal muscle fiber development	P
GO:0048747	76	5.53E-01	1.00E+00	2.08E-01	1.00E+00	6.81E-01	1.00E+00	2.26E-01	1.00E+00	9.08E-01	1.00E+00	5.00E-01	1.00E+00	7.14E-02	1.00E+00	1.59E-01	1.00E+00	muscle fiber development	P
GO:0048754	67	7.87E-01	1.00E+00	9.37E-01	1.00E+00	9.57E-01	1.00E+00	9.94E-01	1.00E+00	9.43E-01	1.00E+00	9.90E-01	1.00E+00	1.17E-01	1.00E+00	2.07E-01	1.00E+00	branching morphogenesis of a tube	P
GO:0048762	45	9.20E-01	1.00E+00	9.29E-01	1.00E+00	7.22E-01	1.00E+00	9.11E-01	1.00E+00	9.80E-01	1.00E+00	8.37E-01	1.00E+00	6.17E-01	1.00E+00	8.72E-01	1.00E+00	mesenchymal cell differentiation	P
GO:0048770	75	8.03E-10	2.57E-03	4.33E-12	0.00E+00	9.73E-07	2.00E-03	4.60E-08	2.89E-03	2.39E-06	1.69E-03	2.84E-06	2.90E-03	1.49E-06	8.23E-04	1.01E-07	9.38E-04	pigment granule	C
GO:0048771	184	5.97E-02	1.00E+00	2.47E-01	1.00E+00	5.58E-01	1.00E+00	5.24E-01	1.00E+00	5.51E-02	1.00E+00	4.28E-01	1.00E+00	3.28E-02	8.38E-01	4.98E-02	1.00E+00	tissue remodeling	P
GO:0048806	18	7.69E-01	1.00E+00	8.07E-01	1.00E+00	9.35E-01	1.00E+00	8.01E-01	1.00E+00	5.31E-01	1.00E+00	9.99E-01	1.00E+00	5.17E-01	1.00E+00	1.91E-01	1.00E+00	genitalia development	P
GO:0048812	195	4.14E-01	1.00E+00	5.17E-01	1.00E+00	7.86E-01	1.00E+00	8.23E-01	1.00E+00	2.42E-01	1.00E+00	6.10E-01	1.00E+00	3.30E-01	1.00E+00	1.32E-01	1.00E+00	neurite morphogenesis	P
GO:0048813	15	3.77E-02	1.00E+00	2.09E-01	1.00E+00	1.22E-01	1.00E+00	3.39E-01	1.00E+00	6.48E-02	1.00E+00	2.66E-01	1.00E+00	1.21E-01	1.00E+00	2.54E-01	1.00E+00	dendrite morphogenesis	P
GO:0048820	16	4.92E-01	1.00E+00	9.69E-02	1.00E+00	6.37E-01	1.00E+00	3.04E-01	1.00E+00	7.03E-01	1.00E+00	7.81E-02	1.00E+00	1.81E-01	1.00E+00	1.22E-01	1.00E+00	hair follicle maturation	P
GO:0048821	15	1.19E-02	6.08E-01	4.38E-02	1.00E+00	4.58E-02	1.00E+00	5.48E-02	1.00E+00	2.52E-01	1.00E+00	9.33E-02	1.00E+00	2.62E-02	8.38E-01	1.21E-01	1.00E+00	erythrocyte development	P
GO:0048839	64	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.65E-01	1.00E+00	9.71E-01	1.00E+00	9.57E-01	1.00E+00	9.43E-01	1.00E+00	inner ear development	P
GO:0048844	10	2.30E-01	1.00E+00	5.49E-01	1.00E+00	9.46E-01	1.00E+00	7.00E-01	1.00E+00	1.15E-01	1.00E+00	4.37E-01	1.00E+00	1.54E-01	1.00E+00	9.18E-01	1.00E+00	artery morphogenesis	P
GO:0048854	13	3.77E-01	1.00E+00	8.84E-03	4.69E-01	4.36E-01	1.00E+00	6.36E-02	1.00E+00	4.72E-01	1.00E+00	9.17E-03	5.03E-01	4.07E-01	1.00E+00	1.41E-01	1.00E+00	brain morphogenesis	P
GO:0048856	2152	1.83E-08	2.57E-03	1.80E-07	3.92E-03	7.25E-04	4.90E-02	1.85E-04	1.30E-02	1.01E-03	1.20E-01	6.51E-03	4.21E-01	3.55E-10	0.00E+00	8.82E-10	0.00E+00	anatomical structure development	P
GO:0048858	195	4.14E-01	1.00E+00	5.17E-01	1.00E+00	7.86E-01	1.00E+00	8.23E-01	1.00E+00	2.42E-01	1.00E+00	6.10E-01	1.00E+00	3.30E-01	1.00E+00	1.32E-01	1.00E+00	cell projection morphogenesis	P
GO:0050136	41	1.14E-01	1.00E+00	4.33E-01	1.00E+00	1.97E-01	1.00E+00	6.70E-01	1.00E+00	1.34E-01	1.00E+00	2.10E-01	1.00E+00	3.27E-01	1.00E+00	5.35E-01	1.00E+00	NADH dehydrogenase (quinone) activity	F
GO:0050381	36	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	unspecific monooxygenase activity	F
GO:0050432	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	9.78E-01	1.00E+00	catecholamine secretion	P
GO:0050435	10	1.12E-01	1.00E+00	7.10E-01	1.00E+00	1.03E-01	1.00E+00	4.48E-01	1.00E+00	1.82E-01	1.00E+00	6.56E-01	1.00E+00	4.15E-01	1.00E+00	9.85E-01	1.00E+00	beta-amyloid metabolism	P
GO:0050650	11	8.33E-01	1.00E+00	5.92E-01	1.00E+00	9.95E-01	1.00E+00	1.81E-01	1.00E+00	9.63E-01	1.00E+00	9.93E-01	1.00E+00	2.73E-01	1.00E+00	5.69E-01	1.00E+00	chondroitin sulfate proteoglycan biosynthes	P
GO:0050654	11	8.33E-01	1.00E+00	5.92E-01	1.00E+00	9.95E-01	1.00E+00	1.81E-01	1.00E+00	9.63E-01	1.00E+00	9.93E-01	1.00E+00	2.73E-01	1.00E+00	5.69E-01	1.00E+00	chondroitin sulfate proteoglycan metabolism	P
GO:0050657	60	3.49E-06	3.02E-03	1.39E-09	8.90E-04	2.08E-05	3.00E-03	3.30E-09	0.00E+00	2.07E-05	5.37E-03	3.79E-05	9.66E-03	2.62E-01	1.00E+00	1.17E-03	6.00E-02	nucleic acid transport	P
GO:0050658	60	3.49E-06	3.02E-03	1.39E-09	8.90E-04	2.08E-05	3.00E-03	3.30E-09	0.00E+00	2.07E-05	5.37E-03	3.79E-05	9.66E-03	2.62E-01	1.00E+00	1.17E-03	6.00E-02	RNA transport	P
GO:0050660	83	1.66E-01	1.00E+00	3.79E-01	1.00E+00	3.19E-01	1.00E+00	5.74E-01	1.00E+00	2.05E-01	1.00E+00	1.59E-01	1.00E+00	1.31E-01	1.00E+00	5.83E-01	1.00E+00	FAD binding	F
GO:0050661	30	4.66E-01	1.00E+00	8.24E-01	1.00E+00	6.52E-01	1.00E+00	7.28E-01	1.00E+00	4.27E-01	1.00E+00	7.01E-01	1.00E+00	3.37E-01	1.00E+00	6.68E-01	1.00E+00	NADP binding	F
GO:0050662	219	5.86E-03	3.09E-01	1.35E-01	1.00E+00	5.60E-02	1.00E+00	2.97E-01	1.00E+00	3.76E-02	1.00E+00	7.42E-02	1.00E+00	1.03E-02	2.75E-01	2.61E-01	1.00E+00	coenzyme binding	F
GO:0050663	21	6.23E-01	1.00E+00	4.49E-01	1.00E+00	5.29E-01	1.00E+00	8.17E-01	1.00E+00	6.21E-01	1.00E+00	1.80E-01	1.00E+00	6.20E-01	1.00E+00	5.09E-01	1.00E+00	cytokine secretion	P
GO:0050670	70	9.13E-01	1.00E+00	9.34E-02	1.00E+00	9.91E-01	1.00E+00	2.02E-01	1.00E+00	9.36E-01	1.00E+00	5.67E-01	1.00E+00	3.24E-01	1.00E+00	1.59E-02	6.56E-01	regulation of lymphocyte proliferation	P
GO:0050671	48	8.73E-01	1.00E+00	2.74E-02	1.00E+00	9.96E-01	1.00E+00	1.26E-01	1.00E+00	8.72E-01	1.00E+00	3.04E-01	1.00E+00	2.51E-01	1.00E+00	6.12E-03	4.28E-01	positive regulation of lymphocyte proliferatic	P
GO:0050672	25	7.97E-01	1.00E+00	3.43E-01	1.00E+00	8.51E-01	1.00E+00	3.69E-01	1.00E+00	7.59E-01	1.00E+00	3.95E-01	1.00E+00	4.99E-01	1.00E+00	2.01E-01	1.00E+00	negative regulation of lymphocyte proliferati	P
GO:0050673	54	6.84E-01	1.00E+00	8.85E-01	1.00E+00	6.81E-01	1.00E+00	9.81E-01	1.00E+00	5.64E-01	1.00E+00	8.20E-01	1.00E+00	4.69E-01	1.00E+00	2.34E-01	1.00E+00	epithelial cell proliferation	P
GO:0050678	45	9.27E-01	1.00E+00	9.87E-01	1.00E+00	9.21E-01	1.00E+00	9.96E-01	1.00E+00	8.36E-01	1.00E+00	9.58E-01	1.00E+00	6.61E-01	1.00E+00	4.77E-01	1.00E+00	regulation of epithelial cell proliferation	P
GO:0050679	24	7.09E-01	1.00E+00	9.81E-01	1.00E+00	6.40E-01	1.00E+00	9.95E-01	1.00E+00	7.32E-01	1.00E+00	9.39E-01	1.00E+00	7.22E-01	1.00E+00	3.19E-01	1.00E+00	positive regulation of epithelial cell proliferat	P
GO:0050680	18	9.50E-01	1.00E+00	8.87E-01	1.00E+00	9.32E-01	1.00E+00	7.64E-01	1.00E+00	9.47E-01	1.00E+00	9.26E-01	1.00E+00	4.14E-01	1.00E+00	6.37E-01	1.00E+00	negative regulation of epithelial cell prolifera	P
GO:0050707	18	4.57E-01	1.00E+00	4.58E-01	1.00E+00	3.54E-01	1.00E+00	8.32E-01	1.00E+00	5.56E-01	1.00E+00	2.46E-01	1.00E+00	5.07E-01	1.00E+00	4.95E-01	1.00E+00	regulation of cytokine secretion	P
GO:0050708	32	5.94E-01	1.00E+00	6.07E-01	1.00E+00	6.35E-01	1.00E+00	9.27E-01	1.00E+00	5.94E-01	1.00E+00	5.50E-01	1.00E+00	5.84E-01	1.00E+00	3.17E-01	1.00E+00	regulation of protein secretion	P
GO:0050709	10	7.11E-02	1.00E+00	2.90E-01	1.00E+00	2.90E-01	1.00E+00	5.87E-01	1.00E+00	3.49E-03	2.13E-01	9.05E-02	1.00E+00	4.47E-01	1.00E+00	6.14E-01	1.00E+00	negative regulation of protein secretion	P
GO:0050714	16	6.38E-01	1.00E+00	9.12E-01	1.00E+00	7.04E-01	1.00E+00	9.97E-01	1.00E+00	8.79E-01	1.00E+00	7.60E-01	1.00E+00	3.58E-01	1.00E+00	4.88E-01	1.00E+00	positive regulation of protein secretion	P
GO:0050715	12	7.01E-01	1.00E+00	8.45E-01	1.00E+00	4.80E-01	1.00E+00	9.63E-01	1.00E+00	8.61E-01	1.00E+00	6.32E-01	1.00E+00	6.50E-01	1.00E+00	6.29E-01	1.00E+00	positive regulation of cytokine secretion	P
GO:0050727	39	7.96E-01	1.00E+00	2.60E-01	1.00E+00	8.29E-01	1.00E+00	4.08E-01	1.00E+00	7.56E-01	1.00E+00	6.87E-01	1.00E+00	7.11E-01	1.00E+00	8.93E-03	4.28E-01	regulation of inflammatory response	P
GO:0050728	16	4.76E-01	1.00E+00	1.13E-01	1.00E+00	4.51E-01	1.00E+00	3.03E-01	1.00E+00	7.16E-01	1.00E+00	5.72E-01	1.00E+00	3.45E-01	1.00E+00	1.18E-03	6.00E-02	negative regulation of inflammatory respons	P
GO:0050729	17	9.94E-01	1.00E+00	5.91E-01	1.00E+00	9.99E-01	1.00E+00	5.76E-01	1.00E+00	9.26E-01	1.00E+00	6.78E-01	1.00E+00	8.69E-01	1.00E+00	4.08E-01	1.00E+00	positive regulation of inflammatory respons	P
GO:0050730	48	9.98E-01	1.00E+00	5.28E-01	1.00E+00	9.95E-01	1.00E+00	8.54E-01	1.00E+00	9.99E-01	1.00E+00	6.74E-01	1.00E+00	7.04E-01	1.00E+00	5.00E-02	1.00E+00	regulation of peptidyl-tyrosine phosphorylati	P
GO:0050731	30	8.78E-01	1.00E+00	2.06E-01	1.00E+00	9.30E-01	1.00E+00	4.20E-01	1.00E+00	9.32E-01	1.00E+00	3.85E-01	1.00E+00	3.85E-01	1.00E+00	3.87E-02	1.00E+00	positive regulation of peptidyl-tyrosine phos	P
GO:0050750	12	1.73E-01	1.00E+00	2.52E-01	1.00E+00	1.97E-01	1.00E+00	3.09E-01	1.00E+00	3.49E-01	1.00E+00	3.18E-01	1.00E+00	3.61E-01	1.00E+00	1.68E-01	1.00E+00	low-density lipoprotein receptor binding	F
GO:0050764	22	9.98E-01	1.00E+00	6.65E-01	1.00E+00	9.53E-01	1.00E+00	8.41E-01	1.00E+00	1.00E+00	1.00E+00	7.72E-01	1.00E+00	9.98E-01	1.00E+00	3.20E-01	1.00E+00	regulation of phagocytosis	P
GO:0050766	20	1.00E+00	1.00E+00	8.07E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	3.30E-01	1.00E+00	positive regulation of phagocytosis	P

GO:0050767	63	5.79E-02	1.00E+00	3.94E-03	1.88E-01	3.79E-01	1.00E+00	9.24E-02	1.00E+00	1.23E-01	1.00E+00	1.03E-02	5.03E-01	6.87E-02	1.00E+00	1.22E-02	4.76E-01	regulation of neurogenesis	P
GO:0050768	26	4.59E-04	4.40E-02	2.51E-05	7.00E-03	2.53E-02	1.00E+00	1.83E-03	1.24E-01	1.65E-02	6.92E-01	1.31E-03	9.00E-02	1.07E-02	2.75E-01	1.68E-02	6.56E-01	negative regulation of neurogenesis	P
GO:0050769	23	2.74E-01	1.00E+00	4.75E-02	1.00E+00	6.84E-01	1.00E+00	2.14E-01	1.00E+00	1.17E-01	1.00E+00	1.09E-01	1.00E+00	4.73E-01	1.00E+00	4.26E-02	1.00E+00	positive regulation of neurogenesis	P
GO:0050770	36	3.90E-01	1.00E+00	1.40E-01	1.00E+00	8.28E-01	1.00E+00	4.31E-01	1.00E+00	4.98E-01	1.00E+00	3.56E-01	1.00E+00	2.61E-01	1.00E+00	2.78E-02	9.99E-01	regulation of axonogenesis	P
GO:0050771	13	1.11E-02	6.08E-01	2.34E-03	1.71E-01	1.70E-01	1.00E+00	8.44E-02	1.00E+00	6.54E-02	1.00E+00	2.54E-02	1.00E+00	6.63E-02	1.00E+00	3.61E-02	1.00E+00	negative regulation of axonogenesis	P
GO:0050772	14	5.91E-01	1.00E+00	3.12E-01	1.00E+00	8.20E-01	1.00E+00	4.00E-01	1.00E+00	5.50E-01	1.00E+00	4.60E-01	1.00E+00	5.69E-01	1.00E+00	2.07E-01	1.00E+00	positive regulation of axonogenesis	P
GO:0050776	124	5.15E-01	1.00E+00	4.78E-01	1.00E+00	6.65E-01	1.00E+00	5.89E-01	1.00E+00	9.55E-01	1.00E+00	6.89E-01	1.00E+00	1.15E-01	1.00E+00	1.69E-01	1.00E+00	regulation of immune response	P
GO:0050777	12	9.42E-02	1.00E+00	1.83E-01	1.00E+00	6.21E-02	1.00E+00	5.68E-02	1.00E+00	2.27E-01	1.00E+00	4.86E-01	1.00E+00	3.08E-01	1.00E+00	1.39E-01	1.00E+00	negative regulation of immune response	P
GO:0050778	104	5.91E-01	1.00E+00	6.71E-01	1.00E+00	8.00E-01	1.00E+00	7.83E-01	1.00E+00	9.54E-01	1.00E+00	5.98E-01	1.00E+00	1.81E-01	1.00E+00	5.68E-01	1.00E+00	positive regulation of immune response	P
GO:0050789	4618	8.55E-44	0.00E+00	0.00E+00	0.00E+00	1.10E-35	0.00E+00	0.00E+00	0.00E+00	4.37E-27	0.00E+00	6.62E-39	0.00E+00	8.33E-17	0.00E+00	3.34E-26	0.00E+00	regulation of biological process	P
GO:0050790	419	5.41E-10	2.57E-03	2.90E-13	0.00E+00	1.66E-07	2.00E-03	1.11E-09	0.00E+00	1.58E-05	5.00E-03	5.51E-09	8.78E-04	2.04E-06	8.23E-04	2.32E-08	0.00E+00	regulation of catalytic activity	P
GO:0050791	4014	2.47E-39	0.00E+00	0.00E+00	0.00E+00	4.66E-34	0.00E+00	0.00E+00	0.00E+00	7.51E-24	0.00E+00	8.80E-35	0.00E+00	1.22E-14	0.00E+00	7.26E-21	0.00E+00	regulation of physiological process	P
GO:0050792	11	6.38E-02	1.00E+00	2.78E-01	1.00E+00	3.85E-01	1.00E+00	3.86E-01	1.00E+00	3.64E-01	1.00E+00	4.33E-01	1.00E+00	8.27E-03	2.75E-01	1.94E-01	1.00E+00	regulation of viral life cycle	P
GO:0050793	292	1.33E-01	1.00E+00	1.83E-01	1.00E+00	2.43E-01	1.00E+00	5.06E-01	1.00E+00	6.03E-01	1.00E+00	4.30E-01	1.00E+00	1.55E-02	4.88E-01	2.11E-02	9.99E-01	regulation of development	P
GO:0050794	4109	1.82E-38	0.00E+00	0.00E+00	0.00E+00	1.69E-32	0.00E+00	0.00E+00	0.00E+00	1.67E-23	0.00E+00	8.03E-35	0.00E+00	1.48E-14	0.00E+00	3.97E-23	0.00E+00	regulation of cellular process	P
GO:0050796	17	6.77E-02	1.00E+00	5.48E-02	1.00E+00	1.31E-01	1.00E+00	1.54E-01	1.00E+00	1.80E-01	1.00E+00	1.90E-01	1.00E+00	1.25E-02	4.24E-01	2.57E-02	9.99E-01	regulation of insulin secretion	P
GO:0050798	16	3.17E-01	1.00E+00	5.15E-03	2.79E-01	4.42E-01	1.00E+00	3.76E-02	1.00E+00	7.66E-01	1.00E+00	2.39E-02	1.00E+00	7.54E-02	1.00E+00	1.76E-03	7.90E-02	activated T cell proliferation	P
GO:0050801	193	5.03E-02	1.00E+00	1.43E-02	6.07E-01	4.00E-01	1.00E+00	6.21E-02	1.00E+00	1.71E-01	1.00E+00	4.45E-02	1.00E+00	1.56E-02	4.88E-01	3.13E-02	9.99E-01	ion homeostasis	P
GO:0050803	73	7.55E-01	1.00E+00	3.43E-01	1.00E+00	7.51E-01	1.00E+00	5.87E-01	1.00E+00	9.42E-01	1.00E+00	1.05E-01	1.00E+00	3.09E-01	1.00E+00	4.34E-01	1.00E+00	regulation of synapse structure and functior	P
GO:0050804	69	7.89E-01	1.00E+00	5.06E-01	1.00E+00	7.27E-01	1.00E+00	6.70E-01	1.00E+00	9.65E-01	1.00E+00	1.78E-01	1.00E+00	4.08E-01	1.00E+00	6.53E-01	1.00E+00	regulation of synaptic transmission	P
GO:0050805	10	9.99E-01	1.00E+00	9.04E-01	1.00E+00	1.00E+00	1.00E+00	8.16E-01	1.00E+00	9.50E-01	1.00E+00	8.44E-01	1.00E+00	9.27E-01	1.00E+00	8.88E-01	1.00E+00	negative regulation of synaptic transmissior	P
GO:0050806	14	1.94E-01	1.00E+00	1.40E-01	1.00E+00	1.27E-01	1.00E+00	3.12E-01	1.00E+00	6.25E-01	1.00E+00	1.74E-02	6.68E-01	1.42E-02	4.78E-01	4.48E-01	1.00E+00	positive regulation of synaptic transmission	P
GO:0050808	33	9.91E-01	1.00E+00	5.81E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.99E-01	1.00E+00	8.15E-01	1.00E+00	4.25E-01	1.00E+00	3.99E-02	1.00E+00	synapse organization and biogenesis	P
GO:0050817	130	7.40E-01	1.00E+00	3.88E-01	1.00E+00	8.27E-01	1.00E+00	7.57E-01	1.00E+00	8.38E-01	1.00E+00	1.83E-01	1.00E+00	4.83E-01	1.00E+00	3.85E-01	1.00E+00	coagulation	P
GO:0050818	27	2.91E-01	1.00E+00	1.37E-01	1.00E+00	5.14E-01	1.00E+00	6.11E-01	1.00E+00	2.58E-01	1.00E+00	8.32E-02	1.00E+00	2.64E-01	1.00E+00	1.55E-01	1.00E+00	regulation of coagulation	P
GO:0050819	19	2.98E-01	1.00E+00	2.46E-01	1.00E+00	5.07E-01	1.00E+00	8.67E-01	1.00E+00	3.86E-01	1.00E+00	8.30E-02	1.00E+00	1.65E-01	1.00E+00	1.94E-01	1.00E+00	negative regulation of coagulation	P
GO:0050821	14	1.44E-01	1.00E+00	6.32E-02	1.00E+00	1.08E-01	1.00E+00	1.03E-01	1.00E+00	2.10E-01	1.00E+00	9.96E-02	1.00E+00	3.27E-01	1.00E+00	9.09E-02	1.00E+00	protein stabilization	P
GO:0050824	191	1.61E-01	1.00E+00	2.05E-01	1.00E+00	8.83E-02	1.00E+00	1.37E-01	1.00E+00	4.03E-01	1.00E+00	3.50E-01	1.00E+00	1.60E-01	1.00E+00	2.89E-01	1.00E+00	water binding	F
GO:0050825	191	1.61E-01	1.00E+00	2.05E-01	1.00E+00	8.83E-02	1.00E+00	1.37E-01	1.00E+00	4.03E-01	1.00E+00	3.50E-01	1.00E+00	1.60E-01	1.00E+00	2.89E-01	1.00E+00	ice binding	F
GO:0050826	191	1.61E-01	1.00E+00	2.05E-01	1.00E+00	8.83E-02	1.00E+00	1.37E-01	1.00E+00	4.03E-01	1.00E+00	3.50E-01	1.00E+00	1.60E-01	1.00E+00	2.89E-01	1.00E+00	response to freezing	P
GO:0050830	12	7.14E-02	1.00E+00	2.15E-01	1.00E+00	1.46E-01	1.00E+00	9.67E-01	1.00E+00	1.67E-01	1.00E+00	2.59E-01	1.00E+00	6.50E-02	1.00E+00	1.24E-01	1.00E+00	defense response to Gram-positive bacteriu	P
GO:0050839	15	7.91E-01	1.00E+00	1.53E-01	1.00E+00	8.22E-01	1.00E+00	4.27E-01	1.00E+00	5.78E-01	1.00E+00	2.95E-02	1.00E+00	8.89E-01	1.00E+00	6.31E-01	1.00E+00	cell adhesion molecule binding	F
GO:0050848	13	2.93E-01	1.00E+00	1.55E-01	1.00E+00	4.03E-01	1.00E+00	5.07E-01	1.00E+00	3.61E-01	1.00E+00	2.18E-01	1.00E+00	1.58E-01	1.00E+00	2.73E-02	9.99E-01	regulation of calcium-mediated signaling	P
GO:0050850	12	4.86E-01	1.00E+00	1.58E-01	1.00E+00	5.08E-01	1.00E+00	5.45E-01	1.00E+00	7.94E-01	1.00E+00	1.49E-01	1.00E+00	1.86E-01	1.00E+00	5.33E-02	1.00E+00	positive regulation of calcium-mediated sigr	P
GO:0050851	35	5.38E-01	1.00E+00	2.09E-01	1.00E+00	4.12E-01	1.00E+00	6.41E-01	1.00E+00	8.12E-01	1.00E+00	2.71E-02	1.00E+00	4.14E-01	1.00E+00	5.06E-01	1.00E+00	antigen receptor-mediated signaling pathwa	P
GO:0050852	23	6.37E-01	1.00E+00	2.16E-01	1.00E+00	5.16E-01	1.00E+00	7.41E-01	1.00E+00	7.48E-01	1.00E+00	3.99E-02	1.00E+00	5.24E-01	1.00E+00	4.27E-01	1.00E+00	T cell receptor signaling pathway	P
GO:0050853	14	4.62E-01	1.00E+00	1.97E-01	1.00E+00	2.78E-01	1.00E+00	1.33E-01	1.00E+00	7.36E-01	1.00E+00	2.66E-01	1.00E+00	4.45E-01	1.00E+00	1.99E-01	1.00E+00	B cell receptor signaling pathway	P
GO:0050854	12	5.15E-01	1.00E+00	5.59E-01	1.00E+00	4.00E-01	1.00E+00	6.23E-01	1.00E+00	7.22E-01	1.00E+00	4.64E-01	1.00E+00	3.52E-01	1.00E+00	4.79E-01	1.00E+00	regulation of antigen receptor-mediated sigi	P
GO:0050856	10	3.52E-01	1.00E+00	5.08E-01	1.00E+00	2.77E-01	1.00E+00	5.81E-01	1.00E+00	5.46E-01	1.00E+00	3.75E-01	1.00E+00	2.72E-01	1.00E+00	6.19E-01	1.00E+00	regulation of T cell receptor signaling pathw	P
GO:0050863	75	2.48E-01	1.00E+00	9.54E-04	8.70E-02	3.49E-01	1.00E+00	6.54E-02	1.00E+00	7.94E-01	1.00E+00	1.45E-02	6.68E-01	2.51E-02	8.38E-01	4.41E-04	3.00E-02	regulation of T cell activation	P
GO:0050864	49	5.30E-01	1.00E+00	2.13E-01	1.00E+00	9.18E-01	1.00E+00	1.97E-01	1.00E+00	5.43E-01	1.00E+00	9.75E-01	1.00E+00	2.23E-01	1.00E+00	2.63E-02	9.99E-01	regulation of B cell activation	P
GO:0050868	21	6.58E-01	1.00E+00	1.40E-01	1.00E+00	6.30E-01	1.00E+00	2.69E-01	1.00E+00	7.06E-01	1.00E+00	9.65E-02	1.00E+00	2.84E-01	1.00E+00	1.56E-01	1.00E+00	negative regulation of T cell activation	P
GO:0050869	14	9.95E-01	1.00E+00	4.97E-01	1.00E+00	9.66E-01	1.00E+00	3.64E-01	1.00E+00	9.84E-01	1.00E+00	5.41E-01	1.00E+00	9.32E-01	1.00E+00	4.84E-01	1.00E+00	negative regulation of B cell activation	P
GO:0050870	53	1.70E-01	1.00E+00	1.34E-03	9.65E-02	4.07E-01	1.00E+00	9.87E-02	1.00E+00	6.48E-01	1.00E+00	8.78E-03	5.03E-01	1.63E-02	4.88E-01	1.83E-03	7.90E-02	positive regulation of T cell activation	P
GO:0050871	34	5.26E-01	1.00E+00	3.20E-01	1.00E+00	9.11E-01	1.00E+00	3.85E-01	1.00E+00	4.20E-01	1.00E+00	1.00E+00	1.00E+00	2.61E-01	1.00E+00	4.05E-02	1.00E+00	positive regulation of B cell activation	P
GO:0050874	2260	9.43E-01	1.00E+00	8.56E-01	1.00E+00	9.93E-01	1.00E+00	9.73E-01	1.00E+00	9.97E-01	1.00E+00	9.10E-01	1.00E+00	6.12E-02	1.00E+00	1.11E-01	1.00E+00	organismal physiological process	P
GO:0050875	11363	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.55E-43	0.00E+00	0.00E+00	0.00E+00	cellular physiological process	P
GO:0050876	116	5.80E-01	1.00E+00	8.70E-01	1.00E+00	7.33E-01	1.00E+00	9.68E-01	1.00E+00	3.66E-01	1.00E+00	8.00E-01	1.00E+00	5.64E-01	1.00E+00	4.97E-01	1.00E+00	reproductive physiological process	P
GO:0050877	675	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	9.87E-01	1.00E+00	neurophysiological process	P
GO:0050878	141	5.98E-01	1.00E+00	6.57E-01	1.00E+00	7.99E-01	1.00E+00	7.02E-01	1.00E+00	8.94E-01	1.00E+00	4.73E-01	1.00E+00	1.72E-01	1.00E+00	7.77E-01	1.00E+00	regulation of body fluids	P
GO:0050879	65	8.54E-01	1.00E+00	9.69E-01	1.00E+00	9.89E-01	1.00E+00	9.45E-01	1.00E+00	8.64E-01	1.00E+00	8.87E-01	1.00E+00	2.61E-01	1.00E+00	7.99E-01	1.00E+00	organismal movement	P
GO:0050880	53	9.53E-01	1.00E+00	9.01E-01	1.00E+00	9.55E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.66E-01	1.00E+00	1.93E-01	1.00E+00	1.85E-01	1.00E+00	regulation of blood vessel size	P
GO:0050881	44	5.31E-01	1.00E+00	7.65E-01	1.00E+00	9.87E-01	1.00E+00	7.93E-01	1.00E+00	4.18E-01	1.00E+00	7.74E-01	1.00E+00	8.68E-02	1.00E+00	3.08E-01	1.00E+00	musculoskeletal movement	P
GO:0050884	10	1.71E-01	1.00E+00	5.35E-01	1.00E+00	3.66E-01	1.00E+00	8.00E-01	1.00E+00	2.14E-01	1.00E+00	3.13E-01	1.00E+00	9.96E-02	1.00E+00	5.56E-01	1.00E+00	regulation of posture	P
GO:0050885	34	3.98E-01	1.00E+00	7.94E-01	1.00E+00	9.69E-01	1.00E+00	7.36E-01	1.00E+00	3.14E-01	1.00E+00	8.42E-01	1.00E+00	8.78E-02	1.00E+00	4.35E-01	1.00E+00	regulation of balance	P
GO:0050886	20	7.44E-01	1.00E+00	1.00E+00	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	7.91E-01	1.00E+00	1.00E+00	1.00E+00	4.12E-01	1.00E+00	9.47E-01	1.00E+00	endocrine physiological process	P
GO:0050892	13	8.83E-02	1.00E+00	1.26E-01	1.00E+00	9.96E-02	1.00E+00	2.02E-01	1.00E+00	2.77E-01	1.00E+00	1.72E-01	1.00E+00	4.31E-02	1.00E+00	1.80E-01	1.00E+00	intestinal absorption	P
GO:0050896	2308	1.43E-02	8.50E-01	1.17E-03	9.65E-02	1.52E-01	1.00E+00	9.73E-03	5.72E-01	2.06E-01	1.00E+00	1.98E-02	7.56E-01	1.34E-03	6.14E-02	1.19E-03	6.00E-02	response to stimulus	P
GO:0050897	13	8.54E-02	1.00E+00	6.00E-02	1.00E+00	7.19E-02	1.00E+00	8.80E-02	1.00E+00	2.86E-01	1.00E+00	5.18E-02	1.00E+00	7.90E-02	1.00E+00	7.39E-01	1.00E+00	cobalt ion binding	F
GO:0050900	48	2.22E-02	1.00E+00	6.00E-02	1.00E+00	1.36E-01	1.00E+00	2.22E-01	1.00E+00	1.03E-01	1.00E+00	6.72E-02	1.00E+00	6.21E-03	2.75E-01	2.86E-02	9.99E-01	leukocyte migration	P
GO:0050905	19	9.86E-01	1.00E+00	9.62E-01	1.00E+00	9.30E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	7.71E-01	1.00E+00	8.82E-01	1.00E+00	6.97E-01	1.00E+00	neuromuscular physiological process	P
GO:0050906	41	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	detection of stimulus during sensory percep	P
GO:0050907	22	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	detection of chemical stimulus during sensc	P
GO:0050909	52	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	sensory perception of taste	P
GO:0050912	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	detection of chemical stimulus during sensc	P
GO:0050913	22	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	sensory perception of bitter taste	P
GO:0050918	14	7.40E-01	1.00E+00	6.66E-01	1.00E+00	3.03E-01	1.00E+00	4.05E-01	1.00E+00	9.67E-01	1.00E+00	6.22E-01	1.00E+00	6.18E-01	1.00E+00	7.94E-01	1.00E+00	positive chemotaxis	P
GO:0050920	14	8.37E-01	1.00E+00	8.57E-01	1.00E+00	5.97E-01	1.00E+00	8.43E-01	1.00E+00	9.46E-01	1.00E+00	5.97E-01	1.00E+00	6.97E-01	1.00E+00	6.26E-01	1.00E+00	regulation of chemotaxis	P
GO:0050921	14	8.37E-01	1.00E+00	8.57E-01	1.00E+00	5.97E-01	1.00E+00	8.43E-01	1.00E+00	9.46E-01	1.00E+00	5.97E-01	1.00E+00	6.97E-01	1.00E+00	6.26E-01	1.00E+00	positive regulation of chemotaxis	P
GO:0050926	12	8.07E-01	1.00E+00	9.38E-01	1.00E+00	4.53E-01	1.00E+00	8.01E-01	1.00E+00	9.59E-01	1.00E+00	6.94E-01	1.00E+00	5.90E-01	1.00E+00	7.91E-01	1.00E+00	regulation of positive chemotaxis	P
GO:0050927	12	8.07E-01	1.00E+00	9.38E-01	1.00E+00	4.53E-01	1.00E+00	8.01E-01	1.00E+00	9.59E-01	1.00E+00	6.94E-01	1.00E+00	5.90E-01	1.00E+00	7.91E-01	1.00E+00	positive regulation of positive chemotaxis	P
GO:0050930	10	8.13E-01	1.00E+00	8.44E-01	1.00E+00	5.68E-01	1.00E+00	7.07E-01	1.00E+00	8.91E-01	1.00E+00	5.06E-01	1.00E+00	6.35E-01	1.00E+00	8.51E-01	1.00E+00	induction of positive chemotaxis	P
GO:0050931	19	2.72E-01	1.00E+00	6.59E-01	1.00E+00	2.24E-01	1.00E+00	6.22E-01	1.00E+00	2.79E-01	1.00E+00	6.27E-01	1.00E+00	3.44E-01	1.00E+00	5.79E-01	1.00E+00	pigment cell differentiation	P
GO:0050953	123	7.31E-01	1.00E+00	7.05E-01	1.00E+00	5.32E-01	1.00E+00	7.32E-01	1.00E+00	9.33E-01	1.00E+00	5.25E-01	1.00E+00	5.50E-01	1.00E+00	8.38E-01	1.00E+00	sensory perception of light stimulus	P
GO:0050954	81	3.66E-01	1.00E+00	6.78E-02	1.00E+00	8.15E-01	1.00E+00	1.09E-01	1.00E+00	5.83E-01	1.00E+00	2.12E-01	1.00E+00	1.97E-02	6.36E-01	1.86E-02	7.36E-01	sensory perception of mechanical stimulus	P

GO:0050974	12	9.99E-01	1.00E+00	9.92E-01	1.00E+00	9.67E-01	1.00E+00	7.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	detection of mechanical stimulus during ser	P
GO:0050982	14	6.40E-01	1.00E+00	8.76E-01	1.00E+00	3.87E-01	1.00E+00	4.54E-01	1.00E+00	9.14E-01	1.00E+00	9.13E-01	1.00E+00	9.94E-01	1.00E+00	9.97E-01	1.00E+00	detection of mechanical stimulus	P
GO:0051015	41	1.75E-03	2.12E-01	1.88E-03	1.30E-01	2.49E-02	1.00E+00	8.79E-03	4.92E-01	1.20E-02	6.92E-01	3.18E-02	1.00E+00	1.68E-03	8.40E-02	2.30E-02	9.99E-01	actin filament binding	F
GO:0051016	18	2.19E-01	1.00E+00	1.09E-02	4.69E-01	6.28E-01	1.00E+00	9.50E-02	1.00E+00	3.84E-01	1.00E+00	4.53E-02	1.00E+00	1.68E-01	1.00E+00	1.62E-02	6.56E-01	barbed-end actin filament capping	P
GO:0051017	18	7.12E-03	3.15E-01	1.52E-03	9.65E-02	2.26E-02	1.00E+00	7.16E-03	4.92E-01	5.87E-02	1.00E+00	4.30E-02	1.00E+00	2.06E-03	8.40E-02	2.95E-04	3.00E-02	actin filament bundle formation	P
GO:0051020	66	9.14E-02	1.00E+00	2.75E-04	4.40E-02	3.28E-01	1.00E+00	2.84E-03	1.61E-01	2.50E-01	1.00E+00	8.42E-03	5.03E-01	4.38E-02	1.00E+00	1.46E-03	6.00E-02	GTPase binding	F
GO:0051028	55	6.90E-05	1.41E-02	2.00E-08	9.59E-04	1.14E-04	1.16E-02	2.16E-08	8.93E-04	1.83E-04	4.90E-02	9.46E-05	1.10E-02	4.80E-01	1.00E+00	7.10E-03	4.28E-01	mRNA transport	P
GO:0051046	90	5.39E-01	1.00E+00	2.44E-01	1.00E+00	8.22E-01	1.00E+00	7.68E-01	1.00E+00	7.95E-01	1.00E+00	4.27E-01	1.00E+00	9.73E-02	1.00E+00	3.01E-02	9.99E-01	regulation of secretion	P
GO:0051047	25	4.17E-01	1.00E+00	4.14E-01	1.00E+00	4.89E-01	1.00E+00	8.47E-01	1.00E+00	7.57E-01	1.00E+00	7.70E-01	1.00E+00	1.21E-01	1.00E+00	1.15E-01	1.00E+00	positive regulation of secretion	P
GO:0051048	28	4.51E-02	1.00E+00	4.93E-03	2.61E-01	1.93E-01	1.00E+00	3.09E-02	1.00E+00	1.40E-01	1.00E+00	4.80E-02	1.00E+00	2.55E-02	8.38E-01	2.48E-02	9.99E-01	negative regulation of secretion	P
GO:0051049	160	5.67E-02	1.00E+00	8.70E-05	1.50E-02	8.00E-02	1.00E+00	1.09E-03	9.40E-02	1.52E-01	1.00E+00	4.98E-03	2.66E-01	7.97E-02	1.00E+00	1.20E-03	6.00E-02	regulation of transport	P
GO:0051050	70	8.22E-01	1.00E+00	5.93E-02	1.00E+00	7.52E-01	1.00E+00	1.78E-01	1.00E+00	8.20E-01	1.00E+00	9.47E-02	1.00E+00	7.58E-01	1.00E+00	4.05E-02	1.00E+00	positive regulation of transport	P
GO:0051051	38	4.88E-03	2.72E-01	3.28E-03	1.88E-01	1.30E-03	7.90E-02	4.97E-03	2.88E-01	4.71E-02	1.00E+00	8.44E-03	5.03E-01	1.31E-01	1.00E+00	7.82E-02	1.00E+00	negative regulation of transport	P
GO:0051052	48	1.06E-04	1.43E-02	1.86E-06	3.92E-03	1.64E-03	9.50E-02	2.10E-04	1.30E-02	1.40E-03	1.20E-01	9.24E-06	5.87E-03	3.21E-02	8.38E-01	9.20E-03	4.28E-01	regulation of DNA metabolism	P
GO:0051053	18	1.00E-02	6.08E-01	5.60E-04	4.74E-02	2.05E-02	1.00E+00	5.68E-03	2.88E-01	4.02E-02	1.00E+00	7.23E-04	4.48E-02	2.07E-01	1.00E+00	3.30E-01	1.00E+00	negative regulation of DNA metabolism	P
GO:0051054	15	1.08E-01	1.00E+00	3.33E-02	1.00E+00	2.20E-01	1.00E+00	2.41E-01	1.00E+00	1.74E-01	1.00E+00	6.32E-02	1.00E+00	1.26E-01	1.00E+00	1.75E-02	6.56E-01	positive regulation of DNA metabolism	P
GO:0051056	170	4.51E-01	1.00E+00	5.60E-03	3.08E-01	8.77E-01	1.00E+00	4.51E-02	1.00E+00	6.12E-01	1.00E+00	2.59E-02	1.00E+00	9.49E-02	1.00E+00	1.16E-02	4.76E-01	regulation of small GTPase mediated signa	P
GO:0051057	12	9.51E-01	1.00E+00	4.89E-01	1.00E+00	1.00E+00	1.00E+00	8.31E-01	1.00E+00	7.28E-01	1.00E+00	4.53E-01	1.00E+00	6.12E-01	1.00E+00	3.70E-01	1.00E+00	positive regulation of small GTPase mediat	P
GO:0051059	23	4.43E-10	2.57E-03	7.08E-04	5.90E-02	4.33E-08	9.80E-04	1.86E-05	9.57E-03	9.00E-04	1.20E-01	1.35E-02	6.68E-01	3.04E-01	1.00E+00	5.49E-01	1.00E+00	NF-kappaB binding	F
GO:0051082	86	7.13E-07	2.76E-03	2.11E-09	8.90E-04	2.02E-05	3.00E-03	6.11E-09	8.93E-04	1.77E-05	5.37E-03	5.97E-05	9.66E-03	4.87E-03	2.23E-01	2.32E-04	2.33E-02	unfolded protein binding	F
GO:0051084	14	4.36E-03	2.14E-01	2.27E-05	7.00E-03	2.12E-02	1.00E+00	2.90E-04	4.20E-02	5.04E-02	1.00E+00	1.65E-03	1.22E-01	1.21E-01	1.00E+00	5.67E-01	1.00E+00	posttranslational protein folding	P
GO:0051085	12	1.65E-03	2.12E-01	2.85E-09	8.90E-04	4.86E-03	3.08E-01	1.54E-05	2.89E-03	4.50E-02	1.00E+00	7.06E-04	4.48E-02	1.43E-01	1.00E+00	3.47E-01	1.00E+00	chaperone cofactor-dependent protein foldi	P
GO:0051087	12	1.91E-03	2.12E-01	2.74E-03	1.88E-01	3.72E-03	2.20E-01	7.90E-03	4.92E-01	1.44E-02	6.92E-01	4.60E-02	1.00E+00	8.52E-02	1.00E+00	2.32E-01	1.00E+00	chaperone binding	F
GO:0051090	51	3.03E-03	2.12E-01	3.12E-05	7.00E-03	5.16E-03	3.08E-01	6.30E-04	4.20E-02	1.49E-01	1.00E+00	5.93E-03	4.21E-01	3.06E-02	8.38E-01	4.84E-05	7.00E-03	regulation of transcription factor activity	P
GO:0051091	29	3.15E-01	1.00E+00	2.17E-02	1.00E+00	4.00E-01	1.00E+00	9.21E-02	1.00E+00	6.00E-01	1.00E+00	1.66E-01	1.00E+00	1.60E-01	1.00E+00	7.32E-03	4.28E-01	positive regulation of transcription factor act	P
GO:0051092	21	3.58E-01	1.00E+00	3.44E-02	1.00E+00	5.91E-01	1.00E+00	1.84E-01	1.00E+00	5.50E-01	1.00E+00	2.21E-01	1.00E+00	1.32E-01	1.00E+00	2.10E-02	9.99E-01	activation of NF-kappaB transcription factor	P
GO:0051093	142	1.98E-01	1.00E+00	6.48E-01	1.00E+00	2.26E-01	1.00E+00	3.75E-01	1.00E+00	5.84E-01	1.00E+00	9.71E-01	1.00E+00	4.71E-02	1.00E+00	3.70E-01	1.00E+00	negative regulation of development	P
GO:0051094	122	5.11E-01	1.00E+00	4.01E-01	1.00E+00	5.98E-01	1.00E+00	8.05E-01	1.00E+00	7.51E-01	1.00E+00	2.73E-01	1.00E+00	1.15E-01	1.00E+00	1.34E-01	1.00E+00	positive regulation of development	P
GO:0051098	36	2.08E-03	2.12E-01	4.15E-04	4.74E-02	5.20E-03	3.08E-01	2.88E-02	1.00E+00	1.68E-02	6.92E-01	2.22E-03	1.27E-01	2.16E-02	6.36E-01	9.77E-03	4.76E-01	regulation of binding	P
GO:0051099	11	7.15E-02	1.00E+00	7.31E-02	1.00E+00	7.54E-02	1.00E+00	2.24E-01	1.00E+00	5.14E-02	1.00E+00	3.95E-02	1.00E+00	1.92E-01	1.00E+00	4.39E-01	1.00E+00	positive regulation of binding	P
GO:0051101	19	1.02E-02	6.08E-01	2.16E-03	1.71E-01	6.12E-03	4.69E-01	2.66E-02	1.00E+00	2.12E-02	9.56E-01	3.00E-03	1.44E-01	1.06E-01	1.00E+00	9.05E-02	1.00E+00	regulation of DNA binding	P
GO:0051119	46	8.84E-02	1.00E+00	2.87E-02	1.00E+00	2.40E-01	1.00E+00	1.30E-01	1.00E+00	7.20E-02	1.00E+00	3.93E-02	1.00E+00	1.85E-01	1.00E+00	8.13E-02	1.00E+00	sugar transporter activity	F
GO:0051128	111	3.93E-05	9.52E-03	1.04E-04	1.50E-02	3.29E-04	4.00E-02	9.52E-04	9.40E-02	2.35E-02	1.00E+00	2.44E-03	1.27E-01	1.40E-04	8.00E-03	3.68E-04	3.00E-02	regulation of cell organization and biogenes	P
GO:0051129	47	7.54E-04	8.86E-02	4.92E-04	4.74E-02	9.46E-03	6.53E-01	5.38E-03	2.88E-01	4.61E-02	1.00E+00	1.22E-02	5.03E-01	1.53E-03	6.14E-02	3.54E-03	1.27E-01	negative regulation of cell organization and	P
GO:0051130	22	5.30E-01	1.00E+00	2.12E-01	1.00E+00	5.03E-01	1.00E+00	2.69E-01	1.00E+00	6.69E-01	1.00E+00	2.78E-01	1.00E+00	3.64E-01	1.00E+00	1.88E-01	1.00E+00	positive regulation of cell organization and b	P
GO:0051145	15	6.40E-01	1.00E+00	9.86E-01	1.00E+00	9.99E-01	1.00E+00	9.19E-01	1.00E+00	5.58E-01	1.00E+00	9.81E-01	1.00E+00	1.90E-01	1.00E+00	9.68E-01	1.00E+00	smooth muscle cell differentiation	P
GO:0051146	39	6.42E-01	1.00E+00	4.28E-01	1.00E+00	8.39E-01	1.00E+00	4.20E-01	1.00E+00	5.81E-01	1.00E+00	3.84E-01	1.00E+00	5.89E-01	1.00E+00	7.06E-01	1.00E+00	striated muscle cell differentiation	P
GO:0051168	41	1.17E-05	7.00E-03	1.52E-06	3.92E-03	4.82E-04	4.90E-02	5.49E-06	2.89E-03	1.01E-04	2.70E-02	4.88E-04	2.33E-02	9.72E-02	1.00E+00	1.37E-03	6.00E-02	nuclear export	P
GO:0051169	121	2.63E-08	2.57E-03	6.30E-11	0.00E+00	8.68E-07	2.00E-03	5.72E-09	8.93E-04	2.81E-06	1.69E-03	7.34E-06	5.87E-03	2.51E-02	8.38E-01	6.25E-06	7.00E-03	nuclear transport	P
GO:0051170	83	3.93E-05	9.52E-03	1.05E-07	3.92E-03	7.51E-05	1.16E-02	4.76E-06	2.89E-03	9.20E-04	1.20E-01	1.49E-03	9.30E-02	9.09E-02	1.00E+00	9.69E-05	1.60E-02	nuclear import	P
GO:0051174	125	3.96E-01	1.00E+00	9.52E-02	1.00E+00	4.62E-01	1.00E+00	1.74E-01	1.00E+00	8.91E-01	1.00E+00	3.66E-01	1.00E+00	3.62E-02	8.38E-01	3.67E-02	1.00E+00	regulation of phosphorus metabolism	P
GO:0051179	3516	5.18E-19	0.00E+00	5.95E-37	0.00E+00	1.00E-10	7.95E-04	4.13E-19	0.00E+00	4.54E-12	0.00E+00	4.18E-22	0.00E+00	3.19E-12	0.00E+00	8.90E-28	0.00E+00	localization	P
GO:0051180	10	9.41E-01	1.00E+00	4.74E-01	1.00E+00	8.65E-01	1.00E+00	8.77E-01	1.00E+00	9.83E-01	1.00E+00	3.03E-01	1.00E+00	8.05E-01	1.00E+00	5.71E-01	1.00E+00	vitamin transport	P
GO:0051181	28	7.06E-01	1.00E+00	3.91E-01	1.00E+00	5.12E-01	1.00E+00	4.27E-01	1.00E+00	9.11E-01	1.00E+00	1.98E-01	1.00E+00	6.49E-01	1.00E+00	8.20E-01	1.00E+00	cofactor transport	P
GO:0051183	12	3.08E-01	1.00E+00	2.29E-01	1.00E+00	3.10E-01	1.00E+00	2.83E-01	1.00E+00	4.27E-01	1.00E+00	2.63E-01	1.00E+00	3.29E-01	1.00E+00	4.38E-01	1.00E+00	vitamin transporter activity	F
GO:0051184	30	4.72E-01	1.00E+00	2.32E-01	1.00E+00	2.99E-01	1.00E+00	1.82E-01	1.00E+00	7.19E-01	1.00E+00	2.36E-01	1.00E+00	4.91E-01	1.00E+00	6.28E-01	1.00E+00	cofactor transporter activity	F
GO:0051186	275	2.41E-07	2.57E-03	5.58E-06	4.51E-03	1.49E-06	2.00E-03	5.56E-04	4.20E-02	5.12E-06	1.69E-03	2.26E-06	2.00E-03	3.01E-02	8.38E-01	2.50E-02	9.99E-01	cofactor metabolism	P
GO:0051187	32	3.79E-03	2.12E-01	1.69E-02	7.63E-01	2.47E-02	1.00E+00	3.59E-02	1.00E+00	7.98E-03	6.92E-01	2.93E-02	1.00E+00	2.10E-01	1.00E+00	1.22E-01	1.00E+00	cofactor catabolism	P
GO:0051188	165	2.34E-03	2.12E-01	2.25E-02	1.00E+00	4.95E-03	3.08E-01	9.96E-02	1.00E+00	3.99E-03	2.13E-01	3.47E-02	1.00E+00	1.23E-01	1.00E+00	1.60E-01	1.00E+00	cofactor biosynthesis	P
GO:0051213	61	1.97E-01	1.00E+00	1.02E-03	9.65E-02	1.65E-01	1.00E+00	2.51E-03	1.39E-01	3.98E-01	1.00E+00	1.82E-02	6.68E-01	3.57E-01	1.00E+00	5.40E-02	1.00E+00	dioxygenase activity	F
GO:0051216	72	3.20E-01	1.00E+00	8.70E-01	1.00E+00	4.16E-01	1.00E+00	8.89E-01	1.00E+00	4.52E-01	1.00E+00	9.10E-01	1.00E+00	2.18E-01	1.00E+00	3.50E-01	1.00E+00	cartilage development	P
GO:0051219	19	5.59E-02	1.00E+00	1.30E-01	1.00E+00	5.74E-02	1.00E+00	3.80E-02	1.00E+00	6.21E-02	1.00E+00	3.85E-01	1.00E+00	1.65E-01	1.00E+00	3.25E-01	1.00E+00	phosphoprotein binding	F
GO:0051222	17	2.79E-02	1.00E+00	1.34E-03	9.65E-02	7.85E-02	1.00E+00	1.11E-03	9.40E-02	1.37E-01	1.00E+00	4.47E-03	2.66E-01	3.06E-02	8.38E-01	2.96E-02	9.99E-01	positive regulation of protein transport	P
GO:0051223	34	7.24E-04	8.86E-02	1.05E-05	4.51E-03	2.24E-03	1.03E-01	7.59E-06	2.89E-03	1.06E-02	6.92E-01	5.65E-04	3.20E-02	1.85E-02	6.36E-01	4.74E-03	2.01E-01	regulation of protein transport	P
GO:0051224	10	7.84E-02	1.00E+00	9.38E-02	1.00E+00	1.31E-01	1.00E+00	1.96E-02	9.37E-01	1.35E-01	1.00E+00	2.57E-01	1.00E+00	5.10E-01	1.00E+00	1.66E-01	1.00E+00	negative regulation of protein transport	P
GO:0051234	3453	2.77E-18	0.00E+00	2.07E-36	0.00E+00	1.38E-10	7.95E-04	8.44E-19	0.00E+00	2.51E-11	0.00E+00	1.35E-21	0.00E+00	6.94E-12	0.00E+00	1.10E-27	0.00E+00	establishment of localization	P
GO:0051235	36	4.42E-02	1.00E+00	7.07E-02	1.00E+00	3.91E-02	1.00E+00	1.80E-01	1.00E+00	2.58E-01	1.00E+00	3.58E-02	1.00E+00	1.20E-01	1.00E+00	2.01E-01	1.00E+00	maintenance of localization	P
GO:0051236	60	3.49E-06	3.02E-03	1.39E-09	8.90E-04	2.08E-05	3.00E-03	3.30E-09	0.00E+00	2.07E-05	5.37E-03	3.79E-05	9.66E-03	2.62E-01	1.00E+00	1.17E-03	6.00E-02	establishment of RNA localization	P
GO:0051238	10	1.44E-01	1.00E+00	9.10E-02	1.00E+00	1.03E-01	1.00E+00	2.90E-01	1.00E+00	8.68E-01	1.00E+00	6.21E-02	1.00E+00	6.59E-02	1.00E+00	1.45E-01	1.00E+00	sequestering of metal ion	P
GO:0051239	321	7.89E-01	1.00E+00	7.64E-01	1.00E+00	9.53E-01	1.00E+00	9.85E-01	1.00E+00	9.89E-01	1.00E+00	7.38E-01	1.00E+00	7.92E-02	1.00E+00	6.23E-02	1.00E+00	regulation of organismal physiological proce	P
GO:0051240	147	9.21E-01	1.00E+00	8.70E-01	1.00E+00	9.82E-01	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	1.42E-01	1.00E+00	3.37E-01	1.00E+00	positive regulation of organismal physiologi	P
GO:0051241	40	2.93E-01	1.00E+00	3.03E-01	1.00E+00	3.07E-01	1.00E+00	3.62E-01	1.00E+00	8.27E-01	1.00E+00	3.81E-01	1.00E+00	2.26E-01	1.00E+00	4.64E-02	1.00E+00	negative regulation of organismal physiolog	P
GO:0051242	1011	1.32E-07	2.57E-03	2.43E-11	0.00E+00	2.14E-06	2.00E-03	5.69E-07	2.89E-03	9.02E-03	6.92E-01	1.78E-07	1.65E-03	4.70E-07	8.23E-04	9.05E-09	0.00E+00	positive regulation of cellular physiological p	P
GO:0051243	969	7.69E-19	0.00E+00	1.45E-19	0.00E+00	1.42E-15	0.00E+00	7.17E-17	0.00E+00	3.52E-08	9.59E-04	3.31E-10	6.20E-04	1.81E-12	0.00E+00	3.94E-12	0.00E+00	negative regulation of cellular physiological	P
GO:0051244	3743	1.36E-37	0.00E+00	0.00E+00	0.00E+00	2.26E-33	0.00E+00	0.00E+00	0.00E+00	3.77E-23	0.00E+00	1.00E-33	0.00E+00	2.76E-13	0.00E+00	3.20E-19	0.00E+00	regulation of cellular physiological process	P
GO:0051246	375	2.30E-06	3.00E-03	5.25E-12	0.00E+00	5.35E-05	9.82E-03	1.63E-07	2.89E-03	8.24E-04	1.20E-01	1.34E-06	2.00E-03	2.36E-04	1.20E-02	3.95E-10	0.00E+00	regulation of protein metabolism	P
GO:0051247	113	4.10E-01	1.00E+00	9.10E-03	4.69E-01	5.86E-01	1.00E+00	7.73E-02	1.00E+00	7.71E-01	1.00E+00	3.04E-01	1.00E+00	8.53E-02	1.00E+00	1.44E-04	1.60E-02	positive regulation of protein metabolism	P
GO:0051248	105	9.91E-05	1.43E-02	3.86E-05	7.00E-03	2.28E-03	1.03E-01	2.84E-03	1.61E-01	4.78E-03	3.75E-01	1.65E-03	1.22E-01	6.14E-04	3.44E-02	1.53E-03	6.00E-02	negative regulation of protein metabolism	P
GO:0051249	103	1.99E-01	1.00E+00	2.04E-03	1.30E-01	5.09E-01	1.00E+00	3.33E-02	1.00E+00	5.07E-01	1.00E+00	1.26E-01	1.00E+00	3.91E-02	9.10E-01	3.86E-04	3.00E-02	regulation of lymphocyte activation	P
GO:0051250	32	8.00E-01	1.00E+00	2.46E-01	1.00E+00	8.77E-01	1.00E+00	2.97E-01	1.00E+00	6.72E-01	1.00E+00	3.49E-01	1.00E+00	4.98E-01	1.00E+00	1.07E-01	1.00E+00	negative regulation of lymphocyte activatior	P
GO:0051251	73	1.96E-01	1.00E+00	3.71E-03	1.88E-01	4.79E-01	1.00E+00	5.86E-02	1.00E+00	5.61E-01	1.00E+00	8.00E-02	1.00E+00	4.39E-02	1.00E+00	2.91E-03	1.27E-01	positive regulation of lymphocyte activation	P
GO:0051252	25	3.65E-03	2.12E-01	8.96E-06	4.51E-03	8.61E-04	4.90E-02	5.95E-03	2.88E-01	8.44E-02	1.00E+00	1.87E-03	1.27E-01	3.30E-02	8.38E-01	6.14E-05	7.00E-03	regulation of RNA metabolism	P
GO:0051258	78	4.46E-03	2.14E-01	4.76E-03	2.61E-01	3.51E-02	1.00E+00	5.78E-02	1.00E+00	8.22E-02	1.00E+00	8.39E-02	1.00E+00	1.91E-03	8.40E-02	3.40E-04	3.00E-02	protein polymerization	P
GO:0051259	111	6.87E-02	1.00E+00	1.56E-02	7.63E-01	2.38E-01	1.00E+00	4.24E-02	1.00E+00	2.74E-01	1.00E+00	1.97E-02	7.56E-01	5.57E-02	1.00E+00	1.44E-01	1.00E+00	protein oligomerization	P
GO:0051260	81	1.53E-01	1.00E+00	5.06E-02	1.00E+00	2.90E-01	1.00E+00	6.22E-02	1.00E+00	3.36E-01	1.00E+00	4.37E-02	1.00E+00	1.42E-01	1.00E+00	2.88E-01	1.00E+00	protein homooligomerization	P

GO:0051261	40	3.95E-03	2.12E-01	2.04E-04	2.40E-02	5.38E-02	1.00E+00	8.21E-03	4.92E-01	4.36E-02	1.00E+00	3.88E-03	1.84E-01	4.78E-03	2.23E-01	2.17E-03	7.90E-02	protein depolymerization	P
GO:0051262	19	1.08E-02	6.08E-01	7.71E-03	4.16E-01	1.60E-01	1.00E+00	3.79E-02	1.00E+00	4.30E-02	1.00E+00	7.91E-02	1.00E+00	9.87E-03	2.75E-01	4.26E-03	2.01E-01	protein tetramerization	P
GO:0051270	95	4.16E-01	1.00E+00	5.04E-02	1.00E+00	7.52E-01	1.00E+00	1.02E-01	1.00E+00	7.72E-01	1.00E+00	1.49E-01	1.00E+00	1.10E-01	1.00E+00	3.47E-02	1.00E+00	regulation of cell motility	P
GO:0051271	29	1.81E-01	1.00E+00	4.08E-02	1.00E+00	4.93E-01	1.00E+00	1.65E-02	6.47E-01	2.56E-01	1.00E+00	7.49E-02	1.00E+00	2.54E-01	1.00E+00	2.87E-01	1.00E+00	negative regulation of cell motility	P
GO:0051272	40	7.29E-01	1.00E+00	2.23E-01	1.00E+00	8.95E-01	1.00E+00	3.67E-01	1.00E+00	9.73E-01	1.00E+00	5.55E-01	1.00E+00	2.26E-01	1.00E+00	9.89E-02	1.00E+00	positive regulation of cell motility	P
GO:0051276	437	7.72E-10	2.57E-03	3.90E-14	0.00E+00	5.78E-13	7.08E-04	1.72E-19	0.00E+00	2.69E-04	4.90E-02	1.07E-07	1.65E-03	1.39E-03	6.14E-02	3.08E-04	3.00E-02	chromosome organization and biogenesis	P
GO:0051287	68	1.64E-01	1.00E+00	1.91E-01	1.00E+00	2.05E-01	1.00E+00	3.29E-01	1.00E+00	6.35E-01	1.00E+00	1.16E-01	1.00E+00	1.03E-01	1.00E+00	3.98E-01	1.00E+00	NAD binding	F
GO:0051297	16	4.24E-03	2.14E-01	9.82E-05	1.50E-02	1.08E-03	7.90E-02	4.53E-04	4.20E-02	5.21E-02	1.00E+00	2.23E-03	1.27E-01	4.03E-01	1.00E+00	6.48E-02	1.00E+00	centrosome organization and biogenesis	P
GO:0051301	246	7.03E-13	0.00E+00	1.53E-16	0.00E+00	8.80E-14	7.08E-04	1.32E-15	0.00E+00	8.32E-08	9.59E-04	7.60E-10	6.20E-04	1.38E-03	6.14E-02	1.08E-05	7.00E-03	cell division	P
GO:0051320	14	6.20E-02	1.00E+00	6.90E-03	3.12E-01	6.39E-02	1.00E+00	2.73E-02	1.00E+00	1.59E-01	1.00E+00	8.15E-03	4.21E-01	5.57E-01	1.00E+00	3.09E-01	1.00E+00	S phase	P
GO:0051321	85	1.28E-04	1.43E-02	1.08E-06	3.92E-03	1.39E-05	3.00E-03	2.99E-05	9.57E-03	3.40E-02	1.00E+00	1.00E-04	1.10E-02	1.59E-02	4.88E-01	3.91E-02	1.00E+00	meiotic cell cycle	P
GO:0051325	69	2.48E-02	1.00E+00	8.93E-03	4.69E-01	6.35E-02	1.00E+00	2.36E-02	9.37E-01	1.64E-01	1.00E+00	4.74E-03	2.66E-01	3.75E-02	8.38E-01	2.76E-01	1.00E+00	interphase	P
GO:0051327	84	2.46E-04	1.90E-02	1.13E-06	3.92E-03	2.90E-05	3.00E-03	2.88E-05	9.57E-03	4.83E-02	1.00E+00	8.08E-05	1.10E-02	2.95E-02	8.38E-01	4.24E-02	1.00E+00	M phase of meiotic cell cycle	P
GO:0051329	68	2.11E-02	1.00E+00	1.02E-02	4.69E-01	4.90E-02	1.00E+00	2.22E-02	9.37E-01	1.54E-01	1.00E+00	5.13E-03	2.66E-01	3.87E-02	8.54E-01	3.22E-01	1.00E+00	interphase of mitotic cell cycle	P
GO:0051336	174	2.79E-08	2.57E-03	1.56E-08	9.59E-04	1.28E-05	3.00E-03	8.72E-06	2.89E-03	3.40E-05	6.33E-03	4.35E-07	1.65E-03	5.00E-05	8.00E-03	1.40E-04	1.60E-02	regulation of hydrolase activity	P
GO:0051338	203	4.40E-04	4.20E-02	3.69E-06	3.92E-03	2.35E-03	1.07E-01	2.29E-04	1.30E-02	2.38E-02	1.00E+00	3.66E-04	2.33E-02	1.23E-03	6.14E-02	4.99E-05	7.00E-03	regulation of transferase activity	P
GO:0051339	23	6.25E-01	1.00E+00	2.51E-01	1.00E+00	7.51E-01	1.00E+00	5.51E-01	1.00E+00	3.89E-01	1.00E+00	2.08E-01	1.00E+00	5.39E-01	1.00E+00	1.22E-01	1.00E+00	regulation of lyase activity	P
GO:0051345	53	1.61E-04	1.72E-02	3.51E-04	4.40E-02	5.96E-03	4.69E-01	1.15E-02	6.47E-01	1.12E-03	1.20E-01	4.22E-04	2.33E-02	8.65E-03	2.75E-01	5.86E-03	4.28E-01	positive regulation of hydrolase activity	P
GO:0051347	138	1.32E-02	6.08E-01	1.07E-02	4.69E-01	1.70E-01	1.00E+00	5.19E-02	1.00E+00	4.31E-02	1.00E+00	6.16E-02	1.00E+00	2.81E-03	8.40E-02	5.69E-03	4.28E-01	positive regulation of transferase activity	P
GO:0051348	54	1.75E-02	1.00E+00	2.82E-05	7.00E-03	1.40E-02	6.53E-01	6.77E-04	4.20E-02	1.90E-01	1.00E+00	3.86E-04	2.33E-02	4.13E-02	1.00E+00	1.50E-03	6.00E-02	negative regulation of transferase activity	P
GO:0051349	17	9.79E-01	1.00E+00	4.00E-01	1.00E+00	9.99E-01	1.00E+00	8.16E-01	1.00E+00	6.46E-01	1.00E+00	3.99E-01	1.00E+00	8.87E-01	1.00E+00	9.54E-02	1.00E+00	positive regulation of lyase activity	P
GO:0051384	21	4.66E-01	1.00E+00	4.02E-01	1.00E+00	3.33E-01	1.00E+00	6.25E-01	1.00E+00	6.13E-01	1.00E+00	2.44E-01	1.00E+00	4.92E-01	1.00E+00	4.13E-01	1.00E+00	response to glucocorticoid stimulus	P
GO:0051402	68	1.10E-02	6.08E-01	1.48E-03	9.65E-02	1.16E-01	1.00E+00	6.62E-03	3.33E-01	2.47E-02	1.00E+00	2.20E-03	1.27E-01	1.70E-02	4.88E-01	3.08E-02	9.99E-01	neuron apoptosis	P
GO:0051427	47	1.04E-03	8.86E-02	1.62E-04	1.50E-02	5.44E-04	4.90E-02	8.96E-05	1.30E-02	7.64E-03	6.92E-01	2.73E-02	1.00E+00	9.57E-02	1.00E+00	7.04E-02	1.00E+00	hormone receptor binding	F
GO:0051480	40	2.06E-01	1.00E+00	1.25E-01	1.00E+00	6.79E-01	1.00E+00	4.28E-01	1.00E+00	7.14E-01	1.00E+00	1.66E-01	1.00E+00	4.55E-03	2.23E-01	3.53E-02	1.00E+00	cytosolic calcium ion homeostasis	P
GO:0051536	63	5.91E-03	3.09E-01	3.44E-01	1.00E+00	1.04E-01	1.00E+00	3.67E-01	1.00E+00	1.62E-02	6.92E-01	2.01E-01	1.00E+00	2.92E-02	8.38E-01	4.91E-01	1.00E+00	iron-sulfur cluster binding	F
GO:0051537	19	1.21E-01	1.00E+00	4.36E-01	1.00E+00	7.20E-01	1.00E+00	8.53E-01	1.00E+00	5.12E-02	1.00E+00	9.68E-02	1.00E+00	6.88E-02	1.00E+00	4.94E-01	1.00E+00	2 iron, 2 sulfur cluster binding	F
GO:0051539	22	1.01E-03	8.86E-02	8.25E-03	4.16E-01	3.12E-03	1.35E-01	3.04E-02	1.00E+00	6.59E-03	6.92E-01	8.12E-03	4.21E-01	6.33E-02	1.00E+00	6.42E-02	1.00E+00	4 iron, 4 sulfur cluster binding	F
GO:0051540	63	5.91E-03	3.09E-01	3.44E-01	1.00E+00	1.04E-01	1.00E+00	3.67E-01	1.00E+00	1.62E-02	6.92E-01	2.01E-01	1.00E+00	2.92E-02	8.38E-01	4.91E-01	1.00E+00	metal cluster binding	F
GO:0051591	13	1.13E-01	1.00E+00	1.55E-01	1.00E+00	3.89E-01	1.00E+00	3.13E-01	1.00E+00	9.98E-02	1.00E+00	1.34E-01	1.00E+00	7.38E-02	1.00E+00	2.15E-01	1.00E+00	response to cAMP	P
GO:0051592	15	2.34E-01	1.00E+00	5.73E-01	1.00E+00	3.82E-01	1.00E+00	5.07E-01	1.00E+00	4.63E-01	1.00E+00	6.64E-01	1.00E+00	1.65E-01	1.00E+00	5.21E-01	1.00E+00	response to calcium ion	P
GO:0051603	183	1.64E-05	7.00E-03	1.50E-08	9.59E-04	6.67E-07	2.00E-03	5.76E-09	8.93E-04	5.12E-03	3.75E-01	3.24E-05	9.52E-03	9.53E-02	1.00E+00	4.79E-04	3.00E-02	proteolysis during cellular protein catabolisr	P
GO:0051604	15	9.61E-01	1.00E+00	7.81E-01	1.00E+00	9.92E-01	1.00E+00	9.47E-01	1.00E+00	9.99E-01	1.00E+00	7.20E-01	1.00E+00	5.03E-01	1.00E+00	4.64E-01	1.00E+00	protein maturation	P
GO:0051605	14	9.22E-01	1.00E+00	7.35E-01	1.00E+00	9.86E-01	1.00E+00	9.05E-01	1.00E+00	9.97E-01	1.00E+00	7.77E-01	1.00E+00	4.09E-01	1.00E+00	3.41E-01	1.00E+00	proteolysis during protein maturation	P
GO:0051606	88	9.81E-01	1.00E+00	9.97E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	8.90E-01	1.00E+00	7.98E-01	1.00E+00	9.87E-01	1.00E+00	detection of stimulus	P
GO:0051607	15	1.74E-01	1.00E+00	2.44E-01	1.00E+00	9.38E-01	1.00E+00	7.12E-01	1.00E+00	6.76E-01	1.00E+00	1.30E-01	1.00E+00	4.09E-03	2.23E-01	2.19E-01	1.00E+00	defense response to virus	P
GO:0051640	33	1.01E-02	6.08E-01	1.05E-04	1.50E-02	2.08E-02	1.00E+00	1.26E-03	9.40E-02	3.45E-02	1.00E+00	1.83E-03	1.27E-01	4.57E-02	1.00E+00	2.35E-03	7.90E-02	organelle localization	P
GO:0051641	835	3.63E-28	0.00E+00	1.18E-39	0.00E+00	2.39E-21	0.00E+00	1.22E-29	0.00E+00	2.34E-22	0.00E+00	3.96E-25	0.00E+00	3.92E-09	0.00E+00	5.05E-16	0.00E+00	cellular localization	P
GO:0051647	10	9.70E-02	1.00E+00	1.88E-02	1.00E+00	1.29E-01	1.00E+00	9.74E-02	1.00E+00	1.56E-02	6.92E-01	5.39E-03	3.43E-01	7.85E-01	1.00E+00	7.34E-02	1.00E+00	nucleus localization	P
GO:0051649	814	1.36E-27	0.00E+00	3.31E-38	0.00E+00	1.97E-21	0.00E+00	7.21E-29	0.00E+00	1.59E-21	0.00E+00	4.35E-24	0.00E+00	5.87E-09	0.00E+00	9.05E-16	0.00E+00	establishment of cellular localization	P
GO:0051656	19	1.43E-02	8.50E-01	4.26E-04	4.74E-02	1.26E-02	6.53E-01	9.61E-04	9.40E-02	5.02E-02	1.00E+00	3.23E-03	1.51E-01	5.89E-02	1.00E+00	7.04E-03	4.28E-01	establishment of organelle localization	P
GO:0051668	10	9.69E-02	1.00E+00	2.33E-02	1.00E+00	3.21E-01	1.00E+00	4.72E-02	1.00E+00	4.84E-02	1.00E+00	3.03E-02	1.00E+00	2.36E-01	1.00E+00	3.64E-01	1.00E+00	localization within membrane	P
GO:0051674	448	2.40E-01	1.00E+00	4.87E-02	1.00E+00	6.96E-01	1.00E+00	3.26E-01	1.00E+00	3.83E-01	1.00E+00	4.06E-01	1.00E+00	6.99E-02	1.00E+00	3.17E-04	3.00E-02	localization of cell	P
GO:0051693	19	1.84E-01	1.00E+00	1.18E-02	6.07E-01	6.80E-01	1.00E+00	1.01E-01	1.00E+00	3.66E-01	1.00E+00	4.69E-02	1.00E+00	1.01E-01	1.00E+00	1.36E-02	4.76E-01	actin filament capping	P
GO:0051701	14	5.91E-01	1.00E+00	5.27E-01	1.00E+00	7.10E-01	1.00E+00	7.11E-01	1.00E+00	7.21E-01	1.00E+00	6.76E-01	1.00E+00	2.62E-01	1.00E+00	3.25E-01	1.00E+00	interaction with host	P
GO:0051704	143	5.06E-01	1.00E+00	9.47E-01	1.00E+00	5.85E-01	1.00E+00	9.89E-01	1.00E+00	6.52E-01	1.00E+00	9.98E-01	1.00E+00	2.68E-01	1.00E+00	4.08E-01	1.00E+00	interaction between organisms	P
GO:0051705	35	4.90E-01	1.00E+00	9.94E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	4.75E-01	1.00E+00	9.61E-01	1.00E+00	2.56E-01	1.00E+00	7.68E-01	1.00E+00	behavioral interaction between organisms	P
GO:0051706	50	8.73E-01	1.00E+00	9.57E-01	1.00E+00	9.75E-01	1.00E+00	9.90E-01	1.00E+00	4.94E-01	1.00E+00	9.91E-01	1.00E+00	7.25E-01	1.00E+00	5.55E-01	1.00E+00	physiological interaction between organisms	P
GO:0051707	184	9.98E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.55E-01	1.00E+00	5.30E-01	1.00E+00	9.18E-01	1.00E+00	response to other organism	P
GO:0051716	24	9.38E-02	1.00E+00	1.93E-01	1.00E+00	6.43E-02	1.00E+00	1.84E-01	1.00E+00	2.55E-01	1.00E+00	2.47E-01	1.00E+00	6.07E-02	1.00E+00	3.01E-01	1.00E+00	cellular response to stimulus	P
GO:0051726	311	8.29E-07	2.76E-03	1.09E-08	8.90E-04	1.69E-06	2.00E-03	1.16E-07	2.89E-03	1.69E-03	1.20E-01	2.01E-06	2.00E-03	2.83E-04	2.29E-02	6.60E-04	6.00E-02	regulation of cell cycle	P
GO:0051789	58	1.65E-03	2.12E-01	2.52E-03	1.80E-01	1.21E-03	7.90E-02	3.53E-04	4.20E-02	7.06E-02	1.00E+00	1.40E-02	6.68E-01	4.56E-02	1.00E+00	4.03E-01	1.00E+00	response to protein stimulus	P
GO:0051869	1279	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	5.51E-01	1.00E+00	8.80E-01	1.00E+00	physiological response to stimulus	P
GO:0051881	11	4.74E-02	1.00E+00	6.52E-02	1.00E+00	4.44E-02	1.00E+00	2.77E-01	1.00E+00	1.47E-01	1.00E+00	2.71E-02	1.00E+00	1.26E-01	1.00E+00	1.80E-01	1.00E+00	regulation of mitochondrial membrane pote	P
GO:0051899	13	3.27E-01	1.00E+00	1.75E-01	1.00E+00	6.85E-01	1.00E+00	8.11E-01	1.00E+00	7.84E-01	1.00E+00	1.11E-01	1.00E+00	1.00E-01	1.00E+00	2.49E-01	1.00E+00	membrane depolarization	P
GO:0051924	29	6.54E-01	1.00E+00	3.08E-01	1.00E+00	9.10E-01	1.00E+00	5.17E-01	1.00E+00	1.93E-01	1.00E+00	7.74E-01	1.00E+00	8.46E-01	1.00E+00	6.48E-02	1.00E+00	regulation of calcium ion transport	P
GO:0051966	12	1.00E+00	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	8.13E-01	1.00E+00	9.06E-01	1.00E+00	9.98E-01	1.00E+00	regulation of synaptic transmission, glutama	P
GO:0051969	71	8.34E-01	1.00E+00	5.25E-01	1.00E+00	7.75E-01	1.00E+00	7.35E-01	1.00E+00	9.77E-01	1.00E+00	1.56E-01	1.00E+00	4.43E-01	1.00E+00	6.92E-01	1.00E+00	regulation of transmission of nerve impulse	P
GO:0051970	11	9.99E-01	1.00E+00	8.68E-01	1.00E+00	1.00E+00	1.00E+00	8.59E-01	1.00E+00	9.60E-01	1.00E+00	6.77E-01	1.00E+00	9.43E-01	1.00E+00	9.31E-01	1.00E+00	negative regulation of transmission of nerve	P
GO:0051971	15	2.87E-01	1.00E+00	1.94E-01	1.00E+00	1.88E-01	1.00E+00	4.13E-01	1.00E+00	7.22E-01	1.00E+00	3.06E-02	1.00E+00	2.43E-02	8.38E-01	4.75E-01	1.00E+00	positive regulation of transmission of nerve	P
GO:0055001	19	1.92E-01	1.00E+00	2.21E-01	1.00E+00	3.69E-01	1.00E+00	3.56E-01	1.00E+00	5.68E-01	1.00E+00	1.87E-01	1.00E+00	6.38E-02	1.00E+00	3.09E-01	1.00E+00	muscle cell development	P
GO:0055002	18	1.36E-01	1.00E+00	1.58E-01	1.00E+00	2.68E-01	1.00E+00	2.98E-01	1.00E+00	5.28E-01	1.00E+00	1.55E-01	1.00E+00	4.89E-02	1.00E+00	2.06E-01	1.00E+00	striated muscle cell development	P
GO:0055007	13	6.92E-01	1.00E+00	8.74E-01	1.00E+00	6.58E-01	1.00E+00	9.17E-01	1.00E+00	4.51E-01	1.00E+00	6.47E-01	1.00E+00	9.85E-01	1.00E+00	9.64E-01	1.00E+00	cardiac muscle cell differentiation	P
GO:0055008	17	5.15E-01	1.00E+00	9.32E-01	1.00E+00	5.14E-01	1.00E+00	9.93E-01	1.00E+00	8.49E-01	1.00E+00	8.51E-01	1.00E+00	1.67E-01	1.00E+00	8.40E-01	1.00E+00	cardiac muscle morphogensis	P
GO:0055010	15	5.20E-01	1.00E+00	8.98E-01	1.00E+00	4.41E-01	1.00E+00	9.99E-01	1.00E+00	6.82E-01	1.00E+00	7.66E-01	1.00E+00	4.01E-01	1.00E+00	7.81E-01	1.00E+00	ventricular cardiac muscle morphogenesis	P

		B+		B-		B1+		B1-		B2+		B2-		B4+		B4-			
GO term id	genes	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	GO term description	GO term catecory
GO:0000003	527	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	reproduction	P
GO:0000030	12	1.28E-03	9.30E-02	5.95E-03	5.59E-01	1.87E-02	8.10E-01	3.31E-02	1.00E+00	1.06E-02	4.14E-01	1.69E-02	1.00E+00	5.95E-02	1.00E+00	1.73E-01	1.00E+00	mannosyltransferase activity	F
GO:0000041	64	2.24E-01	1.00E+00	1.93E-01	1.00E+00	2.26E-01	1.00E+00	1.16E-01	1.00E+00	2.02E-01	1.00E+00	5.02E-01	1.00E+00	4.23E-01	1.00E+00	4.81E-01	1.00E+00	transition metal ion transport	P
GO:0000045	14	1.66E-01	1.00E+00	3.09E-02	1.00E+00	2.29E-01	1.00E+00	1.09E-01	1.00E+00	4.61E-01	1.00E+00	6.84E-01	1.00E+00	9.41E-02	1.00E+00	3.43E-02	1.00E+00	autophagic vacuole formation	P
GO:0000049	18	3.01E-01	1.00E+00	8.00E-02	1.00E+00	1.82E-01	1.00E+00	2.39E-01	1.00E+00	3.64E-01	1.00E+00	9.16E-02	1.00E+00	6.68E-01	1.00E+00	1.41E-01	1.00E+00	tRNA binding	F
GO:0000051	15	2.15E-01	1.00E+00	5.93E-01	1.00E+00	1.32E-01	1.00E+00	7.36E-01	1.00E+00	5.38E-01	1.00E+00	4.67E-01	1.00E+00	3.68E-01	1.00E+00	6.07E-01	1.00E+00	urea cycle intermediate metabolism	P
GO:0000059	15	6.81E-02	1.00E+00	5.61E-07	2.66E-03	2.32E-03	1.18E-01	5.36E-06	1.77E-03	1.37E-01	1.00E+00	2.90E-04	1.36E-02	8.83E-01	1.00E+00	2.95E-04	1.70E-02	protein import into nucleus, docking	P
GO:0000060	22	2.16E-01	1.00E+00	7.35E-01	1.00E+00	4.51E-01	1.00E+00	7.71E-01	1.00E+00	1.17E-01	1.00E+00	6.28E-01	1.00E+00	5.51E-01	1.00E+00	5.08E-01	1.00E+00	protein import into nucleus, translocation	P
GO:0000062	12	3.83E-03	1.86E-01	3.77E-02	1.00E+00	1.39E-02	8.10E-01	1.91E-01	1.00E+00	6.17E-02	1.00E+00	6.10E-02	1.00E+00	7.39E-02	1.00E+00	1.64E-01	1.00E+00	acyl-CoA binding	F
GO:0000070	21	8.54E-02	1.00E+00	1.94E-02	1.00E+00	1.24E-01	1.00E+00	1.15E-02	3.78E-01	3.92E-02	1.00E+00	3.29E-02	1.00E+00	6.85E-01	1.00E+00	2.20E-01	1.00E+00	mitotic sister chromatid segregation	P
GO:0000074	245	7.11E-04	5.20E-02	8.60E-04	7.30E-02	1.25E-03	7.90E-02	9.52E-05	5.80E-03	1.45E-03	4.80E-02	2.05E-02	1.00E+00	1.52E-01	1.00E+00	1.24E-01	1.00E+00	regulation of progression through cell cycle	P
GO:0000075	44	7.50E-05	7.00E-03	3.69E-05	2.80E-02	1.21E-03	7.90E-02	6.63E-06	1.77E-03	2.64E-03	1.35E-01	9.59E-03	3.55E-01	1.72E-02	4.71E-01	1.61E-03	4.50E-02	cell cycle checkpoint	P
GO:0000077	24	6.82E-03	3.64E-01	2.90E-03	1.87E-01	1.29E-02	4.81E-01	1.66E-03	4.40E-02	5.78E-02	1.00E+00	3.76E-02	1.00E+00	3.00E-02	7.53E-01	5.75E-03	2.58E-01	DNA damage checkpoint	P
GO:0000079	20	8.70E-02	1.00E+00	1.67E-01	1.00E+00	1.66E-01	1.00E+00	9.65E-03	3.78E-01	8.83E-02	1.00E+00	6.57E-01	1.00E+00	2.15E-01	1.00E+00	6.61E-01	1.00E+00	regulation of cyclin-dependent protein kinas	P
GO:0000080	10	8.47E-01	1.00E+00	1.09E-01	1.00E+00	8.17E-01	1.00E+00	4.94E-02	1.00E+00	5.87E-01	1.00E+00	1.84E-01	1.00E+00	8.25E-01	1.00E+00	2.19E-01	1.00E+00	G1 phase of mitotic cell cycle	P
GO:0000082	36	8.08E-01	1.00E+00	1.88E-01	1.00E+00	4.06E-01	1.00E+00	6.85E-02	1.00E+00	8.36E-01	1.00E+00	1.92E-01	1.00E+00	8.47E-01	1.00E+00	8.96E-01	1.00E+00	G1/S transition of mitotic cell cycle	P
GO:0000084	14	3.17E-01	1.00E+00	2.62E-01	1.00E+00	3.98E-01	1.00E+00	2.13E-01	1.00E+00	1.63E-01	1.00E+00	2.07E-01	1.00E+00	7.87E-01	1.00E+00	5.50E-01	1.00E+00	S phase of mitotic cell cycle	P
GO:0000086	10	2.48E-01	1.00E+00	1.76E-02	1.00E+00	4.77E-01	1.00E+00	1.98E-03	4.40E-02	7.96E-02	1.00E+00	2.58E-01	1.00E+00	5.71E-01	1.00E+00	6.93E-02	1.00E+00	G2/M transition of mitotic cell cycle	P
GO:0000087	192	6.08E-11	6.62E-04	1.73E-20	0.00E+00	5.21E-11	0.00E+00	5.75E-15	0.00E+00	3.46E-08	0.00E+00	3.90E-13	0.00E+00	1.03E-02	2.17E-01	1.16E-08	0.00E+00	M phase of mitotic cell cycle	P
GO:0000096	20	1.90E-02	9.83E-01	2.54E-02	1.00E+00	6.05E-02	1.00E+00	1.58E-01	1.00E+00	7.42E-02	1.00E+00	3.55E-02	1.00E+00	2.73E-01	1.00E+00	6.98E-02	1.00E+00	sulfur amino acid metabolism	P
GO:0000097	11	3.52E-03	1.86E-01	7.55E-03	5.59E-01	1.10E-01	1.00E+00	1.18E-01	1.00E+00	7.52E-02	1.00E+00	1.23E-01	1.00E+00	2.32E-01	1.00E+00	5.39E-02	1.00E+00	sulfur amino acid biosynthesis	P
GO:0000118	27	1.93E-01	1.00E+00	1.15E-02	7.51E-01	5.00E-01	1.00E+00	3.90E-03	1.42E-01	4.02E-02	1.00E+00	3.71E-02	1.00E+00	7.26E-01	1.00E+00	1.97E-01	1.00E+00	histone deacetylase complex	C
GO:0000119	23	1.19E-03	9.30E-02	2.78E-03	1.87E-01	3.43E-03	1.88E-01	1.93E-04	1.10E-02	1.91E-02	7.19E-01	7.01E-02	1.00E+00	7.46E-01	1.00E+00	3.90E-01	1.00E+00	mediator complex	C
GO:0000122	179	8.81E-01	1.00E+00	8.22E-01	1.00E+00	9.78E-01	1.00E+00	4.97E-01	1.00E+00	8.93E-01	1.00E+00	8.51E-01	1.00E+00	6.15E-01	1.00E+00	9.30E-01	1.00E+00	negative regulation of transcription from RN	P
GO:0000123	10	6.40E-01	1.00E+00	4.37E-02	1.00E+00	3.42E-01	1.00E+00	8.46E-02	1.00E+00	6.93E-01	1.00E+00	2.49E-01	1.00E+00	9.74E-01	1.00E+00	9.69E-03	4.72E-01	histone acetyltransferase complex	C
GO:0000139	310	5.67E-04	5.20E-02	1.66E-04	2.80E-02	2.68E-02	1.00E+00	4.77E-04	1.31E-02	2.21E-02	1.00E+00	6.28E-02	1.00E+00	3.80E-03	6.72E-02	1.43E-03	4.40E-02	Golgi membrane	C
GO:0000149	29	3.13E-01	1.00E+00	7.11E-01	1.00E+00	3.11E-01	1.00E+00	6.46E-01	1.00E+00	4.53E-01	1.00E+00	8.71E-01	1.00E+00	3.78E-01	1.00E+00	4.38E-01	1.00E+00	SNARE binding	F
GO:0000151	85	2.43E-04	1.90E-02	1.40E-05	7.00E-03	5.28E-04	1.61E-02	3.56E-05	5.41E-03	2.33E-04	8.00E-03	5.23E-05	3.82E-03	8.06E-02	1.00E+00	1.71E-02	9.40E-01	ubiquitin ligase complex	C
GO:0000152	10	2.53E-01	1.00E+00	3.94E-02	1.00E+00	1.81E-01	1.00E+00	8.29E-02	1.00E+00	1.72E-01	1.00E+00	3.36E-02	1.00E+00	6.18E-01	1.00E+00	3.82E-02	1.00E+00	nuclear ubiquitin ligase complex	C
GO:0000155	30	7.54E-01	1.00E+00	8.06E-01	1.00E+00	9.52E-01	1.00E+00	9.81E-01	1.00E+00	6.43E-01	1.00E+00	5.92E-01	1.00E+00	6.57E-01	1.00E+00	4.47E-01	1.00E+00	two-component sensor activity	F
GO:0000159	22	4.55E-02	1.00E+00	5.16E-01	1.00E+00	7.21E-02	1.00E+00	3.71E-01	1.00E+00	7.17E-02	1.00E+00	6.38E-01	1.00E+00	5.85E-01	1.00E+00	6.76E-01	1.00E+00	protein phosphatase type 2A complex	C
GO:0000160	32	5.62E-01	1.00E+00	7.52E-01	1.00E+00	9.49E-01	1.00E+00	9.14E-01	1.00E+00	3.51E-01	1.00E+00	6.57E-01	1.00E+00	2.93E-01	1.00E+00	3.62E-01	1.00E+00	two-component signal transduction system	P
GO:0000165	146	9.12E-01	1.00E+00	9.07E-01	1.00E+00	9.95E-01	1.00E+00	9.07E-01	1.00E+00	9.15E-01	1.00E+00	6.91E-01	1.00E+00	6.47E-01	1.00E+00	6.56E-01	1.00E+00	MAPKKK cascade	P
GO:0000166	2206	1.54E-19	0.00E+00	2.30E-32	0.00E+00	1.86E-13	0.00E+00	1.46E-20	0.00E+00	2.44E-15	0.00E+00	1.26E-23	0.00E+00	3.22E-06	2.00E-03	3.32E-10	0.00E+00	nucleotide binding	F
GO:0000178	11	6.36E-02	1.00E+00	9.90E-02	1.00E+00	1.43E-01	1.00E+00	4.33E-01	1.00E+00	7.27E-02	1.00E+00	5.61E-02	1.00E+00	3.08E-01	1.00E+00	4.72E-01	1.00E+00	exosome (RNase complex)	C
GO:0000184	16	1.35E-02	9.83E-01	7.28E-04	7.30E-02	3.41E-03	1.88E-01	7.11E-03	3.78E-01	1.04E-01	1.00E+00	2.06E-01	1.00E+00	7.97E-02	1.00E+00	7.11E-02	1.00E+00	mRNA catabolism, nonsense-mediated dec	P
GO:0000186	15	8.86E-01	1.00E+00	5.63E-01	1.00E+00	7.27E-01	1.00E+00	2.75E-01	1.00E+00	7.61E-01	1.00E+00	5.41E-01	1.00E+00	9.43E-01	1.00E+00	6.94E-01	1.00E+00	activation of MAPKK activity	P
GO:0000187	51	6.79E-01	1.00E+00	6.79E-01	1.00E+00	9.48E-01	1.00E+00	9.84E-01	1.00E+00	3.69E-01	1.00E+00	3.71E-01	1.00E+00	4.29E-01	1.00E+00	1.73E-01	1.00E+00	activation of MAPK activity	P
GO:0000209	17	8.11E-02	1.00E+00	5.88E-02	1.00E+00	5.76E-02	1.00E+00	8.23E-02	1.00E+00	1.25E-02	4.81E-01	2.77E-02	1.00E+00	6.63E-01	1.00E+00	2.80E-01	1.00E+00	protein polyubiquitination	P
GO:0000226	90	4.23E-04	5.20E-02	9.61E-03	7.51E-01	3.94E-03	1.88E-01	1.17E-02	3.78E-01	9.86E-03	3.69E-01	9.56E-02	1.00E+00	6.55E-03	2.01E-01	1.63E-01	1.00E+00	microtubule cytoskeleton organization and b	P
GO:0000228	105	6.21E-07	2.00E-03	1.30E-08	2.66E-03	1.10E-06	9.88E-04	2.82E-07	1.00E-03	1.05E-05	1.56E-03	7.09E-07	2.00E-03	1.01E-02	2.17E-01	1.82E-02	9.40E-01	nuclear chromosome	C
GO:0000245	20	6.43E-02	1.00E+00	6.33E-02	1.00E+00	2.19E-01	1.00E+00	2.25E-01	1.00E+00	1.59E-01	1.00E+00	8.50E-02	1.00E+00	1.92E-01	1.00E+00	6.45E-02	1.00E+00	spliceosome assembly	P
GO:0000267	583	1.67E-01	1.00E+00	9.95E-02	1.00E+00	8.04E-01	1.00E+00	3.34E-01	1.00E+00	2.22E-01	1.00E+00	8.64E-02	1.00E+00	4.26E-02	8.34E-01	1.83E-01	1.00E+00	cell fraction	C
GO:0000271	42	9.85E-02	1.00E+00	7.56E-01	1.00E+00	2.85E-01	1.00E+00	9.89E-01	1.00E+00	5.69E-02	1.00E+00	3.91E-01	1.00E+00	1.66E-01	1.00E+00	4.72E-01	1.00E+00	polysaccharide biosynthesis	P
GO:0000272	15	7.20E-01	1.00E+00	6.52E-01	1.00E+00	8.31E-01	1.00E+00	7.88E-01	1.00E+00	8.89E-01	1.00E+00	6.72E-01	1.00E+00	4.30E-01	1.00E+00	4.01E-01	1.00E+00	polysaccharide catabolism	P
GO:0000278	273	3.45E-08	9.73E-04	5.06E-17	0.00E+00	3.58E-08	0.00E+00	4.33E-13	0.00E+00	1.24E-06	7.65E-04	5.93E-11	0.00E+00	3.65E-02	7.83E-01	3.78E-06	3.91E-03	mitotic cell cycle	P
GO:0000279	261	2.38E-13	6.62E-04	2.91E-23	0.00E+00	1.34E-13	0.00E+00	6.65E-17	0.00E+00	8.03E-09	0.00E+00	1.22E-14	0.00E+00	2.27E-03	5.54E-02	2.92E-09	0.00E+00	M phase	P
GO:0000287	384	2.28E-03	1.02E-01	7.38E-04	7.30E-02	1.45E-02	8.10E-01	1.27E-02	3.78E-01	2.29E-02	1.00E+00	8.10E-03	3.55E-01	3.74E-02	7.83E-01	5.99E-03	2.58E-01	magnesium ion binding	F
GO:0000299	15	7.54E-02	1.00E+00	3.78E-01	1.00E+00	5.22E-01	1.00E+00	5.40E-01	1.00E+00	5.02E-01	1.00E+00	4.66E-01	1.00E+00	7.30E-02	1.00E+00	3.19E-01	1.00E+00	integral to membrane of membrane fraction	C
GO:0000302	31	5.04E-02	1.00E+00	7.83E-02	1.00E+00	1.04E-01	1.00E+00	8.20E-02	1.00E+00	6.69E-02	1.00E+00	8.27E-02	1.00E+00	2.02E-01	1.00E+00	2.79E-01	1.00E+00	response to reactive oxygen species	P
GO:0000313	44	8.04E-03	6.18E-01	2.19E-03	1.62E-01	5.81E-03	1.88E-01	1.12E-01	1.00E+00	2.93E-01	1.00E+00	3.35E-03	1.43E-01	2.55E-01	1.00E+00	8.08E-02	1.00E+00	organellar ribosome	C
GO:0000314	14	3.80E-02	1.00E+00	1.36E-03	7.50E-02	7.90E-02	1.00E+00	4.27E-02	1.00E+00	3.88E-01	1.00E+00	1.66E-02	1.00E+00	2.38E-01	1.00E+00	4.62E-02	1.00E+00	organellar small ribosomal subunit	C
GO:0000315	22	3.11E-01	1.00E+00	6.73E-02	1.00E+00	3.11E-01	1.00E+00	4.01E-01	1.00E+00	2.93E-01	1.00E+00	5.75E-02	1.00E+00	7.80E-01	1.00E+00	2.13E-01	1.00E+00	organellar large ribosomal subunit	C
GO:0000323	198	2.90E-03	1.39E-01	2.33E-04	2.80E-02	9.08E-02	1.00E+00	5.79E-02	1.00E+00	1.14E-01	1.00E+00	8.41E-02	1.00E+00	1.38E-02	4.39E-01	8.06E-05	3.91E-03	lytic vacuole	C
GO:0000375	50	5.55E-04	5.20E-02	4.52E-05	2.80E-02	3.52E-03	1.88E-01	3.61E-03	1.42E-01	1.38E-02	4.81E-01	6.25E-05	5.36E-03	2.04E-01	1.00E+00	2.52E-01	1.00E+00	RNA splicing, via transesterification reaction	P
GO:0000377	50	5.55E-04	5.20E-02	4.52E-05	2.80E-02	3.52E-03	1.88E-01	3.61E-03	1.42E-01	1.38E-02	4.81E-01	6.25E-05	5.36E-03	2.04E-01	1.00E+00	2.52E-01	1.00E+00	RNA splicing, via transesterification reaction	P
GO:0000398	50	5.55E-04	5.20E-02	4.52E-05	2.80E-02	3.52E-03	1.88E-01	3.61E-03	1.42E-01	1.38E-02	4.81E-01	6.25E-05	5.36E-03	2.04E-01	1.00E+00	2.52E-01	1.00E+00	nuclear mRNA splicing, via spliceosome	P
GO:0000502	36	1.56E-03	9.30E-02	1.32E-04	2.80E-02	1.36E-02	8.10E-01	1.23E-02	3.78E-01	2.82E-02	1.00E+00	1.28E-04	1.36E-02	1.62E-01	1.00E+00	6.27E-02	1.00E+00	proteasome complex (sensu Eukaryota)	C
GO:0000723	24	1.57E-02	9.83E-01	2.55E-03	1.87E-01	4.15E-02	1.00E+00	1.42E-03	4.40E-02	7.39E-03	3.18E-01	8.46E-02	1.00E+00	6.14E-02	1.00E+00	4.03E-02	1.00E+00	telomere maintenance	P
GO:0000724	12	2.17E-02	1.00E+00	7.50E-03	5.59E-01	2.90E-01	1.00E+00	1.53E-02	7.69E-01	2.52E-02	1.00E+00	9.09E-03	3.55E-01	2.33E-02	5.60E-01	4.55E-02	1.00E+00	double-strand break repair via homologous	P
GO:0000725	12	2.17E-02	1.00E+00	7.50E-03	5.59E-01	2.90E-01	1.00E+00	1.53E-02	7.69E-01	2.52E-02	1.00E+00	9.09E-03	3.55E-01	2.33E-02	5.60E-01	4.55E-02	1.00E+00	recombinational repair	P
GO:0000775	77	1.13E-06	2.00E-03	7.75E-13	0.00E+00	9.65E-06	1.69E-03	8.71E-10	0.00E+00	1.52E-06	7.65E-04	3.28E-08	7.71E-04	1.02E-01	1.00E+00	2.62E-05	3.91E-03	chromosome, pericentric region	C
GO:0000776	39	1.38E-07	9.73E-04	6.36E-15	0.00E+00	4.13E-06	1.69E-03	1.61E-10	0.00E+00	1.72E-07	0.00E+00	2.81E-08	7.71E-04	2.48E-02	5.60E-01	1.20E-04	4.00E-03	kinetochore	C
GO:0000777	25	2.69E-04	1.90E-02	1.16E-10	2.66E-03	7.07E-04	3.00E-02	1.15E-06	1.00E-03	6.37E-04	4.40E-02	5.80E-05	5.36E-03	2.09E-01	1.00E+00	4.93E-03	2.58E-01	condensed chromosome kinetochore	C
GO:0000779	33	2.67E-05	6.00E-03	2.72E-08	2.66E-03	1.67E-04	1.61E-02	3.58E-05	5.41E-03	1.40E-04	8.00E-03	9.99E-05	5.36E-03	1.98E-01	1.00E+00	1.32E-02	9.40E-01	condensed chromosome, pericentric region	C
GO:0000781	22	1.04E-02	9.83E-01	9.26E-04	7.30E-02	3.67E-02	1.00E+00	1.46E-04	5.80E-03	3.75E-03	1.35E-01	6.36E-02	1.00E+00	6.55E-02	1.00E+00	4.32E-02	1.00E+00	chromosome, telomeric region	C
GO:0000784	10	6.93E-02	1.00E+00	1.04E-01	1.00E+00	2.39E-01	1.00E+00	3.12E-02	1.00E+00	3.26E-02	1.00E+00	6.57E-01	1.00E+00	9.73E-02	1.00E+00	4.04E-01	1.00E+00	nuclear chromosome, telomeric region	C
GO:0000785	210	8.97E-03	9.83E-01	7.97E-05	2.80E-02	4.39E-04	1.61E-02	3.15E-05	5.41E-03	2.80E-02	1.00E+00	9.41E-03	3.55E-01	7.91E-01	1.00E+00	4.69E-01	1.00E+00	chromatin	C
GO:0000786	80	9.86E-02	1.00E+00	1.01E-01	1.00E+00	6.74E-02	1.00E+00	2.02E-02	7.69E-01	1.71E-01	1.00E+00	2.78E-01	1.00E+00	8.10E-01	1.00E+00	9.46E-01	1.00E+00	nucleosome	C
GO:0000790	37	4.74E-04	5.20E-02	4.97E-06	2.86E-03	2.49E-04	1.61E-02	3.26E-05	5.41E-03	1.61E-03	4.80E-02	3.13E-04	1.36E-02	8.17E-02	1.00E+00	2.33E-02	1.00E+00	nuclear chromatin	C
GO:0000792	41	2.68E-04	1.90E-02	6.80E-06	3.00E-03	1.12E-03	7.90E-02	5.39E-05	5.41E-03	1.91E-04	8.00E-03	2.06E-04	1.36E-02	1.06E-01	1.00E+00	1.60E-02	9.40E-01	heterochromatin	C
GO:0000793	81	2.97E-08	9.73E-04	7.50E-11	2.66E-03	2.24E-07	9.88E-04	1.31E-08	0.00E+00	1.76E-07	0.00E+00	1.45E-08	7.71E-04	3.39E-02	7.53E-01	3.13E-03	2.16E-01	condensed chromosome	C
GO:0000794	39	2.51E-04	1.90E-02	6.29E-04	7.30E-02	4.70E-04	1.61E-02	1.74E-03	4.40E-02	8.23E-04	4.40E-02	6.34E-04	2.00E-02	1.11E-01	1.00E+00	8.47E-02	1.00E+00	condensed nuclear chromosome	C

GO:0000795	19	4.15E-03	1.86E-01	2.91E-04	4.20E-02	4.84E-03	1.88E-01	1.42E-03	4.40E-02	5.57E-03	1.65E-01	1.98E-03	1.43E-01	2.17E-01	1.00E+00	1.05E-03	4.40E-02	synaptonemal complex	C
GO:0000803	15	8.92E-04	9.30E-02	7.27E-03	5.59E-01	4.02E-03	1.88E-01	5.08E-03	1.42E-01	1.20E-03	4.40E-02	6.46E-02	1.00E+00	6.03E-02	1.00E+00	1.67E-01	1.00E+00	sex chromosome	C
GO:0000819	22	4.47E-02	1.00E+00	8.78E-03	5.59E-01	9.15E-02	1.00E+00	5.32E-03	1.78E-01	1.91E-02	7.19E-01	1.61E-02	1.00E+00	6.14E-01	1.00E+00	1.48E-01	1.00E+00	sister chromatid segregation	P
GO:0000902	569	8.62E-01	1.00E+00	9.93E-01	1.00E+00	9.61E-01	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	4.75E-02	1.00E+00	7.79E-01	1.00E+00	cell morphogenesis	P
GO:0000904	212	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.35E-01	1.00E+00	9.95E-01	1.00E+00	cellular morphogenesis during differentiatior	P
GO:0000910	29	2.35E-04	1.90E-02	4.59E-04	4.30E-02	1.17E-03	7.90E-02	5.12E-03	1.42E-01	8.57E-03	3.69E-01	3.82E-03	1.43E-01	5.79E-01	1.00E+00	4.61E-02	1.00E+00	cytokinesis	P
GO:0000922	22	1.82E-03	1.02E-01	6.24E-05	2.80E-02	2.11E-02	1.00E+00	3.74E-04	1.30E-02	1.54E-03	4.80E-02	4.85E-04	2.00E-02	6.23E-02	1.00E+00	6.14E-02	1.00E+00	spindle pole	C
GO:0001501	279	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	skeletal development	P
GO:0001502	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	cartilage condensation	P
GO:0001503	143	1.00E+00	1.00E+00	9.63E-01	1.00E+00	9.95E-01	1.00E+00	9.33E-01	1.00E+00	9.94E-01	1.00E+00	9.37E-01	1.00E+00	9.96E-01	1.00E+00	7.33E-01	1.00E+00	ossification	P
GO:0001504	12	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.11E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	neurotransmitter uptake	P
GO:0001505	115	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.66E-01	1.00E+00	7.78E-01	1.00E+00	regulation of neurotransmitter levels	P
GO:0001508	47	4.76E-01	1.00E+00	6.08E-01	1.00E+00	5.80E-01	1.00E+00	7.27E-01	1.00E+00	6.71E-01	1.00E+00	7.84E-01	1.00E+00	3.17E-01	1.00E+00	1.15E-01	1.00E+00	regulation of action potential	P
GO:0001518	11	8.21E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-02	1.00E+00	3.32E-01	1.00E+00	voltage-gated sodium channel complex	C
GO:0001522	13	2.85E-01	1.00E+00	9.91E-03	7.51E-01	2.46E-01	1.00E+00	1.54E-01	1.00E+00	3.71E-01	1.00E+00	4.88E-02	1.00E+00	7.25E-01	1.00E+00	8.73E-02	1.00E+00	pseudouridine synthesis	P
GO:0001523	16	6.23E-01	1.00E+00	4.41E-01	1.00E+00	1.00E+00	1.00E+00	5.82E-01	1.00E+00	4.50E-01	1.00E+00	4.33E-01	1.00E+00	2.16E-01	1.00E+00	4.36E-01	1.00E+00	retinoid metabolism	P
GO:0001525	157	9.95E-01	1.00E+00	9.73E-01	1.00E+00	9.84E-01	1.00E+00	5.36E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.76E-01	1.00E+00	9.95E-01	1.00E+00	angiogenesis	P
GO:0001533	20	8.63E-01	1.00E+00	1.00E+00	1.00E+00	4.17E-01	1.00E+00	1.00E+00	1.00E+00	5.45E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cornified envelope	C
GO:0001539	37	1.26E-01	1.00E+00	9.60E-01	1.00E+00	7.26E-01	1.00E+00	8.55E-01	1.00E+00	1.03E-01	1.00E+00	1.00E+00	1.00E+00	1.20E-01	1.00E+00	5.23E-01	1.00E+00	ciliary or flagellar motility	P
GO:0001541	25	4.93E-01	1.00E+00	1.12E-01	1.00E+00	7.75E-02	1.00E+00	3.37E-01	1.00E+00	8.79E-01	1.00E+00	1.30E-01	1.00E+00	9.64E-01	1.00E+00	7.87E-02	1.00E+00	ovarian follicle development	P
GO:0001542	10	4.38E-01	1.00E+00	7.86E-01	1.00E+00	7.75E-01	1.00E+00	9.93E-01	1.00E+00	6.52E-01	1.00E+00	1.00E+00	1.00E+00	8.04E-02	1.00E+00	1.42E-01	1.00E+00	ovulation (sensu Mammalia)	P
GO:0001558	123	3.35E-01	1.00E+00	7.25E-01	1.00E+00	5.21E-01	1.00E+00	3.55E-01	1.00E+00	9.06E-01	1.00E+00	9.58E-01	1.00E+00	4.56E-02	8.34E-01	6.71E-01	1.00E+00	regulation of cell growth	P
GO:0001565	17	1.24E-01	1.00E+00	2.27E-01	1.00E+00	2.96E-01	1.00E+00	8.14E-01	1.00E+00	1.97E-01	1.00E+00	3.43E-01	1.00E+00	3.13E-02	7.53E-01	4.14E-02	1.00E+00	phorbol ester receptor activity	F
GO:0001568	237	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	9.89E-01	1.00E+00	blood vessel development	P
GO:0001569	21	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	5.61E-01	1.00E+00	8.78E-01	1.00E+00	patterning of blood vessels	P
GO:0001570	33	9.96E-01	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.47E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	4.16E-01	1.00E+00	vasculogenesis	P
GO:0001584	695	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	8.79E-01	1.00E+00	rhodopsin-like receptor activity	F
GO:0001595	53	2.61E-01	1.00E+00	4.53E-01	1.00E+00	3.04E-01	1.00E+00	6.26E-01	1.00E+00	3.85E-01	1.00E+00	8.84E-01	1.00E+00	4.01E-01	1.00E+00	5.77E-02	1.00E+00	angiotensin receptor activity	F
GO:0001603	16	9.62E-01	1.00E+00	8.94E-01	1.00E+00	9.50E-01	1.00E+00	8.97E-01	1.00E+00	9.76E-01	1.00E+00	8.55E-01	1.00E+00	8.75E-01	1.00E+00	7.35E-01	1.00E+00	vasopressin-like receptor activity	F
GO:0001608	108	9.93E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.03E-01	1.00E+00	1.00E+00	1.00E+00	8.75E-01	1.00E+00	2.48E-01	1.00E+00	nucleotide receptor activity, G-protein coupl	F
GO:0001614	109	9.91E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.94E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	2.67E-01	1.00E+00	purinergic nucleotide receptor activity	F
GO:0001619	20	1.45E-01	1.00E+00	2.17E-01	1.00E+00	6.92E-01	1.00E+00	2.05E-01	1.00E+00	1.16E-01	1.00E+00	5.90E-01	1.00E+00	1.98E-01	1.00E+00	6.61E-02	1.00E+00	lysosphingolipid and lysophosphatidic acid r	F
GO:0001633	28	9.97E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.31E-01	1.00E+00	8.11E-01	1.00E+00	9.02E-01	1.00E+00	secretin-like receptor activity	F
GO:0001637	42	2.63E-01	1.00E+00	3.99E-01	1.00E+00	7.51E-01	1.00E+00	7.71E-01	1.00E+00	2.33E-01	1.00E+00	9.10E-01	1.00E+00	1.43E-01	1.00E+00	1.90E-02	9.40E-01	G-protein chemoattractant receptor activity	F
GO:0001649	51	9.95E-01	1.00E+00	5.22E-01	1.00E+00	8.69E-01	1.00E+00	6.05E-01	1.00E+00	9.82E-01	1.00E+00	6.02E-01	1.00E+00	9.97E-01	1.00E+00	1.63E-01	1.00E+00	osteoblast differentiation	P
GO:0001653	301	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	6.79E-01	1.00E+00	7.12E-01	1.00E+00	peptide receptor activity	F
GO:0001654	94	7.94E-01	1.00E+00	9.17E-01	1.00E+00	6.56E-01	1.00E+00	7.84E-01	1.00E+00	8.28E-01	1.00E+00	8.89E-01	1.00E+00	7.15E-01	1.00E+00	7.56E-01	1.00E+00	eye development	P
GO:0001655	92	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.91E-01	1.00E+00	9.03E-01	1.00E+00	urogenital system development	P
GO:0001656	49	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	metanephros development	P
GO:0001657	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ureteric bud development	P
GO:0001658	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.72E-01	1.00E+00	ureteric bud branching	P
GO:0001659	183	1.00E+00	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	3.78E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	thermoregulation	P
GO:0001662	12	9.61E-01	1.00E+00	4.92E-01	1.00E+00	9.87E-01	1.00E+00	7.53E-01	1.00E+00	9.44E-01	1.00E+00	5.11E-01	1.00E+00	8.20E-01	1.00E+00	3.21E-01	1.00E+00	behavioral fear response	P
GO:0001664	85	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	6.44E-01	1.00E+00	G-protein-coupled receptor binding	F
GO:0001666	73	4.48E-01	1.00E+00	5.33E-01	1.00E+00	7.82E-01	1.00E+00	7.05E-01	1.00E+00	6.02E-01	1.00E+00	5.27E-01	1.00E+00	8.41E-02	1.00E+00	2.56E-01	1.00E+00	response to hypoxia	P
GO:0001669	35	3.77E-01	1.00E+00	4.69E-01	1.00E+00	7.04E-01	1.00E+00	7.70E-01	1.00E+00	4.08E-01	1.00E+00	3.87E-01	1.00E+00	3.84E-01	1.00E+00	3.11E-01	1.00E+00	acrosome	C
GO:0001676	15	2.25E-01	1.00E+00	1.23E-01	1.00E+00	2.03E-01	1.00E+00	2.18E-01	1.00E+00	2.83E-01	1.00E+00	5.03E-02	1.00E+00	6.93E-01	1.00E+00	2.63E-01	1.00E+00	long-chain fatty acid metabolism	P
GO:0001701	144	6.63E-01	1.00E+00	1.18E-02	7.51E-01	3.44E-01	1.00E+00	4.72E-03	1.42E-01	8.63E-01	1.00E+00	1.42E-01	1.00E+00	9.18E-01	1.00E+00	1.18E-01	1.00E+00	embryonic development (sensu Mammalia)	P
GO:0001702	26	9.22E-01	1.00E+00	4.04E-01	1.00E+00	9.58E-01	1.00E+00	2.80E-01	1.00E+00	4.75E-01	1.00E+00	5.99E-01	1.00E+00	9.40E-01	1.00E+00	3.35E-01	1.00E+00	gastrulation (sensu Deuterostomia)	P
GO:0001704	37	8.00E-01	1.00E+00	1.18E-01	1.00E+00	9.10E-01	1.00E+00	2.11E-01	1.00E+00	8.39E-01	1.00E+00	3.25E-01	1.00E+00	4.10E-01	1.00E+00	1.18E-01	1.00E+00	formation of primary germ layer	P
GO:0001707	33	7.38E-01	1.00E+00	9.15E-02	1.00E+00	7.79E-01	1.00E+00	2.97E-01	1.00E+00	6.33E-01	1.00E+00	1.93E-01	1.00E+00	7.04E-01	1.00E+00	3.49E-02	1.00E+00	mesoderm formation	P
GO:0001708	33	1.00E+00	1.00E+00	5.86E-01	1.00E+00	1.00E+00	1.00E+00	2.89E-01	1.00E+00	1.00E+00	1.00E+00	9.55E-01	1.00E+00	1.00E+00	1.00E+00	8.73E-01	1.00E+00	cell fate specification	P
GO:0001709	25	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	cell fate determination	P
GO:0001725	24	4.98E-01	1.00E+00	1.00E-01	1.00E+00	8.00E-01	1.00E+00	2.53E-01	1.00E+00	4.13E-01	1.00E+00	1.86E-01	1.00E+00	3.46E-01	1.00E+00	9.28E-02	1.00E+00	stress fiber	C
GO:0001726	46	5.50E-02	1.00E+00	4.26E-02	1.00E+00	1.34E-01	1.00E+00	4.90E-02	1.00E+00	6.20E-02	1.00E+00	1.61E-01	1.00E+00	2.06E-01	1.00E+00	4.22E-01	1.00E+00	ruffle	C
GO:0001727	24	6.75E-02	1.00E+00	8.58E-02	1.00E+00	1.54E-01	1.00E+00	1.51E-01	1.00E+00	2.19E-01	1.00E+00	5.00E-02	1.00E+00	8.65E-02	1.00E+00	1.56E-01	1.00E+00	lipid kinase activity	F
GO:0001738	11	5.31E-01	1.00E+00	7.23E-01	1.00E+00	3.17E-01	1.00E+00	9.32E-01	1.00E+00	7.07E-01	1.00E+00	6.58E-01	1.00E+00	9.93E-01	1.00E+00	3.54E-01	1.00E+00	morphogenesis of a polarized epithelium	P
GO:0001739	14	1.80E-03	1.02E-01	1.69E-02	1.00E+00	4.17E-03	1.88E-01	1.32E-02	3.78E-01	3.80E-03	1.35E-01	1.01E-01	1.00E+00	8.15E-02	1.00E+00	2.32E-01	1.00E+00	sex chromatin	C
GO:0001750	17	5.24E-01	1.00E+00	4.60E-01	1.00E+00	8.31E-01	1.00E+00	4.53E-01	1.00E+00	5.80E-01	1.00E+00	9.01E-01	1.00E+00	2.24E-01	1.00E+00	1.70E-02	9.40E-01	photoreceptor outer segment	C
GO:0001754	15	8.93E-01	1.00E+00	4.60E-01	1.00E+00	2.79E-01	1.00E+00	2.18E-01	1.00E+00	8.86E-01	1.00E+00	4.77E-01	1.00E+00	1.00E+00	1.00E+00	7.74E-01	1.00E+00	eye photoreceptor cell differentiation	P
GO:0001755	23	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	9.92E-01	1.00E+00	neural crest cell migration	P
GO:0001756	34	9.96E-01	1.00E+00	8.81E-01	1.00E+00	9.92E-01	1.00E+00	8.86E-01	1.00E+00	9.98E-01	1.00E+00	7.69E-01	1.00E+00	9.99E-01	1.00E+00	7.77E-01	1.00E+00	somitogenesis	P
GO:0001759	14	9.94E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	8.84E-01	1.00E+00	8.02E-01	1.00E+00	9.26E-01	1.00E+00	9.78E-01	1.00E+00	induction of an organ	P
GO:0001763	75	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	9.63E-01	1.00E+00	morphogenesis of a branching structure	P
GO:0001764	63	9.89E-01	1.00E+00	9.55E-01	1.00E+00	9.74E-01	1.00E+00	9.92E-01	1.00E+00	9.74E-01	1.00E+00	8.34E-01	1.00E+00	9.43E-01	1.00E+00	8.98E-01	1.00E+00	neuron migration	P
GO:0001772	22	3.91E-01	1.00E+00	7.61E-01	1.00E+00	3.54E-01	1.00E+00	3.01E-01	1.00E+00	8.59E-01	1.00E+00	1.00E+00	1.00E+00	1.16E-01	1.00E+00	5.15E-01	1.00E+00	immunological synapse	C
GO:0001775	283	1.55E-01	1.00E+00	2.26E-01	1.00E+00	6.15E-01	1.00E+00	8.91E-02	1.00E+00	6.34E-01	1.00E+00	9.91E-01	1.00E+00	4.56E-02	8.34E-01	7.43E-02	1.00E+00	cell activation	P
GO:0001776	37	3.20E-01	1.00E+00	5.30E-01	1.00E+00	2.37E-01	1.00E+00	5.66E-01	1.00E+00	7.24E-01	1.00E+00	4.58E-01	1.00E+00	3.88E-01	1.00E+00	6.92E-01	1.00E+00	leukocyte homeostasis	P
GO:0001782	13	1.59E-01	1.00E+00	6.92E-01	1.00E+00	1.71E-01	1.00E+00	2.75E-01	1.00E+00	9.36E-01	1.00E+00	7.04E-01	1.00E+00	2.27E-01	1.00E+00	6.33E-01	1.00E+00	B cell homeostasis	P
GO:0001816	118	5.24E-01	1.00E+00	9.94E-01	1.00E+00	5.95E-01	1.00E+00	9.98E-01	1.00E+00	6.74E-01	1.00E+00	9.33E-01	1.00E+00	3.13E-01	1.00E+00	8.38E-01	1.00E+00	cytokine production	P
GO:0001817	13	2.40E-01	1.00E+00	9.35E-01	1.00E+00	6.07E-01	1.00E+00	9.76E-01	1.00E+00	2.59E-01	1.00E+00	7.60E-01	1.00E+00	4.79E-01	1.00E+00	9.41E-01	1.00E+00	regulation of cytokine production	P
GO:0001822	82	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.62E-01	1.00E+00	8.25E-01	1.00E+00	kidney development	P
GO:0001824	38	2.99E-01	1.00E+00	9.94E-03	7.51E-01	1.28E-01	1.00E+00	8.19E-03	3.78E-01	1.23E-01	1.00E+00	8.57E-02	1.00E+00	9.92E-01	1.00E+00	5.04E-02	1.00E+00	blastocyst development	P
GO:0001825	12	3.21E-01	1.00E+00	2.23E-01	1.00E+00	2.46E-01	1.00E+00	1.35E-01	1.00E+00	1.75E-01	1.00E+00	6.23E-01	1.00E+00	7.80E-01	1.00E+00	2.25E-01	1.00E+00	blastocyst formation	P
GO:0001832	14	6.93E-02	1.00E+00	3.09E-03	2.13E-01	3.18E-02	1.00E+00	1.66E-02	7.69E-01	1.15E-01	1.00E+00	7.52E-03	3.55E-01	6.98E-01	1.00E+00	4.67E-02	1.00E+00	blastocyst growth	P

GO:0001836	16	1.50E-01	1.00E+00	1.81E-01	1.00E+00	8.00E-01	1.00E+00	7.50E-02	1.00E+00	2.84E-01	1.00E+00	2.22E-01	1.00E+00	3.71E-01	1.00E+00	6.01E-01	1.00E+00	release of cytochrome c from mitochondria	P
GO:0001837	11	6.42E-01	1.00E+00	1.45E-01	1.00E+00	6.98E-01	1.00E+00	9.31E-02	1.00E+00	5.06E-01	1.00E+00	9.99E-01	1.00E+00	7.59E-01	1.00E+00	9.09E-01	1.00E+00	epithelial to mesenchymal transition	P
GO:0001838	48	8.00E-01	1.00E+00	2.25E-01	1.00E+00	7.40E-01	1.00E+00	1.66E-01	1.00E+00	6.87E-01	1.00E+00	3.53E-01	1.00E+00	9.66E-01	1.00E+00	4.50E-01	1.00E+00	embryonic epithelial tube formation	P
GO:0001839	49	8.01E-01	1.00E+00	1.74E-01	1.00E+00	7.82E-01	1.00E+00	1.74E-01	1.00E+00	6.92E-01	1.00E+00	3.02E-01	1.00E+00	9.19E-01	1.00E+00	2.74E-01	1.00E+00	neural plate morphogenesis	P
GO:0001841	45	7.09E-01	1.00E+00	1.45E-01	1.00E+00	6.81E-01	1.00E+00	1.11E-01	1.00E+00	5.57E-01	1.00E+00	2.61E-01	1.00E+00	9.49E-01	1.00E+00	3.30E-01	1.00E+00	neural tube formation	P
GO:0001843	33	8.95E-01	1.00E+00	4.18E-01	1.00E+00	6.72E-01	1.00E+00	4.81E-01	1.00E+00	6.40E-01	1.00E+00	4.11E-01	1.00E+00	9.99E-01	1.00E+00	5.47E-01	1.00E+00	neural tube closure	P
GO:0001871	103	8.26E-01	1.00E+00	9.89E-01	1.00E+00	9.88E-01	1.00E+00	9.61E-01	1.00E+00	9.55E-01	1.00E+00	9.97E-01	1.00E+00	6.19E-02	1.00E+00	6.79E-01	1.00E+00	pattern binding	F
GO:0001889	32	5.86E-01	1.00E+00	2.13E-01	1.00E+00	6.08E-01	1.00E+00	2.24E-01	1.00E+00	3.49E-01	1.00E+00	2.10E-01	1.00E+00	9.17E-01	1.00E+00	3.55E-01	1.00E+00	liver development	P
GO:0001890	37	3.93E-01	1.00E+00	1.31E-01	1.00E+00	5.95E-01	1.00E+00	2.37E-01	1.00E+00	2.07E-01	1.00E+00	2.12E-01	1.00E+00	4.09E-01	1.00E+00	9.07E-02	1.00E+00	placenta development	P
GO:0001892	16	3.22E-01	1.00E+00	5.39E-02	1.00E+00	2.74E-01	1.00E+00	7.86E-02	1.00E+00	1.23E-01	1.00E+00	1.46E-01	1.00E+00	8.01E-01	1.00E+00	6.58E-02	1.00E+00	embryonic placenta development	P
GO:0001894	47	6.17E-01	1.00E+00	5.53E-01	1.00E+00	4.89E-01	1.00E+00	6.70E-01	1.00E+00	8.96E-01	1.00E+00	5.15E-01	1.00E+00	6.41E-01	1.00E+00	5.43E-01	1.00E+00	tissue homeostasis	P
GO:0001906	33	4.77E-01	1.00E+00	7.70E-01	1.00E+00	3.73E-01	1.00E+00	6.65E-01	1.00E+00	9.70E-01	1.00E+00	5.55E-01	1.00E+00	9.33E-02	1.00E+00	7.48E-01	1.00E+00	cell killing	P
GO:0001909	32	3.98E-01	1.00E+00	7.17E-01	1.00E+00	3.17E-01	1.00E+00	6.13E-01	1.00E+00	9.58E-01	1.00E+00	5.01E-01	1.00E+00	7.30E-02	1.00E+00	7.02E-01	1.00E+00	leukocyte mediated cytotoxicity	P
GO:0001910	24	7.32E-01	1.00E+00	9.72E-01	1.00E+00	9.16E-01	1.00E+00	9.34E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	3.32E-02	7.53E-01	7.96E-01	1.00E+00	regulation of leukocyte mediated cytotoxicity	P
GO:0001912	18	7.34E-01	1.00E+00	9.55E-01	1.00E+00	9.15E-01	1.00E+00	8.93E-01	1.00E+00	1.00E+00	1.00E+00	7.66E-01	1.00E+00	8.21E-02	1.00E+00	8.38E-01	1.00E+00	positive regulation of leukocyte mediated cy	P
GO:0001932	96	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.21E-01	1.00E+00	6.76E-01	1.00E+00	regulation of protein amino acid phosphoryl	P
GO:0001933	15	9.56E-01	1.00E+00	9.70E-01	1.00E+00	9.94E-01	1.00E+00	6.79E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	3.64E-01	1.00E+00	9.80E-01	1.00E+00	negative regulation of protein amino acid ph	P
GO:0001934	46	9.32E-01	1.00E+00	8.65E-01	1.00E+00	9.46E-01	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	3.81E-01	1.00E+00	4.53E-01	1.00E+00	positive regulation of protein amino acid pho	P
GO:0001935	28	8.30E-01	1.00E+00	8.05E-01	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	5.55E-01	1.00E+00	4.87E-01	1.00E+00	6.82E-01	1.00E+00	8.68E-01	1.00E+00	endothelial cell proliferation	P
GO:0001936	22	8.21E-01	1.00E+00	8.05E-01	1.00E+00	9.09E-01	1.00E+00	1.00E+00	1.00E+00	5.12E-01	1.00E+00	5.17E-01	1.00E+00	7.45E-01	1.00E+00	9.01E-01	1.00E+00	regulation of endothelial cell proliferation	P
GO:0001937	14	4.95E-01	1.00E+00	5.41E-01	1.00E+00	7.67E-01	1.00E+00	9.71E-01	1.00E+00	3.24E-01	1.00E+00	3.39E-01	1.00E+00	4.70E-01	1.00E+00	8.96E-01	1.00E+00	negative regulation of endothelial cell prolife	P
GO:0001942	40	6.58E-01	1.00E+00	3.53E-01	1.00E+00	5.23E-01	1.00E+00	2.33E-01	1.00E+00	4.28E-01	1.00E+00	9.74E-01	1.00E+00	7.26E-01	1.00E+00	3.64E-01	1.00E+00	hair follicle development	P
GO:0001944	240	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.38E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	9.88E-01	1.00E+00	vasculature development	P
GO:0001947	16	6.59E-01	1.00E+00	6.09E-01	1.00E+00	6.12E-01	1.00E+00	4.16E-01	1.00E+00	5.06E-01	1.00E+00	9.78E-01	1.00E+00	9.29E-01	1.00E+00	4.18E-01	1.00E+00	heart looping	P
GO:0001948	14	9.34E-01	1.00E+00	1.58E-01	1.00E+00	9.81E-01	1.00E+00	4.28E-01	1.00E+00	8.65E-01	1.00E+00	5.05E-01	1.00E+00	4.19E-01	1.00E+00	1.10E-02	6.43E-01	glycoprotein binding	F
GO:0001952	18	8.59E-01	1.00E+00	5.72E-01	1.00E+00	7.32E-01	1.00E+00	7.35E-01	1.00E+00	8.04E-01	1.00E+00	4.78E-01	1.00E+00	6.00E-01	1.00E+00	4.15E-01	1.00E+00	regulation of cell-matrix adhesion	P
GO:0001963	13	8.35E-01	1.00E+00	9.99E-01	1.00E+00	8.46E-01	1.00E+00	9.99E-01	1.00E+00	7.29E-01	1.00E+00	9.79E-01	1.00E+00	7.87E-01	1.00E+00	9.98E-01	1.00E+00	synaptic transmission, dopaminergic	P
GO:0001964	11	5.18E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	9.98E-01	1.00E+00	4.12E-01	1.00E+00	1.00E+00	1.00E+00	1.69E-01	1.00E+00	7.90E-01	1.00E+00	startle response	P
GO:0001974	16	9.96E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	8.97E-01	1.00E+00	7.91E-01	1.00E+00	blood vessel remodeling	P
GO:0001975	11	4.27E-01	1.00E+00	9.04E-01	1.00E+00	4.18E-01	1.00E+00	9.55E-01	1.00E+00	5.61E-01	1.00E+00	8.93E-01	1.00E+00	2.49E-01	1.00E+00	5.80E-01	1.00E+00	response to amphetamine	P
GO:0001976	19	8.70E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.04E-01	1.00E+00	1.00E+00	1.00E+00	7.78E-01	1.00E+00	9.00E-01	1.00E+00	fast regulation of arterial pressure	P
GO:0001990	15	7.95E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.95E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	6.14E-01	1.00E+00	8.04E-01	1.00E+00	regulation of blood pressure by hormones	P
GO:0002009	137	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	morphogenesis of an epithelium	P
GO:0002026	12	4.24E-01	1.00E+00	9.00E-01	1.00E+00	4.75E-01	1.00E+00	6.79E-01	1.00E+00	6.03E-01	1.00E+00	9.68E-01	1.00E+00	1.02E-01	1.00E+00	5.75E-01	1.00E+00	cardiac inotropy	P
GO:0002053	14	9.15E-01	1.00E+00	9.63E-01	1.00E+00	9.98E-01	1.00E+00	9.90E-01	1.00E+00	7.61E-01	1.00E+00	9.58E-01	1.00E+00	7.75E-01	1.00E+00	7.80E-01	1.00E+00	positive regulation of mesenchymal cell prol	P
GO:0002062	20	9.81E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	8.62E-01	1.00E+00	chondrocyte differentiation	P
GO:0002064	14	8.65E-01	1.00E+00	6.91E-01	1.00E+00	9.31E-01	1.00E+00	8.93E-01	1.00E+00	8.97E-01	1.00E+00	4.77E-01	1.00E+00	4.43E-01	1.00E+00	5.37E-01	1.00E+00	epithelial cell development	P
GO:0002088	12	3.58E-01	1.00E+00	8.29E-01	1.00E+00	8.77E-01	1.00E+00	9.43E-01	1.00E+00	6.15E-01	1.00E+00	6.94E-01	1.00E+00	8.26E-02	1.00E+00	5.45E-01	1.00E+00	lens development (sensu Vertebrata)	P
GO:0002200	30	1.77E-02	9.83E-01	2.33E-02	1.00E+00	3.96E-02	1.00E+00	6.16E-02	1.00E+00	2.24E-01	1.00E+00	2.44E-01	1.00E+00	3.38E-02	7.53E-01	5.70E-03	2.58E-01	somatic diversification of immune receptors	P
GO:0002204	25	1.38E-02	9.83E-01	4.47E-02	1.00E+00	7.95E-02	1.00E+00	4.05E-02	1.00E+00	1.23E-01	1.00E+00	5.06E-01	1.00E+00	1.85E-02	4.71E-01	8.56E-03	4.48E-01	somatic recombination of immunoglobulin g	P
GO:0002208	25	1.38E-02	9.83E-01	4.47E-02	1.00E+00	7.95E-02	1.00E+00	4.05E-02	1.00E+00	1.23E-01	1.00E+00	5.06E-01	1.00E+00	1.85E-02	4.71E-01	8.56E-03	4.48E-01	somatic diversification of immunoglobulins d	P
GO:0002209	12	9.61E-01	1.00E+00	4.92E-01	1.00E+00	9.87E-01	1.00E+00	7.53E-01	1.00E+00	9.44E-01	1.00E+00	5.11E-01	1.00E+00	8.20E-01	1.00E+00	3.21E-01	1.00E+00	behavioral defense response	P
GO:0002217	425	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.64E-01	1.00E+00	9.99E-01	1.00E+00	physiological defense response	P
GO:0002228	21	2.94E-01	1.00E+00	6.18E-01	1.00E+00	2.65E-01	1.00E+00	7.20E-01	1.00E+00	9.19E-01	1.00E+00	3.80E-01	1.00E+00	7.01E-02	1.00E+00	5.21E-01	1.00E+00	natural killer cell mediated immunity	P
GO:0002245	434	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.23E-01	1.00E+00	9.22E-01	1.00E+00	physiological response to wounding	P
GO:0002250	152	5.98E-01	1.00E+00	9.04E-01	1.00E+00	7.52E-01	1.00E+00	7.63E-01	1.00E+00	7.85E-01	1.00E+00	8.61E-01	1.00E+00	4.66E-01	1.00E+00	9.60E-01	1.00E+00	adaptive immune response	P
GO:0002252	188	5.63E-01	1.00E+00	8.62E-01	1.00E+00	5.29E-01	1.00E+00	8.34E-01	1.00E+00	9.99E-01	1.00E+00	7.73E-01	1.00E+00	6.33E-02	1.00E+00	8.31E-01	1.00E+00	immune effector process	P
GO:0002253	80	6.04E-01	1.00E+00	8.05E-01	1.00E+00	4.06E-01	1.00E+00	5.72E-01	1.00E+00	9.59E-01	1.00E+00	9.44E-01	1.00E+00	1.82E-01	1.00E+00	5.58E-01	1.00E+00	activation of immune response	P
GO:0002260	29	6.66E-02	1.00E+00	7.88E-02	1.00E+00	5.04E-02	1.00E+00	8.44E-02	1.00E+00	4.61E-01	1.00E+00	1.37E-01	1.00E+00	1.34E-01	1.00E+00	2.66E-01	1.00E+00	lymphocyte homeostasis	P
GO:0002263	18	3.59E-02	1.00E+00	2.60E-01	1.00E+00	1.31E-01	1.00E+00	1.08E-01	1.00E+00	7.00E-02	1.00E+00	8.21E-01	1.00E+00	9.84E-02	1.00E+00	1.69E-01	1.00E+00	cell activation during immune response	P
GO:0002274	35	1.34E-01	1.00E+00	1.41E-01	1.00E+00	2.96E-01	1.00E+00	1.10E-01	1.00E+00	5.74E-01	1.00E+00	8.93E-01	1.00E+00	5.25E-02	1.00E+00	3.55E-02	1.00E+00	myeloid leukocyte activation	P
GO:0002285	16	5.23E-02	1.00E+00	4.56E-01	1.00E+00	1.47E-01	1.00E+00	3.15E-01	1.00E+00	1.08E-01	1.00E+00	8.80E-01	1.00E+00	1.34E-01	1.00E+00	2.53E-01	1.00E+00	lymphocyte activation during immune respo	P
GO:0002286	14	2.66E-02	1.00E+00	4.25E-01	1.00E+00	8.56E-02	1.00E+00	2.28E-01	1.00E+00	7.22E-02	1.00E+00	8.73E-01	1.00E+00	9.44E-02	1.00E+00	2.94E-01	1.00E+00	T cell activation during immune response	P
GO:0002292	12	3.41E-02	1.00E+00	4.94E-01	1.00E+00	1.44E-01	1.00E+00	2.69E-01	1.00E+00	7.67E-02	1.00E+00	9.22E-01	1.00E+00	1.05E-01	1.00E+00	3.38E-01	1.00E+00	T cell differentiation during immune respons	P
GO:0002293	12	3.41E-02	1.00E+00	4.94E-01	1.00E+00	1.44E-01	1.00E+00	2.69E-01	1.00E+00	7.67E-02	1.00E+00	9.22E-01	1.00E+00	1.05E-01	1.00E+00	3.38E-01	1.00E+00	alpha-beta T cell differentiation during immu	P
GO:0002294	12	3.41E-02	1.00E+00	4.94E-01	1.00E+00	1.44E-01	1.00E+00	2.69E-01	1.00E+00	7.67E-02	1.00E+00	9.22E-01	1.00E+00	1.05E-01	1.00E+00	3.38E-01	1.00E+00	CD4-positive, alpha-beta T cell differentiatio	P
GO:0002366	18	3.59E-02	1.00E+00	2.60E-01	1.00E+00	1.31E-01	1.00E+00	1.08E-01	1.00E+00	7.00E-02	1.00E+00	8.21E-01	1.00E+00	9.84E-02	1.00E+00	1.69E-01	1.00E+00	leukocyte activation during immune respons	P
GO:0002367	10	7.80E-01	1.00E+00	1.00E+00	1.00E+00	6.68E-01	1.00E+00	1.00E+00	1.00E+00	6.73E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cytokine production during immune respons	P
GO:0002376	839	9.94E-01	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	8.97E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	3.74E-01	1.00E+00	9.23E-01	1.00E+00	immune system process	P
GO:0002377	43	1.83E-02	9.83E-01	1.22E-01	1.00E+00	3.56E-02	1.00E+00	2.82E-01	1.00E+00	3.60E-01	1.00E+00	3.28E-01	1.00E+00	2.25E-02	5.60E-01	4.25E-02	1.00E+00	immunoglobulin production	P
GO:0002381	27	1.02E-02	9.83E-01	5.44E-02	1.00E+00	5.56E-02	1.00E+00	4.94E-02	1.00E+00	1.55E-01	1.00E+00	5.17E-01	1.00E+00	1.12E-02	4.39E-01	9.22E-03	4.48E-01	immunoglobulin production during immune r	P
GO:0002429	39	3.91E-02	1.00E+00	3.31E-01	1.00E+00	1.26E-01	1.00E+00	1.65E-01	1.00E+00	3.24E-01	1.00E+00	8.78E-01	1.00E+00	5.78E-02	1.00E+00	1.97E-01	1.00E+00	immune response-activating cell surface rec	P
GO:0002437	59	9.96E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	9.69E-01	1.00E+00	9.98E-01	1.00E+00	8.80E-01	1.00E+00	7.63E-01	1.00E+00	1.00E+00	1.00E+00	inflammatory response to antigenic stimulus	P
GO:0002438	52	9.97E-01	1.00E+00	9.80E-01	1.00E+00	9.88E-01	1.00E+00	9.34E-01	1.00E+00	9.87E-01	1.00E+00	8.41E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	acute inflammatory response to antigenic st	P
GO:0002440	48	3.23E-02	1.00E+00	2.49E-01	1.00E+00	5.27E-02	1.00E+00	4.36E-01	1.00E+00	3.93E-01	1.00E+00	4.65E-01	1.00E+00	4.41E-02	8.34E-01	1.15E-01	1.00E+00	production of molecular mediator of immune	P
GO:0002443	166	5.52E-01	1.00E+00	7.56E-01	1.00E+00	6.38E-01	1.00E+00	6.05E-01	1.00E+00	9.94E-01	1.00E+00	7.35E-01	1.00E+00	7.91E-02	1.00E+00	7.56E-01	1.00E+00	leukocyte mediated immunity	P
GO:0002444	17	1.44E-01	1.00E+00	3.79E-01	1.00E+00	2.98E-01	1.00E+00	2.19E-01	1.00E+00	6.85E-01	1.00E+00	9.48E-01	1.00E+00	7.81E-02	1.00E+00	1.45E-01	1.00E+00	myeloid leukocyte mediated immunity	P
GO:0002449	155	7.36E-01	1.00E+00	7.99E-01	1.00E+00	7.26E-01	1.00E+00	7.15E-01	1.00E+00	9.92E-01	1.00E+00	6.60E-01	1.00E+00	2.28E-01	1.00E+00	8.77E-01	1.00E+00	lymphocyte mediated immunity	P
GO:0002455	33	9.14E-01	1.00E+00	9.70E-01	1.00E+00	8.45E-01	1.00E+00	9.63E-01	1.00E+00	9.98E-01	1.00E+00	8.65E-01	1.00E+00	5.28E-01	1.00E+00	9.08E-01	1.00E+00	humoral immune response mediated by circ	P
GO:0002456	18	2.58E-01	1.00E+00	2.55E-01	1.00E+00	3.53E-01	1.00E+00	1.37E-01	1.00E+00	4.97E-01	1.00E+00	5.00E-01	1.00E+00	2.11E-01	1.00E+00	3.92E-01	1.00E+00	T cell mediated immunity	P
GO:0002460	152	5.98E-01	1.00E+00	9.04E-01	1.00E+00	7.52E-01	1.00E+00	7.63E-01	1.00E+00	7.85E-01	1.00E+00	8.61E-01	1.00E+00	4.66E-01	1.00E+00	9.60E-01	1.00E+00	adaptive immune response (sensu Gnathos	P
GO:0002474	18	9.69E-01	1.00E+00	1.19E-01	1.00E+00	8.16E-01	1.00E+00	5.61E-02	1.00E+00	8.28E-01	1.00E+00	1.06E-01	1.00E+00	9.99E-01	1.00E+00	8.75E-01	1.00E+00	antigen processing and presentation of pept	P
GO:0002478	18	7.69E-01	1.00E+00	1.76E-01	1.00E+00	7.08E-01	1.00E+00	1.84E-01	1.00E+00	2.67E-01	1.00E+00	3.22E-01	1.00E+00	9.98E-01	1.00E+00	8.08E-01	1.00E+00	antigen processing and presentation of exog	P
GO:0002495	16	9.41E-01	1.00E+00	2.76E-01	1.00E+00	9.66E-01	1.00E+00	2.42E-01	1.00E+00	3.33E-01	1.00E+00	4.68E-01	1.00E+00	9.99E-01	1.00E+00	8.42E-01	1.00E+00	antigen processing and presentation of pept	P
GO:0002504	18	9.20E-01	1.00E+00	3.22E-01	1.00E+00	9.17E-01	1.00E+00	2.51E-01	1.00E+00	4.34E-01	1.00E+00	5.07E-01	1.00E+00	9.90E-01	1.00E+00	8.63E-01	1.00E+00	antigen processing and presentation of pept	P

GO:0002520	308	8.02E-01	1.00E+00	5.34E-01	1.00E+00	8.71E-01	1.00E+00	2.24E-01	1.00E+00	7.46E-01	1.00E+00	9.60E-01	1.00E+00	9.02E-01	1.00E+00	8.29E-01	1.00E+00	immune system development	P
GO:0002521	154	5.60E-01	1.00E+00	3.53E-01	1.00E+00	6.87E-01	1.00E+00	1.39E-01	1.00E+00	6.69E-01	1.00E+00	9.85E-01	1.00E+00	5.74E-01	1.00E+00	5.07E-01	1.00E+00	leukocyte differentiation	P
GO:0002524	52	9.97E-01	1.00E+00	9.80E-01	1.00E+00	9.88E-01	1.00E+00	9.34E-01	1.00E+00	9.87E-01	1.00E+00	8.41E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	hypersensitivity	P
GO:0002526	121	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.83E-01	1.00E+00	9.97E-01	1.00E+00	acute inflammatory response	P
GO:0002541	37	9.88E-01	1.00E+00	9.98E-01	1.00E+00	8.33E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	5.78E-01	1.00E+00	9.61E-01	1.00E+00	activation of plasma proteins during acute ir	P
GO:0002562	28	9.04E-03	9.83E-01	2.12E-02	1.00E+00	4.45E-02	1.00E+00	5.88E-02	1.00E+00	1.55E-01	1.00E+00	2.56E-01	1.00E+00	1.54E-02	4.39E-01	2.95E-03	2.16E-01	somatic diversification of immune receptors	P
GO:0002573	53	6.60E-01	1.00E+00	7.71E-01	1.00E+00	7.56E-01	1.00E+00	6.26E-01	1.00E+00	3.77E-01	1.00E+00	8.57E-01	1.00E+00	8.93E-01	1.00E+00	5.94E-01	1.00E+00	myeloid leukocyte differentiation	P
GO:0002673	10	8.34E-01	1.00E+00	8.20E-01	1.00E+00	7.43E-01	1.00E+00	7.32E-01	1.00E+00	6.74E-01	1.00E+00	8.88E-01	1.00E+00	7.28E-01	1.00E+00	7.24E-01	1.00E+00	regulation of acute inflammatory response	P
GO:0002682	127	4.05E-01	1.00E+00	9.44E-01	1.00E+00	7.36E-01	1.00E+00	9.58E-01	1.00E+00	9.61E-01	1.00E+00	9.79E-01	1.00E+00	1.80E-02	4.71E-01	3.20E-01	1.00E+00	regulation of immune system process	P
GO:0002683	12	5.14E-02	1.00E+00	7.66E-01	1.00E+00	6.55E-01	1.00E+00	6.66E-01	1.00E+00	9.58E-02	1.00E+00	9.90E-01	1.00E+00	5.18E-02	1.00E+00	5.61E-01	1.00E+00	negative regulation of immune system proce	P
GO:0002684	108	7.68E-01	1.00E+00	9.37E-01	1.00E+00	7.55E-01	1.00E+00	8.71E-01	1.00E+00	9.95E-01	1.00E+00	9.76E-01	1.00E+00	1.24E-01	1.00E+00	5.89E-01	1.00E+00	positive regulation of immune system proce	P
GO:0002697	25	5.84E-01	1.00E+00	9.47E-01	1.00E+00	7.51E-01	1.00E+00	8.65E-01	1.00E+00	7.99E-01	1.00E+00	9.82E-01	1.00E+00	2.32E-01	1.00E+00	8.91E-01	1.00E+00	regulation of immune effector process	P
GO:0002699	21	5.14E-01	1.00E+00	9.02E-01	1.00E+00	5.89E-01	1.00E+00	9.03E-01	1.00E+00	7.61E-01	1.00E+00	9.69E-01	1.00E+00	2.98E-01	1.00E+00	7.40E-01	1.00E+00	positive regulation of immune effector proce	P
GO:0002703	24	5.41E-01	1.00E+00	9.38E-01	1.00E+00	7.10E-01	1.00E+00	8.36E-01	1.00E+00	7.69E-01	1.00E+00	9.78E-01	1.00E+00	2.21E-01	1.00E+00	9.01E-01	1.00E+00	regulation of leukocyte mediated immunity	P
GO:0002705	20	4.66E-01	1.00E+00	8.87E-01	1.00E+00	5.37E-01	1.00E+00	8.75E-01	1.00E+00	7.25E-01	1.00E+00	9.63E-01	1.00E+00	2.85E-01	1.00E+00	7.56E-01	1.00E+00	positive regulation of leukocyte mediated im	P
GO:0002706	24	5.41E-01	1.00E+00	9.38E-01	1.00E+00	7.10E-01	1.00E+00	8.36E-01	1.00E+00	7.69E-01	1.00E+00	9.78E-01	1.00E+00	2.21E-01	1.00E+00	9.01E-01	1.00E+00	regulation of lymphocyte mediated immunity	P
GO:0002708	20	4.66E-01	1.00E+00	8.87E-01	1.00E+00	5.37E-01	1.00E+00	8.75E-01	1.00E+00	7.25E-01	1.00E+00	9.63E-01	1.00E+00	2.85E-01	1.00E+00	7.56E-01	1.00E+00	positive regulation of lymphocyte mediated i	P
GO:0002712	14	7.32E-01	1.00E+00	8.77E-01	1.00E+00	8.37E-01	1.00E+00	6.87E-01	1.00E+00	8.41E-01	1.00E+00	9.73E-01	1.00E+00	2.50E-01	1.00E+00	6.58E-01	1.00E+00	regulation of B cell mediated immunity	P
GO:0002714	11	7.89E-01	1.00E+00	8.51E-01	1.00E+00	7.40E-01	1.00E+00	7.96E-01	1.00E+00	8.66E-01	1.00E+00	9.77E-01	1.00E+00	4.10E-01	1.00E+00	4.52E-01	1.00E+00	positive regulation of B cell mediated immur	P
GO:0002757	43	5.38E-02	1.00E+00	1.63E-01	1.00E+00	1.15E-01	1.00E+00	7.44E-02	1.00E+00	2.91E-01	1.00E+00	6.62E-01	1.00E+00	9.34E-02	1.00E+00	1.54E-01	1.00E+00	immune response-activating signal transduc	P
GO:0002761	24	9.40E-01	1.00E+00	8.51E-01	1.00E+00	7.73E-01	1.00E+00	8.14E-01	1.00E+00	9.08E-01	1.00E+00	7.42E-01	1.00E+00	1.00E+00	1.00E+00	7.93E-01	1.00E+00	regulation of myeloid leukocyte differentiatic	P
GO:0002762	10	8.05E-01	1.00E+00	2.02E-01	1.00E+00	2.81E-01	1.00E+00	3.94E-01	1.00E+00	9.48E-01	1.00E+00	2.12E-01	1.00E+00	9.82E-01	1.00E+00	3.44E-01	1.00E+00	negative regulation of myeloid leukocyte diff	P
GO:0002763	11	9.43E-01	1.00E+00	9.45E-01	1.00E+00	9.65E-01	1.00E+00	9.10E-01	1.00E+00	8.74E-01	1.00E+00	9.22E-01	1.00E+00	9.95E-01	1.00E+00	8.58E-01	1.00E+00	positive regulation of myeloid leukocyte diffe	P
GO:0002764	46	2.88E-02	1.00E+00	1.77E-01	1.00E+00	1.64E-01	1.00E+00	7.66E-02	1.00E+00	2.43E-01	1.00E+00	7.08E-01	1.00E+00	3.15E-02	7.53E-01	1.36E-01	1.00E+00	immune response-regulating signal transduc	P
GO:0002768	42	1.99E-02	1.00E+00	3.51E-01	1.00E+00	1.80E-01	1.00E+00	1.69E-01	1.00E+00	2.68E-01	1.00E+00	9.05E-01	1.00E+00	1.75E-02	4.71E-01	1.73E-01	1.00E+00	immune response-regulating cell surface re	P
GO:0002790	45	7.33E-01	1.00E+00	6.81E-01	1.00E+00	9.04E-01	1.00E+00	8.84E-01	1.00E+00	2.22E-01	1.00E+00	5.60E-01	1.00E+00	9.29E-01	1.00E+00	3.08E-01	1.00E+00	peptide secretion	P
GO:0002819	26	5.72E-01	1.00E+00	8.78E-01	1.00E+00	8.29E-01	1.00E+00	6.60E-01	1.00E+00	5.20E-01	1.00E+00	9.96E-01	1.00E+00	3.72E-01	1.00E+00	9.14E-01	1.00E+00	regulation of adaptive immune response	P
GO:0002821	20	5.15E-01	1.00E+00	7.53E-01	1.00E+00	6.01E-01	1.00E+00	6.19E-01	1.00E+00	6.08E-01	1.00E+00	9.90E-01	1.00E+00	4.50E-01	1.00E+00	7.43E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002822	26	5.72E-01	1.00E+00	8.78E-01	1.00E+00	8.29E-01	1.00E+00	6.60E-01	1.00E+00	5.20E-01	1.00E+00	9.96E-01	1.00E+00	3.72E-01	1.00E+00	9.14E-01	1.00E+00	regulation of adaptive immune response (se	P
GO:0002824	20	5.15E-01	1.00E+00	7.53E-01	1.00E+00	6.01E-01	1.00E+00	6.19E-01	1.00E+00	6.08E-01	1.00E+00	9.90E-01	1.00E+00	4.50E-01	1.00E+00	7.43E-01	1.00E+00	positive regulation of adaptive immune resp	P
GO:0002861	14	7.44E-01	1.00E+00	8.23E-01	1.00E+00	9.39E-01	1.00E+00	8.05E-01	1.00E+00	9.18E-01	1.00E+00	9.52E-01	1.00E+00	3.07E-01	1.00E+00	7.50E-01	1.00E+00	regulation of inflammatory response to antic	P
GO:0002863	10	9.03E-01	1.00E+00	5.74E-01	1.00E+00	7.83E-01	1.00E+00	5.22E-01	1.00E+00	8.23E-01	1.00E+00	8.73E-01	1.00E+00	7.70E-01	1.00E+00	6.51E-01	1.00E+00	positive regulation of inflammatory response	P
GO:0002864	10	8.34E-01	1.00E+00	8.20E-01	1.00E+00	7.43E-01	1.00E+00	7.32E-01	1.00E+00	6.74E-01	1.00E+00	8.88E-01	1.00E+00	7.28E-01	1.00E+00	7.24E-01	1.00E+00	regulation of acute inflammatory response t	P
GO:0002883	10	8.34E-01	1.00E+00	8.20E-01	1.00E+00	7.43E-01	1.00E+00	7.32E-01	1.00E+00	6.74E-01	1.00E+00	8.88E-01	1.00E+00	7.28E-01	1.00E+00	7.24E-01	1.00E+00	regulation of hypersensitivity	P
GO:0002889	14	7.32E-01	1.00E+00	8.77E-01	1.00E+00	8.37E-01	1.00E+00	6.87E-01	1.00E+00	8.41E-01	1.00E+00	9.73E-01	1.00E+00	2.50E-01	1.00E+00	6.58E-01	1.00E+00	regulation of immunoglobulin mediated imm	P
GO:0002891	11	7.89E-01	1.00E+00	8.51E-01	1.00E+00	7.40E-01	1.00E+00	7.96E-01	1.00E+00	8.66E-01	1.00E+00	9.77E-01	1.00E+00	4.10E-01	1.00E+00	4.52E-01	1.00E+00	positive regulation of immunoglobulin media	P
GO:0003674	15302	1.21E-29	0.00E+00	1.40E-45	0.00E+00	4.91E-14	0.00E+00	6.21E-26	0.00E+00	6.05E-17	0.00E+00	3.39E-16	0.00E+00	2.81E-09	0.00E+00	4.50E-20	0.00E+00	molecular_function	F
GO:0003676	3286	1.20E-04	1.90E-02	1.41E-22	0.00E+00	1.01E-07	9.88E-04	1.08E-23	0.00E+00	2.31E-05	1.56E-03	1.11E-15	0.00E+00	9.87E-01	1.00E+00	1.49E-01	1.00E+00	nucleic acid binding	F
GO:0003677	2156	2.78E-02	1.00E+00	1.58E-07	2.66E-03	2.86E-03	1.27E-01	1.36E-09	0.00E+00	1.38E-02	4.81E-01	7.30E-04	2.06E-02	9.19E-01	1.00E+00	1.25E-01	1.00E+00	DNA binding	F
GO:0003678	25	7.86E-03	6.18E-01	8.89E-05	2.80E-02	1.37E-01	1.00E+00	1.81E-03	4.40E-02	5.03E-03	1.35E-01	1.48E-02	1.00E+00	6.79E-02	1.00E+00	4.15E-05	3.91E-03	DNA helicase activity	F
GO:0003682	129	1.36E-01	1.00E+00	1.45E-03	7.50E-02	1.14E-01	1.00E+00	3.50E-02	1.00E+00	2.23E-01	1.00E+00	2.05E-02	1.00E+00	3.11E-01	1.00E+00	2.08E-02	1.00E+00	chromatin binding	F
GO:0003684	33	4.72E-02	1.00E+00	6.73E-04	7.30E-02	1.14E-01	1.00E+00	1.85E-03	4.40E-02	2.66E-02	1.00E+00	1.45E-02	1.00E+00	3.42E-01	1.00E+00	1.33E-02	9.40E-01	damaged DNA binding	F
GO:0003690	41	3.27E-01	1.00E+00	7.83E-02	1.00E+00	3.58E-01	1.00E+00	4.46E-02	1.00E+00	3.75E-01	1.00E+00	9.80E-02	1.00E+00	4.77E-01	1.00E+00	5.66E-01	1.00E+00	double-stranded DNA binding	F
GO:0003697	37	4.91E-02	1.00E+00	6.32E-02	1.00E+00	6.20E-02	1.00E+00	1.41E-01	1.00E+00	1.36E-01	1.00E+00	4.36E-02	1.00E+00	2.06E-01	1.00E+00	3.12E-01	1.00E+00	single-stranded DNA binding	F
GO:0003700	883	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.84E-01	1.00E+00	9.51E-01	1.00E+00	transcription factor activity	F
GO:0003702	91	1.33E-01	1.00E+00	4.30E-02	1.00E+00	2.29E-02	1.00E+00	9.87E-03	3.78E-01	6.17E-01	1.00E+00	2.03E-01	1.00E+00	4.15E-01	1.00E+00	4.16E-01	1.00E+00	RNA polymerase II transcription factor activi	F
GO:0003705	21	9.27E-01	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	9.98E-01	1.00E+00	8.99E-01	1.00E+00	9.89E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	RNA polymerase II transcription factor activi	F
GO:0003707	53	8.25E-01	1.00E+00	9.76E-01	1.00E+00	8.71E-01	1.00E+00	9.57E-01	1.00E+00	9.53E-01	1.00E+00	8.64E-01	1.00E+00	1.65E-01	1.00E+00	8.89E-01	1.00E+00	steroid hormone receptor activity	F
GO:0003708	24	7.34E-01	1.00E+00	8.67E-01	1.00E+00	5.75E-01	1.00E+00	3.39E-01	1.00E+00	8.63E-01	1.00E+00	8.95E-01	1.00E+00	4.59E-01	1.00E+00	9.98E-01	1.00E+00	retinoic acid receptor activity	F
GO:0003711	13	3.28E-02	1.00E+00	1.29E-02	7.51E-01	2.23E-02	1.00E+00	2.19E-03	4.50E-02	2.83E-01	1.00E+00	5.83E-02	1.00E+00	5.53E-02	1.00E+00	1.52E-01	1.00E+00	transcriptional elongation regulator activity	F
GO:0003712	163	9.90E-03	9.83E-01	6.64E-04	7.30E-02	2.66E-03	1.18E-01	9.72E-04	3.60E-02	7.39E-02	1.00E+00	3.95E-02	1.00E+00	4.04E-01	1.00E+00	5.13E-02	1.00E+00	transcription cofactor activity	F
GO:0003713	92	3.04E-03	1.39E-01	7.04E-04	7.30E-02	1.47E-03	7.90E-02	1.46E-03	4.40E-02	3.97E-02	1.00E+00	6.86E-02	1.00E+00	1.81E-01	1.00E+00	5.51E-02	1.00E+00	transcription coactivator activity	F
GO:0003714	59	1.66E-01	1.00E+00	1.15E-01	1.00E+00	2.05E-01	1.00E+00	2.33E-01	1.00E+00	2.01E-01	1.00E+00	1.29E-01	1.00E+00	5.34E-01	1.00E+00	2.08E-01	1.00E+00	transcription corepressor activity	F
GO:0003723	608	8.25E-09	9.73E-04	1.60E-27	0.00E+00	1.92E-08	0.00E+00	3.53E-18	0.00E+00	5.43E-05	1.56E-03	7.79E-19	0.00E+00	2.34E-01	1.00E+00	8.25E-04	3.30E-02	RNA binding	F
GO:0003725	37	8.05E-02	1.00E+00	1.57E-03	7.50E-02	1.33E-01	1.00E+00	1.87E-02	7.69E-01	7.71E-02	1.00E+00	3.78E-03	1.43E-01	1.15E-01	1.00E+00	8.05E-03	4.48E-01	double-stranded RNA binding	F
GO:0003727	19	4.40E-01	1.00E+00	5.63E-01	1.00E+00	1.80E-01	1.00E+00	2.06E-01	1.00E+00	4.36E-01	1.00E+00	6.14E-01	1.00E+00	8.83E-01	1.00E+00	9.90E-01	1.00E+00	single-stranded RNA binding	F
GO:0003729	41	8.49E-01	1.00E+00	2.04E-02	1.00E+00	3.11E-01	1.00E+00	3.03E-03	1.42E-01	8.03E-01	1.00E+00	1.53E-01	1.00E+00	9.98E-01	1.00E+00	6.33E-01	1.00E+00	mRNA binding	F
GO:0003735	221	7.99E-01	1.00E+00	4.45E-02	1.00E+00	7.50E-01	1.00E+00	1.04E-02	3.78E-01	4.39E-01	1.00E+00	3.19E-01	1.00E+00	1.00E+00	1.00E+00	6.59E-01	1.00E+00	structural constituent of ribosome	F
GO:0003743	83	7.04E-05	7.00E-03	1.21E-09	2.66E-03	5.75E-04	2.20E-02	8.74E-05	5.80E-03	3.84E-05	1.56E-03	1.08E-08	7.71E-04	3.17E-01	1.00E+00	3.90E-02	1.00E+00	translation initiation factor activity	F
GO:0003746	35	4.57E-01	1.00E+00	5.10E-01	1.00E+00	1.85E-01	1.00E+00	3.30E-01	1.00E+00	6.38E-01	1.00E+00	5.46E-01	1.00E+00	6.42E-01	1.00E+00	4.83E-01	1.00E+00	translation elongation factor activity	F
GO:0003755	33	3.74E-04	5.20E-02	4.31E-05	2.80E-02	1.33E-03	7.90E-02	4.66E-03	1.42E-01	1.30E-02	4.81E-01	9.88E-05	5.36E-03	6.59E-03	2.01E-01	2.10E-02	1.00E+00	peptidyl-prolyl cis-trans isomerase activity	F
GO:0003774	161	7.82E-06	5.00E-03	1.85E-02	1.00E+00	2.01E-03	1.18E-01	2.39E-02	7.69E-01	3.94E-04	1.90E-02	9.75E-02	1.00E+00	1.41E-03	3.80E-02	7.01E-02	1.00E+00	motor activity	F
GO:0003777	78	6.74E-05	7.00E-03	5.46E-05	2.80E-02	1.98E-04	1.61E-02	3.17E-04	1.30E-02	1.37E-03	4.80E-02	1.58E-03	5.10E-02	6.07E-02	1.00E+00	1.26E-02	9.40E-01	microtubule motor activity	F
GO:0003779	305	2.10E-03	1.02E-01	1.04E-01	1.00E+00	8.34E-02	1.00E+00	5.77E-01	1.00E+00	6.90E-02	1.00E+00	3.00E-01	1.00E+00	1.01E-04	3.00E-03	1.65E-02	9.40E-01	actin binding	F
GO:0003796	11	1.95E-01	1.00E+00	5.92E-01	1.00E+00	8.09E-01	1.00E+00	3.73E-01	1.00E+00	9.62E-01	1.00E+00	4.26E-01	1.00E+00	5.84E-02	1.00E+00	4.37E-01	1.00E+00	lysozyme activity	F
GO:0003810	11	9.78E-01	1.00E+00	9.44E-01	1.00E+00	9.94E-01	1.00E+00	9.27E-01	1.00E+00	9.64E-01	1.00E+00	7.32E-01	1.00E+00	8.11E-01	1.00E+00	9.76E-01	1.00E+00	protein-glutamine gamma-glutamyltransfera	F
GO:0003823	49	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	antigen binding	F
GO:0003824	5745	8.01E-35	0.00E+00	3.84E-42	0.00E+00	5.33E-20	0.00E+00	2.41E-20	0.00E+00	1.74E-20	0.00E+00	1.85E-28	0.00E+00	3.37E-15	0.00E+00	8.55E-24	0.00E+00	catalytic activity	F
GO:0003854	20	9.18E-01	1.00E+00	7.64E-01	1.00E+00	6.83E-01	1.00E+00	9.60E-01	1.00E+00	6.09E-01	1.00E+00	4.86E-01	1.00E+00	9.93E-01	1.00E+00	5.78E-01	1.00E+00	3-beta-hydroxy-delta5-steroid dehydrogena	F
GO:0003887	32	3.98E-01	1.00E+00	1.82E-01	1.00E+00	1.56E-01	1.00E+00	1.48E-01	1.00E+00	2.82E-01	1.00E+00	1.53E-01	1.00E+00	9.77E-01	1.00E+00	5.86E-01	1.00E+00	DNA-directed DNA polymerase activity	F
GO:0003899	38	8.52E-05	7.00E-03	3.07E-05	2.80E-02	2.72E-04	1.61E-02	2.62E-05	1.92E-03	3.70E-03	1.35E-01	5.77E-04	2.00E-02	2.89E-01	1.00E+00	3.79E-02	1.00E+00	DNA-directed RNA polymerase activity	F
GO:0003916	20	1.06E-01	1.00E+00	1.32E-01	1.00E+00	5.73E-02	1.00E+00	4.44E-01	1.00E+00	2.23E-01	1.00E+00	9.97E-02	1.00E+00	4.64E-01	1.00E+00	6.30E-01	1.00E+00	DNA topoisomerase activity	F
GO:0003918	17	1.43E-01	1.00E+00	1.25E-01	1.00E+00	2.87E-02	1.00E+00	4.87E-01	1.00E+00	3.54E-01	1.00E+00	1.10E-01	1.00E+00	6.26E-01	1.00E+00	5.92E-01	1.00E+00	DNA topoisomerase (ATP-hydrolyzing) activ	F
GO:0003924	231	3.91E-02	1.00E+00	5.33E-02	1.00E+00	1.68E-01	1.00E+00	5.95E-02	1.00E+00	4.16E-02	1.00E+00	9.66E-02	1.00E+00	1.06E-01	1.00E+00	2.66E-01	1.00E+00	GTPase activity	F
GO:0003950	19	1.61E-03	9.30E-02	1.50E-04	2.80E-02	1.51E-02	8.10E-01	5.82E-05	5.80E-03	3.89E-03	1.35E-01	8.26E-04	4.80E-02	1.42E-02	4.39E-01	2.52E-02	1.00E+00	NAD+ ADP-ribosyltransferase activity	F

GO:0003954	34	4.49E-02	1.00E+00	4.42E-04	4.30E-02	6.32E-02	1.00E+00	1.51E-04	5.80E-03	5.79E-01	1.00E+00	2.15E-02	1.00E+00	8.09E-02	1.00E+00	1.10E-01	1.00E+00	NADH dehydrogenase activity	F
GO:0003993	16	3.19E-02	1.00E+00	1.36E-01	1.00E+00	3.09E-01	1.00E+00	3.74E-01	1.00E+00	1.18E-01	1.00E+00	1.24E-01	1.00E+00	2.77E-02	6.06E-01	1.72E-01	1.00E+00	acid phosphatase activity	F
GO:0003995	17	3.52E-03	1.86E-01	2.50E-02	1.00E+00	3.66E-03	1.88E-01	3.55E-02	1.00E+00	6.09E-03	1.65E-01	4.19E-02	1.00E+00	9.73E-02	1.00E+00	6.43E-01	1.00E+00	acyl-CoA dehydrogenase activity	F
GO:0004003	14	1.91E-02	9.83E-01	3.28E-03	2.13E-01	6.14E-02	1.00E+00	3.51E-02	1.00E+00	3.22E-02	1.00E+00	2.21E-02	1.00E+00	3.83E-02	7.83E-01	3.66E-04	2.10E-02	ATP-dependent DNA helicase activity	F
GO:0004012	16	8.31E-01	1.00E+00	8.67E-01	1.00E+00	9.74E-01	1.00E+00	9.63E-01	1.00E+00	8.86E-01	1.00E+00	8.98E-01	1.00E+00	2.23E-01	1.00E+00	7.63E-01	1.00E+00	phospholipid-translocating ATPase activity	F
GO:0004016	11	8.74E-01	1.00E+00	9.81E-01	1.00E+00	9.46E-01	1.00E+00	5.58E-01	1.00E+00	7.16E-01	1.00E+00	1.00E+00	1.00E+00	6.07E-01	1.00E+00	6.58E-01	1.00E+00	adenylate cyclase activity	F
GO:0004022	35	3.00E-01	1.00E+00	4.48E-01	1.00E+00	5.66E-01	1.00E+00	9.34E-01	1.00E+00	3.35E-01	1.00E+00	2.94E-01	1.00E+00	1.11E-01	1.00E+00	1.77E-01	1.00E+00	alcohol dehydrogenase activity	F
GO:0004033	11	9.17E-01	1.00E+00	3.77E-01	1.00E+00	9.05E-01	1.00E+00	6.20E-01	1.00E+00	7.47E-01	1.00E+00	1.55E-01	1.00E+00	8.73E-01	1.00E+00	7.95E-01	1.00E+00	aldo-keto reductase activity	F
GO:0004089	19	5.69E-01	1.00E+00	8.42E-01	1.00E+00	4.90E-01	1.00E+00	7.18E-01	1.00E+00	4.07E-01	1.00E+00	9.49E-01	1.00E+00	9.11E-01	1.00E+00	5.42E-01	1.00E+00	carbonate dehydratase activity	F
GO:0004091	36	3.69E-01	1.00E+00	9.14E-01	1.00E+00	7.50E-01	1.00E+00	9.36E-01	1.00E+00	4.85E-01	1.00E+00	7.35E-01	1.00E+00	1.76E-01	1.00E+00	6.34E-01	1.00E+00	carboxylesterase activity	F
GO:0004104	18	8.68E-01	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	9.94E-01	1.00E+00	3.77E-01	1.00E+00	1.00E+00	1.00E+00	cholinesterase activity	F
GO:0004112	27	4.04E-01	1.00E+00	6.06E-01	1.00E+00	3.16E-01	1.00E+00	9.08E-01	1.00E+00	3.61E-01	1.00E+00	2.03E-01	1.00E+00	3.75E-01	1.00E+00	6.21E-01	1.00E+00	cyclic-nucleotide phosphodiesterase activity	F
GO:0004114	25	4.78E-01	1.00E+00	6.92E-01	1.00E+00	5.51E-01	1.00E+00	9.80E-01	1.00E+00	3.52E-01	1.00E+00	2.09E-01	1.00E+00	3.04E-01	1.00E+00	6.21E-01	1.00E+00	3',5'-cyclic-nucleotide phosphodiesterase ac	F
GO:0004129	25	1.54E-01	1.00E+00	7.74E-02	1.00E+00	5.86E-02	1.00E+00	3.32E-01	1.00E+00	1.31E-01	1.00E+00	8.33E-02	1.00E+00	7.86E-01	1.00E+00	1.77E-01	1.00E+00	cytochrome-c oxidase activity	F
GO:0004143	15	7.85E-01	1.00E+00	6.67E-01	1.00E+00	5.99E-01	1.00E+00	5.70E-01	1.00E+00	6.74E-01	1.00E+00	5.99E-01	1.00E+00	9.86E-01	1.00E+00	8.70E-01	1.00E+00	diacylglycerol kinase activity	F
GO:0004175	497	4.40E-01	1.00E+00	6.06E-01	1.00E+00	7.17E-01	1.00E+00	9.91E-01	1.00E+00	9.58E-01	1.00E+00	7.28E-01	1.00E+00	1.74E-02	4.71E-01	5.58E-03	2.58E-01	endopeptidase activity	F
GO:0004176	17	2.83E-01	1.00E+00	3.86E-01	1.00E+00	2.73E-01	1.00E+00	2.22E-01	1.00E+00	7.09E-01	1.00E+00	7.69E-01	1.00E+00	3.81E-01	1.00E+00	4.27E-01	1.00E+00	ATP-dependent peptidase activity	F
GO:0004177	42	5.67E-01	1.00E+00	3.94E-01	1.00E+00	3.34E-01	1.00E+00	2.78E-01	1.00E+00	7.61E-01	1.00E+00	4.63E-01	1.00E+00	8.02E-01	1.00E+00	5.51E-01	1.00E+00	aminopeptidase activity	F
GO:0004179	12	5.82E-01	1.00E+00	5.50E-01	1.00E+00	3.65E-01	1.00E+00	4.12E-01	1.00E+00	6.80E-01	1.00E+00	4.43E-01	1.00E+00	7.66E-01	1.00E+00	9.34E-01	1.00E+00	membrane alanyl aminopeptidase activity	F
GO:0004180	46	9.50E-01	1.00E+00	8.46E-01	1.00E+00	9.41E-01	1.00E+00	7.29E-01	1.00E+00	7.98E-01	1.00E+00	9.16E-01	1.00E+00	7.84E-01	1.00E+00	6.08E-01	1.00E+00	carboxypeptidase activity	F
GO:0004181	33	8.71E-01	1.00E+00	8.37E-01	1.00E+00	8.33E-01	1.00E+00	6.62E-01	1.00E+00	7.63E-01	1.00E+00	8.20E-01	1.00E+00	5.80E-01	1.00E+00	8.71E-01	1.00E+00	metallocarboxypeptidase activity	F
GO:0004182	30	8.32E-01	1.00E+00	8.53E-01	1.00E+00	8.12E-01	1.00E+00	7.11E-01	1.00E+00	6.70E-01	1.00E+00	8.72E-01	1.00E+00	6.05E-01	1.00E+00	7.38E-01	1.00E+00	carboxypeptidase A activity	F
GO:0004190	29	7.87E-02	1.00E+00	1.17E-01	1.00E+00	2.98E-01	1.00E+00	2.69E-01	1.00E+00	6.78E-02	1.00E+00	1.10E-01	1.00E+00	1.91E-01	1.00E+00	1.69E-01	1.00E+00	aspartic-type endopeptidase activity	F
GO:0004197	97	1.38E-01	1.00E+00	3.31E-01	1.00E+00	3.95E-01	1.00E+00	2.52E-01	1.00E+00	4.55E-01	1.00E+00	5.93E-01	1.00E+00	1.34E-02	4.39E-01	1.50E-01	1.00E+00	cysteine-type endopeptidase activity	F
GO:0004198	16	2.61E-01	1.00E+00	5.97E-01	1.00E+00	4.63E-01	1.00E+00	9.98E-01	1.00E+00	6.73E-01	1.00E+00	4.42E-01	1.00E+00	3.41E-02	7.53E-01	2.48E-01	1.00E+00	calpain activity	F
GO:0004221	65	3.25E-02	1.00E+00	4.06E-04	4.30E-02	8.15E-02	1.00E+00	1.53E-04	5.80E-03	3.70E-03	1.35E-01	1.39E-02	1.00E+00	6.03E-01	1.00E+00	1.02E-02	4.72E-01	ubiquitin thiolesterase activity	F
GO:0004222	112	4.30E-01	1.00E+00	9.31E-01	1.00E+00	6.00E-01	1.00E+00	9.64E-01	1.00E+00	4.43E-01	1.00E+00	8.40E-01	1.00E+00	1.75E-01	1.00E+00	8.49E-01	1.00E+00	metalloendopeptidase activity	F
GO:0004252	233	9.36E-01	1.00E+00	7.90E-01	1.00E+00	8.83E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.16E-01	1.00E+00	2.58E-01	1.00E+00	5.71E-03	2.58E-01	serine-type endopeptidase activity	F
GO:0004263	15	4.66E-01	1.00E+00	4.37E-01	1.00E+00	4.38E-01	1.00E+00	8.63E-01	1.00E+00	8.45E-01	1.00E+00	3.50E-01	1.00E+00	3.60E-01	1.00E+00	3.32E-01	1.00E+00	chymotrypsin activity	F
GO:0004289	21	2.50E-01	1.00E+00	4.72E-01	1.00E+00	6.32E-01	1.00E+00	9.26E-01	1.00E+00	2.45E-01	1.00E+00	1.49E-01	1.00E+00	2.34E-01	1.00E+00	3.27E-01	1.00E+00	subtilase activity	F
GO:0004293	13	1.00E+00	1.00E+00	6.10E-06	3.00E-03	1.00E+00	1.00E+00	2.06E-02	7.69E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.14E-21	0.00E+00	tissue kallikrein activity	F
GO:0004295	19	9.98E-01	1.00E+00	8.19E-01	1.00E+00	1.00E+00	1.00E+00	9.75E-01	1.00E+00	9.07E-01	1.00E+00	8.60E-01	1.00E+00	9.41E-01	1.00E+00	4.24E-01	1.00E+00	trypsin activity	F
GO:0004298	19	3.26E-02	1.00E+00	1.06E-02	7.51E-01	7.88E-02	1.00E+00	2.20E-01	1.00E+00	2.34E-01	1.00E+00	5.08E-03	2.02E-01	2.32E-01	1.00E+00	1.14E-01	1.00E+00	threonine endopeptidase activity	F
GO:0004303	10	1.77E-01	1.00E+00	4.63E-01	1.00E+00	2.07E-01	1.00E+00	6.21E-01	1.00E+00	1.34E-01	1.00E+00	3.67E-01	1.00E+00	1.84E-01	1.00E+00	4.63E-01	1.00E+00	estradiol 17-beta-dehydrogenase activity	F
GO:0004364	28	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.92E-01	1.00E+00	9.23E-01	1.00E+00	9.73E-01	1.00E+00	9.79E-01	1.00E+00	glutathione transferase activity	F
GO:0004365	22	1.00E+00	1.00E+00	7.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.63E-01	1.00E+00	2.93E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	glyceraldehyde-3-phosphate dehydrogenas	F
GO:0004383	11	4.33E-01	1.00E+00	9.96E-01	1.00E+00	6.88E-01	1.00E+00	8.34E-01	1.00E+00	6.48E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-02	1.00E+00	7.78E-01	1.00E+00	guanylate cyclase activity	F
GO:0004386	141	4.14E-08	9.73E-04	9.80E-15	0.00E+00	5.45E-08	9.88E-04	6.07E-12	0.00E+00	1.84E-07	0.00E+00	3.49E-08	7.71E-04	2.23E-02	5.60E-01	1.16E-07	0.00E+00	helicase activity	F
GO:0004396	10	1.49E-01	1.00E+00	3.58E-01	1.00E+00	9.93E-02	1.00E+00	1.66E-01	1.00E+00	3.74E-01	1.00E+00	5.33E-01	1.00E+00	2.95E-01	1.00E+00	4.43E-01	1.00E+00	hexokinase activity	F
GO:0004402	20	2.14E-03	1.02E-01	8.13E-04	7.30E-02	5.75E-03	1.88E-01	2.75E-03	1.42E-01	1.89E-02	7.19E-01	1.52E-02	1.00E+00	8.63E-02	1.00E+00	4.40E-03	2.58E-01	histone acetyltransferase activity	F
GO:0004407	18	1.70E-02	9.83E-01	2.80E-02	1.00E+00	4.04E-02	1.00E+00	4.32E-02	1.00E+00	4.85E-02	1.00E+00	2.15E-01	1.00E+00	2.50E-01	1.00E+00	4.34E-02	1.00E+00	histone deacetylase activity	F
GO:0004428	35	4.49E-04	5.20E-02	3.06E-03	2.13E-01	6.85E-04	3.00E-02	1.78E-02	7.69E-01	1.13E-02	4.14E-01	4.81E-03	2.02E-01	3.43E-02	7.53E-01	4.92E-03	2.58E-01	inositol or phosphatidylinositol kinase activit	F
GO:0004434	16	8.92E-01	1.00E+00	7.68E-01	1.00E+00	6.60E-01	1.00E+00	9.35E-01	1.00E+00	9.99E-01	1.00E+00	7.27E-01	1.00E+00	4.87E-01	1.00E+00	2.47E-01	1.00E+00	inositol or phosphatidylinositol phosphodies	F
GO:0004435	16	8.92E-01	1.00E+00	7.68E-01	1.00E+00	6.60E-01	1.00E+00	9.35E-01	1.00E+00	9.99E-01	1.00E+00	7.27E-01	1.00E+00	4.87E-01	1.00E+00	2.47E-01	1.00E+00	phosphoinositide phospholipase C activity	F
GO:0004437	34	2.29E-01	1.00E+00	3.28E-02	1.00E+00	3.10E-01	1.00E+00	1.02E-01	1.00E+00	3.88E-01	1.00E+00	8.94E-02	1.00E+00	3.52E-01	1.00E+00	6.47E-02	1.00E+00	inositol or phosphatidylinositol phosphatase	F
GO:0004467	13	2.99E-01	1.00E+00	5.27E-02	1.00E+00	1.60E-01	1.00E+00	9.54E-02	1.00E+00	8.10E-01	1.00E+00	9.36E-02	1.00E+00	4.35E-01	1.00E+00	1.50E-01	1.00E+00	long-chain-fatty-acid-CoA ligase activity	F
GO:0004468	20	2.14E-03	1.02E-01	8.13E-04	7.30E-02	5.75E-03	1.88E-01	2.75E-03	1.42E-01	1.89E-02	7.19E-01	1.52E-02	1.00E+00	8.63E-02	1.00E+00	4.40E-03	2.58E-01	lysine N-acetyltransferase activity	F
GO:0004497	174	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.23E-01	1.00E+00	1.00E+00	1.00E+00	2.63E-01	1.00E+00	8.12E-01	1.00E+00	monooxygenase activity	F
GO:0004499	23	1.87E-01	1.00E+00	9.94E-01	1.00E+00	7.99E-01	1.00E+00	9.99E-01	1.00E+00	2.03E-01	1.00E+00	1.00E+00	1.00E+00	2.00E-02	4.71E-01	4.61E-01	1.00E+00	dimethylaniline monooxygenase (N-oxide-fo	F
GO:0004518	153	9.58E-03	9.83E-01	7.40E-03	5.59E-01	3.33E-02	1.00E+00	1.48E-02	7.69E-01	3.67E-02	1.00E+00	5.48E-03	2.02E-01	4.38E-02	8.34E-01	6.66E-01	1.00E+00	nuclease activity	F
GO:0004519	97	4.70E-02	1.00E+00	8.10E-02	1.00E+00	7.00E-02	1.00E+00	4.65E-02	1.00E+00	1.85E-01	1.00E+00	1.10E-01	1.00E+00	7.06E-02	1.00E+00	9.15E-01	1.00E+00	endonuclease activity	F
GO:0004520	15	7.81E-02	1.00E+00	4.73E-02	1.00E+00	2.35E-01	1.00E+00	1.63E-01	1.00E+00	5.50E-02	1.00E+00	1.87E-01	1.00E+00	3.97E-01	1.00E+00	3.31E-01	1.00E+00	endodeoxyribonuclease activity	F
GO:0004521	40	4.25E-01	1.00E+00	6.96E-01	1.00E+00	1.96E-01	1.00E+00	4.75E-01	1.00E+00	6.53E-01	1.00E+00	3.30E-01	1.00E+00	5.63E-01	1.00E+00	9.99E-01	1.00E+00	endoribonuclease activity	F
GO:0004522	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	8.78E-01	1.00E+00	pancreatic ribonuclease activity	F
GO:0004526	10	1.02E-01	1.00E+00	9.60E-01	1.00E+00	2.51E-01	1.00E+00	2.50E-01	1.00E+00	3.70E-01	1.00E+00	9.95E-01	1.00E+00	7.08E-02	1.00E+00	1.00E+00	1.00E+00	ribonuclease P activity	F
GO:0004527	53	2.45E-02	1.00E+00	1.44E-02	1.00E+00	5.28E-02	1.00E+00	4.32E-02	1.00E+00	4.28E-02	1.00E+00	4.77E-03	2.02E-01	1.61E-01	1.00E+00	2.03E-01	1.00E+00	exonuclease activity	F
GO:0004532	12	9.13E-02	1.00E+00	8.21E-02	1.00E+00	2.06E-01	1.00E+00	4.73E-01	1.00E+00	1.87E-01	1.00E+00	1.82E-01	1.00E+00	1.37E-01	1.00E+00	7.14E-02	1.00E+00	exoribonuclease activity	F
GO:0004536	26	7.48E-02	1.00E+00	2.12E-01	1.00E+00	1.05E-01	1.00E+00	3.60E-01	1.00E+00	1.17E-01	1.00E+00	3.78E-01	1.00E+00	1.68E-01	1.00E+00	6.10E-01	1.00E+00	deoxyribonuclease activity	F
GO:0004540	58	1.96E-01	1.00E+00	3.68E-01	1.00E+00	1.27E-01	1.00E+00	3.84E-01	1.00E+00	4.98E-01	1.00E+00	1.81E-01	1.00E+00	3.01E-01	1.00E+00	8.83E-01	1.00E+00	ribonuclease activity	F
GO:0004549	13	3.23E-02	1.00E+00	6.80E-01	1.00E+00	1.01E-01	1.00E+00	1.21E-01	1.00E+00	2.27E-01	1.00E+00	8.59E-01	1.00E+00	9.11E-02	1.00E+00	1.00E+00	1.00E+00	tRNA-specific ribonuclease activity	F
GO:0004550	11	1.04E-01	1.00E+00	1.02E-01	1.00E+00	5.89E-02	1.00E+00	1.63E-01	1.00E+00	5.18E-02	1.00E+00	9.12E-02	1.00E+00	7.68E-01	1.00E+00	2.83E-01	1.00E+00	nucleoside diphosphate kinase activity	F
GO:0004553	113	4.49E-02	1.00E+00	1.43E-01	1.00E+00	8.74E-03	4.69E-01	1.79E-01	1.00E+00	5.59E-01	1.00E+00	4.98E-01	1.00E+00	1.38E-01	1.00E+00	1.19E-02	9.40E-01	hydrolase activity, hydrolyzing O-glycosyl cc	F
GO:0004568	10	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.79E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	chitinase activity	F
GO:0004601	49	1.32E-01	1.00E+00	1.50E-01	1.00E+00	8.61E-01	1.00E+00	2.39E-01	1.00E+00	2.15E-01	1.00E+00	2.27E-01	1.00E+00	5.02E-02	1.00E+00	2.09E-01	1.00E+00	peroxidase activity	F
GO:0004602	10	1.57E-01	1.00E+00	5.15E-01	1.00E+00	6.68E-01	1.00E+00	4.59E-01	1.00E+00	7.44E-01	1.00E+00	3.47E-01	1.00E+00	8.36E-02	1.00E+00	9.98E-01	1.00E+00	glutathione peroxidase activity	F
GO:0004620	57	7.00E-02	1.00E+00	2.61E-01	1.00E+00	4.24E-02	1.00E+00	3.96E-01	1.00E+00	8.57E-01	1.00E+00	3.47E-01	1.00E+00	2.47E-02	5.60E-01	1.04E-01	1.00E+00	phospholipase activity	F
GO:0004623	27	1.94E-01	1.00E+00	2.93E-01	1.00E+00	3.02E-01	1.00E+00	5.29E-01	1.00E+00	5.94E-01	1.00E+00	2.83E-01	1.00E+00	8.40E-02	1.00E+00	1.89E-01	1.00E+00	phospholipase A2 activity	F
GO:0004629	20	6.58E-01	1.00E+00	7.93E-01	1.00E+00	2.62E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	7.78E-01	1.00E+00	3.74E-01	1.00E+00	4.43E-01	1.00E+00	phospholipase C activity	F
GO:0004653	15	9.11E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.60E-01	1.00E+00	9.47E-01	1.00E+00	4.14E-01	1.00E+00	3.36E-01	1.00E+00	polypeptide N-acetylgalactosaminyltransfera	F
GO:0004659	18	9.22E-02	1.00E+00	3.15E-01	1.00E+00	3.04E-01	1.00E+00	8.90E-02	1.00E+00	2.31E-01	1.00E+00	5.06E-01	1.00E+00	1.08E-01	1.00E+00	6.54E-01	1.00E+00	prenyltransferase activity	F
GO:0004672	669	1.05E-02	9.83E-01	2.67E-03	1.87E-01	1.56E-01	1.00E+00	1.29E-01	1.00E+00	4.08E-02	1.00E+00	3.42E-03	1.43E-01	2.13E-02	5.29E-01	1.75E-02	9.40E-01	protein kinase activity	F
GO:0004673	30	7.54E-01	1.00E+00	8.06E-01	1.00E+00	9.52E-01	1.00E+00	9.81E-01	1.00E+00	6.43E-01	1.00E+00	5.92E-01	1.00E+00	6.57E-01	1.00E+00	4.47E-01	1.00E+00	protein histidine kinase activity	F
GO:0004674	546	1.38E-04	1.90E-02	5.38E-06	3.00E-03	8.00E-03	3.43E-01	3.47E-03	1.42E-01	3.16E-03	1.35E-01	1.73E-04	1.36E-02	1.27E-02	4.39E-01	3.05E-03	2.16E-01	protein serine/threonine kinase activity	F
GO:0004675	13	2.69E-01	1.00E+00	3.18E-01	1.00E+00	6.27E-01	1.00E+00	2.92E-01	1.00E+00	3.94E-01	1.00E+00	3.04E-01	1.00E+00	5.69E-01	1.00E+00	5.32E-01	1.00E+00	transmembrane receptor protein serine/thre	F
GO:0004683	22	1.34E-01	1.00E+00	8.90E-01	1.00E+00	2.63E-01	1.00E+00	9.84E-01	1.00E+00	1.17E-01	1.00E+00	6.63E-01	1.00E+00	2.35E-01	1.00E+00	7.78E-01	1.00E+00	calmodulin regulated protein kinase activity	F

GO:0004689	15	1.70E-01	1.00E+00	9.09E-01	1.00E+00	3.00E-01	1.00E+00	9.89E-01	1.00E+00	1.12E-01	1.00E+00	5.48E-01	1.00E+00	3.61E-01	1.00E+00	8.73E-01	1.00E+00	phosphorylase kinase activity	F
GO:0004693	31	1.42E-02	9.83E-01	4.01E-02	1.00E+00	1.01E-01	1.00E+00	2.41E-02	7.69E-01	3.75E-02	1.00E+00	5.95E-02	1.00E+00	8.43E-02	1.00E+00	8.23E-01	1.00E+00	cyclin-dependent protein kinase activity	F
GO:0004697	15	1.07E-01	1.00E+00	1.94E-01	1.00E+00	2.70E-01	1.00E+00	7.59E-01	1.00E+00	2.02E-01	1.00E+00	2.94E-01	1.00E+00	2.37E-02	5.60E-01	5.49E-02	1.00E+00	protein kinase C activity	F
GO:0004702	55	1.09E-01	1.00E+00	6.20E-02	1.00E+00	9.91E-02	1.00E+00	7.07E-02	1.00E+00	3.90E-01	1.00E+00	1.15E-01	1.00E+00	2.29E-01	1.00E+00	2.50E-01	1.00E+00	receptor signaling protein serine/threonine k	F
GO:0004707	18	3.25E-01	1.00E+00	9.31E-02	1.00E+00	1.49E-01	1.00E+00	2.70E-02	1.00E+00	1.86E-01	1.00E+00	1.39E-01	1.00E+00	8.42E-01	1.00E+00	5.11E-01	1.00E+00	MAP kinase activity	F
GO:0004709	17	1.77E-01	1.00E+00	4.88E-01	1.00E+00	2.23E-01	1.00E+00	8.22E-01	1.00E+00	6.65E-01	1.00E+00	3.68E-01	1.00E+00	6.99E-02	1.00E+00	4.56E-01	1.00E+00	MAP kinase kinase kinase activity	F
GO:0004712	10	9.78E-01	1.00E+00	9.06E-01	1.00E+00	9.66E-01	1.00E+00	9.51E-01	1.00E+00	8.93E-01	1.00E+00	9.56E-01	1.00E+00	9.31E-01	1.00E+00	5.15E-01	1.00E+00	protein threonine/tyrosine kinase activity	F
GO:0004713	553	3.64E-02	1.00E+00	2.81E-03	1.87E-01	2.23E-01	1.00E+00	1.13E-01	1.00E+00	8.22E-02	1.00E+00	6.83E-03	3.55E-01	2.70E-02	6.06E-01	1.37E-02	9.40E-01	protein-tyrosine kinase activity	F
GO:0004714	111	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.96E-01	1.00E+00	7.83E-01	1.00E+00	transmembrane receptor protein tyrosine kir	F
GO:0004715	38	2.12E-01	1.00E+00	5.88E-02	1.00E+00	4.68E-01	1.00E+00	4.12E-02	1.00E+00	3.10E-01	1.00E+00	3.37E-01	1.00E+00	7.60E-02	1.00E+00	2.75E-02	1.00E+00	non-membrane spanning protein tyrosine ki	F
GO:0004721	158	2.43E-02	1.00E+00	2.65E-03	1.87E-01	9.81E-02	1.00E+00	3.55E-02	1.00E+00	4.17E-02	1.00E+00	6.04E-02	1.00E+00	6.08E-02	1.00E+00	8.30E-04	3.30E-02	phosphoprotein phosphatase activity	F
GO:0004722	37	6.55E-02	1.00E+00	6.73E-03	5.59E-01	1.96E-02	8.10E-01	6.22E-03	3.78E-01	3.42E-01	1.00E+00	5.59E-02	1.00E+00	3.06E-01	1.00E+00	4.37E-02	1.00E+00	protein serine/threonine phosphatase activit	F
GO:0004725	109	3.25E-01	1.00E+00	9.00E-02	1.00E+00	7.34E-01	1.00E+00	2.22E-01	1.00E+00	2.27E-01	1.00E+00	3.88E-01	1.00E+00	1.02E-01	1.00E+00	1.98E-02	1.00E+00	protein tyrosine phosphatase activity	F
GO:0004745	10	1.65E-01	1.00E+00	1.53E-01	1.00E+00	1.30E-01	1.00E+00	5.27E-02	1.00E+00	4.96E-02	1.00E+00	1.50E-01	1.00E+00	5.65E-01	1.00E+00	5.55E-01	1.00E+00	retinol dehydrogenase activity	F
GO:0004765	12	2.02E-02	1.00E+00	2.56E-02	1.00E+00	4.47E-02	1.00E+00	5.86E-02	1.00E+00	1.58E-02	7.19E-01	4.48E-02	1.00E+00	8.59E-02	1.00E+00	2.33E-01	1.00E+00	shikimate kinase activity	F
GO:0004806	15	4.72E-01	1.00E+00	9.96E-01	1.00E+00	4.24E-01	1.00E+00	9.93E-01	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	2.05E-01	1.00E+00	8.26E-01	1.00E+00	triacylglycerol lipase activity	F
GO:0004812	69	1.74E-03	1.02E-01	2.06E-04	2.80E-02	4.63E-03	1.88E-01	1.90E-04	1.10E-02	5.78E-03	1.65E-01	4.96E-03	2.02E-01	8.55E-02	1.00E+00	1.12E-01	1.00E+00	aminoacyl-tRNA ligase activity	F
GO:0004835	16	8.43E-02	1.00E+00	1.68E-01	1.00E+00	8.96E-02	1.00E+00	3.00E-01	1.00E+00	1.15E-01	1.00E+00	1.15E-01	1.00E+00	1.03E-01	1.00E+00	9.97E-02	1.00E+00	tubulin-tyrosine ligase activity	F
GO:0004842	146	1.15E-05	5.00E-03	1.41E-07	2.66E-03	3.15E-05	3.00E-03	2.87E-06	1.00E-03	2.34E-06	7.65E-04	1.90E-07	1.75E-03	8.67E-02	1.00E+00	4.79E-04	2.10E-02	ubiquitin-protein ligase activity	F
GO:0004843	67	2.32E-02	1.00E+00	1.52E-04	2.80E-02	9.76E-02	1.00E+00	6.30E-05	5.80E-03	3.58E-03	1.35E-01	5.51E-03	2.02E-01	4.60E-01	1.00E+00	6.16E-03	2.58E-01	ubiquitin-specific protease activity	F
GO:0004857	298	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	5.74E-01	1.00E+00	8.59E-01	1.00E+00	enzyme inhibitor activity	F
GO:0004859	11	8.79E-01	1.00E+00	5.93E-01	1.00E+00	9.61E-01	1.00E+00	9.95E-01	1.00E+00	5.64E-01	1.00E+00	4.84E-01	1.00E+00	9.80E-01	1.00E+00	3.90E-01	1.00E+00	phospholipase inhibitor activity	F
GO:0004860	22	3.08E-01	1.00E+00	6.77E-01	1.00E+00	2.93E-01	1.00E+00	8.26E-02	1.00E+00	5.28E-01	1.00E+00	9.91E-01	1.00E+00	2.43E-01	1.00E+00	9.49E-01	1.00E+00	protein kinase inhibitor activity	F
GO:0004864	17	3.54E-01	1.00E+00	2.46E-01	1.00E+00	3.70E-01	1.00E+00	3.76E-01	1.00E+00	8.01E-01	1.00E+00	4.02E-01	1.00E+00	1.42E-01	1.00E+00	1.33E-01	1.00E+00	protein phosphatase inhibitor activity	F
GO:0004866	200	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	9.94E-01	1.00E+00	endopeptidase inhibitor activity	F
GO:0004867	139	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.74E-01	1.00E+00	9.98E-01	1.00E+00	serine-type endopeptidase inhibitor activity	F
GO:0004869	41	9.49E-01	1.00E+00	8.60E-01	1.00E+00	9.92E-01	1.00E+00	1.42E-01	1.00E+00	5.01E-02	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	8.26E-01	1.00E+00	cysteine protease inhibitor activity	F
GO:0004871	2382	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.20E-01	1.00E+00	9.38E-01	1.00E+00	signal transducer activity	F
GO:0004872	2044	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	9.88E-01	1.00E+00	receptor activity	F
GO:0004879	165	6.67E-01	1.00E+00	2.32E-01	1.00E+00	5.70E-01	1.00E+00	1.39E-01	1.00E+00	7.89E-01	1.00E+00	2.12E-01	1.00E+00	2.91E-01	1.00E+00	4.95E-01	1.00E+00	ligand-dependent nuclear receptor activity	F
GO:0004887	19	1.14E-01	1.00E+00	3.06E-01	1.00E+00	1.80E-01	1.00E+00	3.51E-01	1.00E+00	4.19E-01	1.00E+00	2.72E-01	1.00E+00	3.09E-02	7.53E-01	3.89E-01	1.00E+00	thyroid hormone receptor activity	F
GO:0004888	1263	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.96E-01	1.00E+00	transmembrane receptor activity	F
GO:0004889	17	1.98E-01	1.00E+00	7.29E-01	1.00E+00	4.53E-01	1.00E+00	9.47E-01	1.00E+00	9.34E-01	1.00E+00	6.82E-01	1.00E+00	3.58E-02	7.53E-01	3.23E-01	1.00E+00	nicotinic acetylcholine-activated cation-selec	F
GO:0004890	32	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	1.00E+00	1.00E+00	GABA-A receptor activity	F
GO:0004896	81	9.90E-01	1.00E+00	9.69E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.12E-01	1.00E+00	9.91E-01	1.00E+00	6.85E-01	1.00E+00	1.13E-01	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0004907	50	9.90E-01	1.00E+00	8.75E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.25E-01	1.00E+00	9.40E-01	1.00E+00	6.78E-01	1.00E+00	1.14E-01	1.00E+00	interleukin receptor activity	F
GO:0004908	27	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.25E-01	1.00E+00	interleukin-1 receptor activity	F
GO:0004918	10	1.43E-01	1.00E+00	1.08E-01	1.00E+00	1.00E+00	1.00E+00	5.20E-01	1.00E+00	8.55E-02	1.00E+00	2.37E-01	1.00E+00	3.09E-01	1.00E+00	2.00E-02	1.00E+00	interleukin-8 receptor activity	F
GO:0004930	897	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	G-protein coupled receptor activity	F
GO:0004935	26	6.32E-01	1.00E+00	9.64E-01	1.00E+00	6.39E-01	1.00E+00	6.71E-01	1.00E+00	9.22E-01	1.00E+00	9.99E-01	1.00E+00	4.12E-01	1.00E+00	7.14E-01	1.00E+00	adrenoceptor activity	F
GO:0004936	10	7.10E-01	1.00E+00	8.25E-01	1.00E+00	5.12E-01	1.00E+00	4.48E-01	1.00E+00	8.78E-01	1.00E+00	1.00E+00	1.00E+00	4.06E-01	1.00E+00	3.80E-01	1.00E+00	alpha-adrenergic receptor activity	F
GO:0004942	17	4.88E-03	3.48E-01	1.63E-02	1.00E+00	4.76E-02	1.00E+00	1.07E-01	1.00E+00	3.63E-02	1.00E+00	1.03E-01	1.00E+00	3.29E-02	7.53E-01	4.61E-03	2.58E-01	anaphylatoxin receptor activity	F
GO:0004945	52	2.40E-01	1.00E+00	4.35E-01	1.00E+00	2.93E-01	1.00E+00	6.09E-01	1.00E+00	3.77E-01	1.00E+00	8.73E-01	1.00E+00	3.78E-01	1.00E+00	5.78E-02	1.00E+00	angiotensin type II receptor activity	F
GO:0004946	17	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	4.14E-01	1.00E+00	1.00E+00	1.00E+00	bombesin receptor activity	F
GO:0004947	29	2.77E-01	1.00E+00	3.78E-01	1.00E+00	4.71E-01	1.00E+00	5.71E-01	1.00E+00	5.76E-01	1.00E+00	7.54E-01	1.00E+00	3.11E-01	1.00E+00	6.31E-02	1.00E+00	bradykinin receptor activity	F
GO:0004949	23	9.94E-01	1.00E+00	3.97E-01	1.00E+00	9.09E-01	1.00E+00	2.55E-01	1.00E+00	9.90E-01	1.00E+00	7.66E-01	1.00E+00	9.92E-01	1.00E+00	2.60E-01	1.00E+00	cannabinoid receptor activity	F
GO:0004950	42	2.63E-01	1.00E+00	3.99E-01	1.00E+00	7.51E-01	1.00E+00	7.71E-01	1.00E+00	2.33E-01	1.00E+00	9.10E-01	1.00E+00	1.43E-01	1.00E+00	1.90E-02	9.40E-01	chemokine receptor activity	F
GO:0004952	52	8.46E-01	1.00E+00	6.10E-01	1.00E+00	8.34E-01	1.00E+00	3.19E-01	1.00E+00	9.64E-01	1.00E+00	8.53E-01	1.00E+00	7.14E-01	1.00E+00	5.24E-01	1.00E+00	dopamine receptor activity	F
GO:0004953	15	4.17E-01	1.00E+00	4.01E-01	1.00E+00	1.16E-01	1.00E+00	4.81E-01	1.00E+00	8.48E-01	1.00E+00	3.90E-01	1.00E+00	9.72E-01	1.00E+00	2.82E-01	1.00E+00	icosanoid receptor activity	F
GO:0004954	15	4.17E-01	1.00E+00	4.01E-01	1.00E+00	1.16E-01	1.00E+00	4.81E-01	1.00E+00	8.48E-01	1.00E+00	3.90E-01	1.00E+00	9.72E-01	1.00E+00	2.82E-01	1.00E+00	prostanoid receptor activity	F
GO:0004955	15	4.17E-01	1.00E+00	4.01E-01	1.00E+00	1.16E-01	1.00E+00	4.81E-01	1.00E+00	8.48E-01	1.00E+00	3.90E-01	1.00E+00	9.72E-01	1.00E+00	2.82E-01	1.00E+00	prostaglandin receptor activity	F
GO:0004957	11	3.23E-01	1.00E+00	5.19E-01	1.00E+00	5.73E-02	1.00E+00	7.05E-01	1.00E+00	9.56E-01	1.00E+00	4.50E-01	1.00E+00	9.99E-01	1.00E+00	4.73E-01	1.00E+00	prostaglandin E receptor activity	F
GO:0004965	34	9.94E-01	1.00E+00	7.77E-01	1.00E+00	7.74E-01	1.00E+00	6.47E-01	1.00E+00	9.95E-01	1.00E+00	8.17E-01	1.00E+00	9.92E-01	1.00E+00	4.91E-01	1.00E+00	GABA-B receptor activity	F
GO:0004966	41	9.97E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	8.49E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	7.44E-01	1.00E+00	7.60E-01	1.00E+00	galanin receptor activity	F
GO:0004969	41	1.83E-01	1.00E+00	3.43E-02	1.00E+00	4.40E-01	1.00E+00	6.63E-02	1.00E+00	1.68E-01	1.00E+00	6.97E-02	1.00E+00	3.31E-01	1.00E+00	1.34E-01	1.00E+00	histamine receptor activity	F
GO:0004970	18	7.34E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.20E-01	1.00E+00	7.20E-01	1.00E+00	1.00E+00	1.00E+00	7.41E-02	1.00E+00	9.53E-01	1.00E+00	ionotropic glutamate receptor activity	F
GO:0004974	16	5.39E-01	1.00E+00	8.89E-01	1.00E+00	2.14E-01	1.00E+00	4.67E-01	1.00E+00	7.83E-01	1.00E+00	9.93E-01	1.00E+00	7.98E-01	1.00E+00	9.65E-01	1.00E+00	leukotriene receptor activity	F
GO:0004977	103	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	7.28E-01	1.00E+00	9.82E-01	1.00E+00	melanocortin receptor activity	F
GO:0004981	10	7.71E-01	1.00E+00	9.97E-01	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	8.46E-01	1.00E+00	9.71E-01	1.00E+00	4.13E-01	1.00E+00	3.60E-01	1.00E+00	muscarinic acetylcholine receptor activity	F
GO:0004982	27	1.03E-01	1.00E+00	2.64E-01	1.00E+00	6.01E-02	1.00E+00	4.43E-01	1.00E+00	8.95E-01	1.00E+00	4.65E-01	1.00E+00	1.47E-01	1.00E+00	9.99E-02	1.00E+00	N-formyl peptide receptor activity	F
GO:0004983	81	9.98E-01	1.00E+00	9.65E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.83E-01	1.00E+00	9.93E-01	1.00E+00	5.36E-01	1.00E+00	2.86E-01	1.00E+00	neuropeptide Y receptor activity	F
GO:0004984	195	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	olfactory receptor activity	F
GO:0004985	16	9.98E-01	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	5.80E-01	1.00E+00	9.29E-01	1.00E+00	6.25E-01	1.00E+00	opioid receptor activity	F
GO:0004992	13	6.27E-01	1.00E+00	2.67E-01	1.00E+00	9.43E-01	1.00E+00	4.28E-01	1.00E+00	8.06E-01	1.00E+00	3.47E-01	1.00E+00	1.87E-01	1.00E+00	9.92E-02	1.00E+00	platelet activating factor receptor activity	F
GO:0004994	17	9.99E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.92E-01	1.00E+00	9.04E-01	1.00E+00	9.47E-01	1.00E+00	7.43E-01	1.00E+00	somatostatin receptor activity	F
GO:0005000	11	9.24E-01	1.00E+00	8.23E-01	1.00E+00	9.69E-01	1.00E+00	7.42E-01	1.00E+00	9.60E-01	1.00E+00	8.52E-01	1.00E+00	7.34E-01	1.00E+00	7.17E-01	1.00E+00	vasopressin receptor activity	F
GO:0005003	14	9.06E-01	1.00E+00	9.73E-01	1.00E+00	9.28E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.05E-01	1.00E+00	2.37E-01	1.00E+00	7.76E-01	1.00E+00	ephrin receptor activity	F
GO:0005021	65	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	7.70E-01	1.00E+00	vascular endothelial growth factor receptor a	F
GO:0005024	13	2.69E-01	1.00E+00	3.18E-01	1.00E+00	6.27E-01	1.00E+00	2.92E-01	1.00E+00	3.94E-01	1.00E+00	3.04E-01	1.00E+00	5.69E-01	1.00E+00	5.32E-01	1.00E+00	transforming growth factor beta receptor act	F
GO:0005044	34	4.75E-01	1.00E+00	8.03E-01	1.00E+00	3.87E-01	1.00E+00	9.95E-01	1.00E+00	7.48E-01	1.00E+00	8.36E-01	1.00E+00	2.13E-01	1.00E+00	1.39E-01	1.00E+00	scavenger receptor activity	F
GO:0005048	10	7.25E-02	1.00E+00	1.88E-03	1.62E-01	2.22E-01	1.00E+00	7.24E-02	1.00E+00	4.11E-02	1.00E+00	1.31E-02	1.00E+00	3.88E-01	1.00E+00	1.58E-01	1.00E+00	signal sequence binding	F
GO:0005057	108	1.89E-01	1.00E+00	9.52E-02	1.00E+00	3.11E-01	1.00E+00	1.50E-01	1.00E+00	7.36E-01	1.00E+00	4.06E-01	1.00E+00	5.26E-02	1.00E+00	2.63E-02	1.00E+00	receptor signaling protein activity	F
GO:0005070	17	1.91E-01	1.00E+00	5.06E-01	1.00E+00	1.74E-01	1.00E+00	2.66E-01	1.00E+00	4.37E-01	1.00E+00	8.81E-01	1.00E+00	1.90E-01	1.00E+00	3.27E-01	1.00E+00	SH3/SH2 adaptor activity	F
GO:0005083	215	1.74E-04	1.90E-02	8.49E-03	5.59E-01	2.57E-02	1.00E+00	3.21E-01	1.00E+00	4.34E-03	1.35E-01	2.47E-02	1.00E+00	1.76E-04	6.45E-03	3.12E-04	1.70E-02	small GTPase regulator activity	F
GO:0005085	157	5.23E-01	1.00E+00	7.58E-01	1.00E+00	8.20E-01	1.00E+00	9.69E-01	1.00E+00	4.41E-01	1.00E+00	7.64E-01	1.00E+00	2.82E-01	1.00E+00	2.53E-01	1.00E+00	guanyl-nucleotide exchange factor activity	F

GO:0005086	16	8.39E-01	1.00E+00	7.65E-01	1.00E+00	9.59E-01	1.00E+00	7.32E-01	1.00E+00	7.04E-01	1.00E+00	9.07E-01	1.00E+00	8.00E-01	1.00E+00	5.03E-01	1.00E+00	ARF guanyl-nucleotide exchange factor acti	F
GO:0005088	84	8.22E-02	1.00E+00	3.49E-01	1.00E+00	6.11E-01	1.00E+00	9.39E-01	1.00E+00	1.76E-01	1.00E+00	1.57E-01	1.00E+00	9.11E-03	2.17E-01	1.39E-01	1.00E+00	Ras guanyl-nucleotide exchange factor activ	F
GO:0005089	74	2.28E-01	1.00E+00	7.47E-01	1.00E+00	7.97E-01	1.00E+00	9.96E-01	1.00E+00	4.27E-01	1.00E+00	3.20E-01	1.00E+00	2.37E-02	5.60E-01	4.95E-01	1.00E+00	Rho guanyl-nucleotide exchange factor activ	F
GO:0005096	199	4.07E-03	1.86E-01	7.08E-02	1.00E+00	2.31E-02	1.00E+00	5.82E-01	1.00E+00	2.70E-02	1.00E+00	4.41E-01	1.00E+00	3.66E-02	7.83E-01	1.80E-03	6.30E-02	GTPase activator activity	F
GO:0005097	44	2.69E-03	1.39E-01	3.71E-03	3.82E-01	1.46E-02	8.10E-01	3.60E-02	1.00E+00	2.56E-02	1.00E+00	8.56E-03	3.55E-01	1.97E-02	4.71E-01	7.74E-03	4.48E-01	Rab GTPase activator activity	F
GO:0005099	67	1.58E-03	9.30E-02	3.12E-03	2.13E-01	1.16E-02	4.74E-01	4.79E-02	1.00E+00	1.82E-02	7.19E-01	4.35E-02	1.00E+00	2.24E-02	5.60E-01	7.96E-04	3.30E-02	Ras GTPase activator activity	F
GO:0005100	17	2.06E-01	1.00E+00	2.67E-01	1.00E+00	1.81E-01	1.00E+00	3.65E-01	1.00E+00	4.33E-01	1.00E+00	9.04E-01	1.00E+00	3.45E-01	1.00E+00	6.42E-02	1.00E+00	Rho GTPase activator activity	F
GO:0005102	776	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.69E-01	1.00E+00	receptor binding	F
GO:0005125	241	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.50E-01	1.00E+00	cytokine activity	F
GO:0005126	39	9.50E-01	1.00E+00	9.98E-01	1.00E+00	5.70E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	8.49E-01	1.00E+00	hematopoietin/interferon-class (D200-doma	F
GO:0005149	13	7.19E-01	1.00E+00	9.71E-01	1.00E+00	6.30E-01	1.00E+00	9.39E-01	1.00E+00	5.70E-01	1.00E+00	8.74E-01	1.00E+00	4.78E-01	1.00E+00	7.17E-01	1.00E+00	interleukin-1 receptor binding	F
GO:0005158	17	8.53E-01	1.00E+00	6.82E-01	1.00E+00	6.12E-01	1.00E+00	3.15E-01	1.00E+00	7.07E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	insulin receptor binding	F
GO:0005160	11	4.15E-01	1.00E+00	8.38E-01	1.00E+00	2.30E-01	1.00E+00	8.89E-01	1.00E+00	4.71E-01	1.00E+00	1.00E+00	1.00E+00	5.61E-01	1.00E+00	3.69E-01	1.00E+00	transforming growth factor beta receptor bin	F
GO:0005164	32	7.91E-01	1.00E+00	9.65E-01	1.00E+00	8.00E-01	1.00E+00	8.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	2.52E-01	1.00E+00	2.93E-01	1.00E+00	tumor necrosis factor receptor binding	F
GO:0005178	29	9.10E-01	1.00E+00	9.63E-01	1.00E+00	9.39E-01	1.00E+00	9.33E-01	1.00E+00	5.73E-01	1.00E+00	8.88E-01	1.00E+00	9.31E-01	1.00E+00	7.22E-01	1.00E+00	integrin binding	F
GO:0005179	161	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	7.02E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.89E-01	1.00E+00	hormone activity	F
GO:0005184	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	neuropeptide hormone activity	F
GO:0005198	739	7.44E-01	1.00E+00	9.10E-01	1.00E+00	8.96E-01	1.00E+00	5.11E-01	1.00E+00	4.32E-01	1.00E+00	9.86E-01	1.00E+00	8.30E-01	1.00E+00	8.79E-01	1.00E+00	structural molecule activity	F
GO:0005199	59	5.27E-01	1.00E+00	4.89E-01	1.00E+00	6.43E-01	1.00E+00	4.63E-01	1.00E+00	2.76E-01	1.00E+00	2.76E-01	1.00E+00	8.68E-01	1.00E+00	7.67E-01	1.00E+00	structural constituent of cell wall	F
GO:0005200	49	5.28E-02	1.00E+00	6.15E-01	1.00E+00	1.01E-01	1.00E+00	5.21E-01	1.00E+00	1.22E-01	1.00E+00	7.87E-01	1.00E+00	4.15E-02	8.34E-01	6.64E-01	1.00E+00	structural constituent of cytoskeleton	F
GO:0005201	49	7.12E-01	1.00E+00	1.00E+00	1.00E+00	4.66E-01	1.00E+00	1.00E+00	1.00E+00	8.51E-01	1.00E+00	1.00E+00	1.00E+00	6.39E-01	1.00E+00	9.95E-01	1.00E+00	extracellular matrix structural constituent	F
GO:0005212	20	4.60E-01	1.00E+00	9.82E-01	1.00E+00	7.01E-01	1.00E+00	7.36E-01	1.00E+00	4.98E-01	1.00E+00	9.19E-01	1.00E+00	3.34E-01	1.00E+00	8.72E-01	1.00E+00	structural constituent of eye lens	F
GO:0005215	1485	4.74E-02	1.00E+00	4.33E-01	1.00E+00	9.11E-01	1.00E+00	4.78E-01	1.00E+00	4.62E-01	1.00E+00	9.53E-01	1.00E+00	1.61E-04	6.45E-03	5.56E-02	1.00E+00	transporter activity	F
GO:0005216	424	2.49E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.99E-01	1.00E+00	6.04E-01	1.00E+00	1.00E+00	1.00E+00	1.36E-03	3.80E-02	7.19E-01	1.00E+00	ion channel activity	F
GO:0005217	12	5.77E-01	1.00E+00	9.99E-01	1.00E+00	9.75E-01	1.00E+00	1.00E+00	1.00E+00	3.84E-01	1.00E+00	9.99E-01	1.00E+00	9.24E-02	1.00E+00	8.47E-01	1.00E+00	intracellular ligand-gated ion channel activit	F
GO:0005230	71	8.19E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.98E-01	1.00E+00	6.39E-02	1.00E+00	9.72E-01	1.00E+00	extracellular ligand-gated ion channel activit	F
GO:0005231	47	1.68E-01	1.00E+00	9.75E-01	1.00E+00	6.52E-01	1.00E+00	9.65E-01	1.00E+00	7.52E-01	1.00E+00	9.30E-01	1.00E+00	2.96E-03	5.54E-02	5.94E-01	1.00E+00	excitatory extracellular ligand-gated ion cha	F
GO:0005234	18	7.34E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	8.20E-01	1.00E+00	7.20E-01	1.00E+00	1.00E+00	1.00E+00	7.41E-02	1.00E+00	9.53E-01	1.00E+00	glutamate-gated ion channel activity	F
GO:0005242	18	9.76E-01	1.00E+00	9.95E-01	1.00E+00	9.87E-01	1.00E+00	9.52E-01	1.00E+00	9.99E-01	1.00E+00	9.34E-01	1.00E+00	5.59E-01	1.00E+00	9.70E-01	1.00E+00	inward rectifier potassium channel activity	F
GO:0005244	256	3.43E-01	1.00E+00	9.91E-01	1.00E+00	9.70E-01	1.00E+00	9.88E-01	1.00E+00	4.55E-01	1.00E+00	1.00E+00	1.00E+00	8.15E-02	1.00E+00	6.48E-01	1.00E+00	voltage-gated ion channel activity	F
GO:0005245	40	1.90E-01	1.00E+00	6.33E-01	1.00E+00	6.61E-01	1.00E+00	6.94E-01	1.00E+00	7.48E-01	1.00E+00	7.41E-01	1.00E+00	1.12E-02	4.39E-01	2.35E-01	1.00E+00	voltage-gated calcium channel activity	F
GO:0005246	13	8.04E-01	1.00E+00	9.78E-01	1.00E+00	9.59E-01	1.00E+00	9.96E-01	1.00E+00	4.44E-01	1.00E+00	9.97E-01	1.00E+00	6.53E-01	1.00E+00	5.66E-01	1.00E+00	calcium channel regulator activity	F
GO:0005247	19	1.26E-01	1.00E+00	3.54E-01	1.00E+00	5.20E-01	1.00E+00	3.48E-01	1.00E+00	8.77E-02	1.00E+00	3.20E-01	1.00E+00	1.49E-01	1.00E+00	3.24E-01	1.00E+00	voltage-gated chloride channel activity	F
GO:0005248	13	9.26E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.31E-01	1.00E+00	1.00E+00	1.00E+00	1.16E-01	1.00E+00	3.79E-01	1.00E+00	voltage-gated sodium channel activity	F
GO:0005249	191	6.23E-01	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	9.99E-01	1.00E+00	6.89E-01	1.00E+00	1.00E+00	1.00E+00	3.40E-01	1.00E+00	9.98E-01	1.00E+00	voltage-gated potassium channel activity	F
GO:0005253	66	3.34E-01	1.00E+00	9.56E-01	1.00E+00	7.20E-01	1.00E+00	9.60E-01	1.00E+00	2.89E-01	1.00E+00	8.14E-01	1.00E+00	1.50E-01	1.00E+00	9.27E-01	1.00E+00	anion channel activity	F
GO:0005254	61	4.48E-01	1.00E+00	9.99E-01	1.00E+00	8.06E-01	1.00E+00	9.98E-01	1.00E+00	4.94E-01	1.00E+00	9.93E-01	1.00E+00	1.24E-01	1.00E+00	9.87E-01	1.00E+00	chloride channel activity	F
GO:0005261	324	1.96E-01	1.00E+00	9.98E-01	1.00E+00	9.50E-01	1.00E+00	9.96E-01	1.00E+00	6.33E-01	1.00E+00	1.00E+00	1.00E+00	4.10E-03	7.75E-02	5.41E-01	1.00E+00	cation channel activity	F
GO:0005262	88	1.31E-01	1.00E+00	4.88E-01	1.00E+00	7.04E-01	1.00E+00	6.45E-01	1.00E+00	2.42E-01	1.00E+00	8.12E-01	1.00E+00	2.88E-03	5.54E-02	9.84E-02	1.00E+00	calcium channel activity	F
GO:0005267	213	6.29E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	7.55E-01	1.00E+00	1.00E+00	1.00E+00	1.85E-01	1.00E+00	9.96E-01	1.00E+00	potassium channel activity	F
GO:0005272	28	9.10E-01	1.00E+00	9.12E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	7.67E-01	1.00E+00	9.73E-01	1.00E+00	1.10E-01	1.00E+00	2.64E-01	1.00E+00	sodium channel activity	F
GO:0005275	72	9.56E-01	1.00E+00	8.58E-01	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	9.99E-01	1.00E+00	8.47E-01	1.00E+00	3.52E-01	1.00E+00	2.67E-01	1.00E+00	amine transporter activity	F
GO:0005279	19	9.86E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	2.65E-01	1.00E+00	4.67E-01	1.00E+00	amino acid-polyamine transporter activity	F
GO:0005283	14	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	4.62E-01	1.00E+00	9.91E-01	1.00E+00	sodium:amino acid symporter activity	F
GO:0005310	57	5.64E-01	1.00E+00	9.94E-01	1.00E+00	5.44E-01	1.00E+00	9.83E-01	1.00E+00	7.76E-01	1.00E+00	9.98E-01	1.00E+00	4.86E-01	1.00E+00	8.99E-01	1.00E+00	dicarboxylic acid transporter activity	F
GO:0005313	10	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	9.91E-01	1.00E+00	9.91E-01	1.00E+00	9.87E-01	1.00E+00	9.01E-01	1.00E+00	9.09E-01	1.00E+00	L-glutamate transporter activity	F
GO:0005319	60	4.00E-01	1.00E+00	8.46E-01	1.00E+00	2.55E-01	1.00E+00	4.67E-01	1.00E+00	8.12E-01	1.00E+00	1.00E+00	1.00E+00	2.47E-01	1.00E+00	4.97E-01	1.00E+00	lipid transporter activity	F
GO:0005326	29	8.51E-01	1.00E+00	8.39E-01	1.00E+00	7.12E-01	1.00E+00	8.35E-01	1.00E+00	5.27E-01	1.00E+00	8.28E-01	1.00E+00	9.82E-01	1.00E+00	5.38E-01	1.00E+00	neurotransmitter transporter activity	F
GO:0005328	27	8.30E-01	1.00E+00	8.79E-01	1.00E+00	6.83E-01	1.00E+00	9.73E-01	1.00E+00	6.01E-01	1.00E+00	7.84E-01	1.00E+00	9.54E-01	1.00E+00	5.55E-01	1.00E+00	neurotransmitter:sodium symporter activity	F
GO:0005337	12	4.78E-01	1.00E+00	1.11E-01	1.00E+00	6.37E-01	1.00E+00	2.59E-01	1.00E+00	2.10E-01	1.00E+00	1.25E-01	1.00E+00	4.06E-01	1.00E+00	2.15E-01	1.00E+00	nucleoside transporter activity	F
GO:0005342	123	8.80E-01	1.00E+00	9.98E-01	1.00E+00	7.89E-01	1.00E+00	9.95E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	6.92E-01	1.00E+00	8.13E-01	1.00E+00	organic acid transporter activity	F
GO:0005343	73	5.91E-01	1.00E+00	9.98E-01	1.00E+00	4.22E-01	1.00E+00	9.65E-01	1.00E+00	8.88E-01	1.00E+00	1.00E+00	1.00E+00	6.61E-01	1.00E+00	9.44E-01	1.00E+00	organic acid:sodium symporter activity	F
GO:0005344	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen transporter activity	F
GO:0005351	44	1.09E-01	1.00E+00	5.83E-01	1.00E+00	5.00E-01	1.00E+00	8.53E-01	1.00E+00	2.76E-01	1.00E+00	6.41E-01	1.00E+00	1.87E-02	4.71E-01	4.01E-01	1.00E+00	sugar porter activity	F
GO:0005355	12	1.06E-01	1.00E+00	8.67E-01	1.00E+00	3.07E-01	1.00E+00	9.70E-01	1.00E+00	2.62E-01	1.00E+00	7.79E-01	1.00E+00	6.12E-02	1.00E+00	8.71E-01	1.00E+00	glucose transporter activity	F
GO:0005372	11	7.14E-01	1.00E+00	6.63E-01	1.00E+00	7.32E-01	1.00E+00	3.64E-01	1.00E+00	8.18E-01	1.00E+00	8.15E-01	1.00E+00	4.39E-01	1.00E+00	6.54E-01	1.00E+00	water transporter activity	F
GO:0005385	12	5.22E-01	1.00E+00	6.95E-02	1.00E+00	2.31E-01	1.00E+00	2.54E-02	7.69E-01	3.14E-01	1.00E+00	6.69E-01	1.00E+00	9.98E-01	1.00E+00	2.29E-01	1.00E+00	zinc ion transporter activity	F
GO:0005386	395	2.64E-01	1.00E+00	6.85E-01	1.00E+00	9.18E-01	1.00E+00	8.99E-01	1.00E+00	5.49E-01	1.00E+00	8.34E-01	1.00E+00	2.28E-02	5.60E-01	2.33E-01	1.00E+00	carrier activity	F
GO:0005416	17	9.72E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	2.08E-01	1.00E+00	6.64E-01	1.00E+00	cation:amino acid symporter activity	F
GO:0005451	16	8.48E-01	1.00E+00	9.05E-01	1.00E+00	9.74E-01	1.00E+00	7.75E-01	1.00E+00	4.25E-01	1.00E+00	9.70E-01	1.00E+00	7.86E-01	1.00E+00	8.78E-01	1.00E+00	monovalent cation:proton antiporter activity	F
GO:0005452	16	6.95E-01	1.00E+00	4.01E-01	1.00E+00	8.33E-01	1.00E+00	4.57E-01	1.00E+00	1.00E+00	1.00E+00	3.82E-01	1.00E+00	2.75E-01	1.00E+00	3.99E-01	1.00E+00	inorganic anion exchanger activity	F
GO:0005478	28	2.73E-02	1.00E+00	1.87E-03	1.62E-01	7.38E-02	1.00E+00	4.16E-03	1.42E-01	3.74E-02	1.00E+00	4.16E-03	1.52E-01	7.12E-02	1.00E+00	2.27E-02	1.00E+00	intracellular transporter activity	F
GO:0005484	21	1.54E-01	1.00E+00	8.47E-02	1.00E+00	3.25E-01	1.00E+00	1.60E-01	1.00E+00	1.30E-01	1.00E+00	1.28E-01	1.00E+00	1.96E-01	1.00E+00	5.49E-02	1.00E+00	SNAP receptor activity	F
GO:0005488	12054	2.90E-28	0.00E+00	0.00E+00	0.00E+00	2.17E-18	0.00E+00	4.44E-32	0.00E+00	6.99E-16	0.00E+00	8.77E-23	0.00E+00	4.26E-07	6.33E-04	1.46E-13	0.00E+00	binding	F
GO:0005496	65	3.21E-01	1.00E+00	9.44E-01	1.00E+00	2.08E-01	1.00E+00	8.16E-01	1.00E+00	5.81E-01	1.00E+00	9.80E-01	1.00E+00	2.90E-01	1.00E+00	5.40E-01	1.00E+00	steroid binding	F
GO:0005501	17	8.77E-01	1.00E+00	9.25E-01	1.00E+00	8.26E-01	1.00E+00	4.94E-01	1.00E+00	9.20E-01	1.00E+00	7.95E-01	1.00E+00	6.31E-01	1.00E+00	8.98E-01	1.00E+00	retinoid binding	F
GO:0005504	20	1.12E-02	9.83E-01	9.54E-02	1.00E+00	1.01E-01	1.00E+00	2.99E-01	1.00E+00	8.58E-02	1.00E+00	1.08E-01	1.00E+00	3.23E-02	7.53E-01	2.73E-01	1.00E+00	fatty acid binding	F
GO:0005506	357	6.51E-01	1.00E+00	6.88E-01	1.00E+00	9.93E-01	1.00E+00	4.30E-01	1.00E+00	3.84E-01	1.00E+00	9.19E-01	1.00E+00	5.35E-02	1.00E+00	4.25E-01	1.00E+00	iron ion binding	F
GO:0005507	75	9.83E-01	1.00E+00	1.00E+00	1.00E+00	8.09E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.64E-01	1.00E+00	8.98E-01	1.00E+00	copper ion binding	F
GO:0005509	962	7.51E-02	1.00E+00	1.00E+00	1.00E+00	7.93E-01	1.00E+00	1.00E+00	1.00E+00	6.58E-01	1.00E+00	1.00E+00	1.00E+00	8.79E-07	8.79E-04	8.04E-02	1.00E+00	calcium ion binding	F
GO:0005515	6722	3.31E-38	0.00E+00	1.81E-37	0.00E+00	2.93E-24	0.00E+00	1.11E-24	0.00E+00	1.64E-20	0.00E+00	3.34E-16	0.00E+00	1.59E-10	0.00E+00	2.57E-16	0.00E+00	protein binding	F
GO:0005516	120	1.14E-01	1.00E+00	8.17E-01	1.00E+00	4.57E-01	1.00E+00	9.95E-01	1.00E+00	7.79E-02	1.00E+00	6.04E-01	1.00E+00	1.01E-01	1.00E+00	5.24E-01	1.00E+00	calmodulin binding	F
GO:0005520	24	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	8.62E-01	1.00E+00	8.18E-01	1.00E+00	insulin-like growth factor binding	F
GO:0005524	1514	3.61E-17	0.00E+00	3.26E-25	0.00E+00	4.44E-11	0.00E+00	1.38E-15	0.00E+00	7.89E-13	0.00E+00	7.51E-17	0.00E+00	1.84E-07	6.33E-04	1.05E-11	0.00E+00	ATP binding	F
GO:0005525	366	6.77E-05	7.00E-03	1.20E-04	2.80E-02	3.51E-04	1.61E-02	7.16E-04	2.70E-02	3.49E-04	1.90E-02	1.15E-03	5.10E-02	4.81E-02	1.00E+00	1.07E-01	1.00E+00	GTP binding	F

GO:0005529	206	9.92E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	4.76E-02	1.00E+00	3.44E-01	1.00E+00	sugar binding	F
GO:0005537	15	2.76E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.60E-01	1.00E+00	9.54E-01	1.00E+00	1.06E-02	2.62E-01	5.42E-01	1.00E+00	mannose binding	F
GO:0005539	83	8.97E-01	1.00E+00	9.98E-01	1.00E+00	9.68E-01	1.00E+00	9.96E-01	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	1.37E-01	1.00E+00	7.49E-01	1.00E+00	glycosaminoglycan binding	F
GO:0005540	17	5.05E-01	1.00E+00	4.06E-01	1.00E+00	6.27E-01	1.00E+00	4.09E-01	1.00E+00	5.58E-01	1.00E+00	5.48E-01	1.00E+00	3.22E-01	1.00E+00	1.94E-01	1.00E+00	hyaluronic acid binding	F
GO:0005542	11	4.16E-02	1.00E+00	1.14E-01	1.00E+00	3.11E-01	1.00E+00	3.42E-01	1.00E+00	4.50E-02	1.00E+00	7.44E-02	1.00E+00	8.84E-02	1.00E+00	3.67E-01	1.00E+00	folic acid binding	F
GO:0005543	127	6.78E-02	1.00E+00	9.31E-04	7.30E-02	2.43E-01	1.00E+00	4.59E-02	1.00E+00	1.52E-01	1.00E+00	5.58E-03	2.02E-01	5.18E-02	1.00E+00	8.92E-03	4.48E-01	phospholipid binding	F
GO:0005544	23	6.48E-01	1.00E+00	3.67E-01	1.00E+00	7.75E-01	1.00E+00	5.67E-01	1.00E+00	2.43E-01	1.00E+00	4.29E-01	1.00E+00	4.92E-01	1.00E+00	1.26E-01	1.00E+00	calcium-dependent phospholipid binding	F
GO:0005545	10	6.86E-01	1.00E+00	1.40E-01	1.00E+00	9.94E-01	1.00E+00	5.34E-01	1.00E+00	3.80E-01	1.00E+00	1.02E-01	1.00E+00	5.52E-01	1.00E+00	8.07E-02	1.00E+00	phosphatidylinositol binding	F
GO:0005548	19	4.55E-01	1.00E+00	8.45E-01	1.00E+00	6.94E-01	1.00E+00	9.83E-01	1.00E+00	7.95E-01	1.00E+00	8.70E-01	1.00E+00	1.39E-01	1.00E+00	6.47E-01	1.00E+00	phospholipid transporter activity	F
GO:0005549	39	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	odorant binding	F
GO:0005550	38	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	pheromone binding	F
GO:0005575	14763	6.00E-34	0.00E+00	0.00E+00	0.00E+00	4.18E-16	0.00E+00	1.80E-33	0.00E+00	3.16E-18	0.00E+00	7.16E-19	0.00E+00	7.34E-11	0.00E+00	9.61E-25	0.00E+00	cellular_component	C
GO:0005576	2551	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.80E-01	1.00E+00	9.98E-01	1.00E+00	extracellular region	C
GO:0005578	314	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	2.82E-01	1.00E+00	9.99E-01	1.00E+00	extracellular matrix (sensu Metazoa)	C
GO:0005581	21	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.18E-01	1.00E+00	9.55E-01	1.00E+00	collagen	C
GO:0005604	70	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.98E-01	1.00E+00	5.58E-01	1.00E+00	8.83E-01	1.00E+00	basement membrane	C
GO:0005605	25	9.95E-01	1.00E+00	9.51E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	7.72E-01	1.00E+00	8.86E-01	1.00E+00	9.21E-01	1.00E+00	7.12E-01	1.00E+00	basal lamina	C
GO:0005615	1786	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.05E-01	1.00E+00	9.33E-01	1.00E+00	extracellular space	C
GO:0005622	9786	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.32E-11	0.00E+00	5.52E-34	0.00E+00	intracellular	C
GO:0005623	13388	1.33E-43	0.00E+00	0.00E+00	0.00E+00	1.20E-21	0.00E+00	0.00E+00	0.00E+00	1.92E-25	0.00E+00	1.81E-29	0.00E+00	1.05E-12	0.00E+00	7.22E-29	0.00E+00	cell	C
GO:0005624	497	3.01E-01	1.00E+00	1.98E-01	1.00E+00	9.02E-01	1.00E+00	5.40E-01	1.00E+00	2.08E-01	1.00E+00	2.53E-01	1.00E+00	6.80E-02	1.00E+00	1.27E-01	1.00E+00	membrane fraction	C
GO:0005625	97	6.85E-02	1.00E+00	1.29E-01	1.00E+00	2.94E-01	1.00E+00	1.40E-01	1.00E+00	1.61E-01	1.00E+00	4.48E-02	1.00E+00	1.44E-01	1.00E+00	7.55E-01	1.00E+00	soluble fraction	C
GO:0005626	21	5.52E-02	1.00E+00	3.88E-01	1.00E+00	9.32E-02	1.00E+00	4.44E-01	1.00E+00	1.71E-01	1.00E+00	4.40E-01	1.00E+00	3.12E-01	1.00E+00	1.40E-01	1.00E+00	insoluble fraction	C
GO:0005634	4334	2.48E-28	0.00E+00	0.00E+00	0.00E+00	1.60E-29	0.00E+00	0.00E+00	0.00E+00	2.72E-20	0.00E+00	1.51E-43	0.00E+00	5.92E-02	1.00E+00	3.51E-11	0.00E+00	nucleus	C
GO:0005635	167	3.84E-06	2.00E-03	6.29E-15	0.00E+00	2.04E-05	3.00E-03	1.62E-10	0.00E+00	1.31E-04	8.00E-03	1.03E-09	7.71E-04	4.25E-02	8.34E-01	5.18E-06	3.91E-03	nuclear envelope	C
GO:0005637	17	1.07E-01	1.00E+00	5.91E-04	7.30E-02	5.99E-02	1.00E+00	2.29E-02	7.69E-01	2.05E-01	1.00E+00	1.43E-03	5.10E-02	3.34E-01	1.00E+00	5.64E-01	1.00E+00	nuclear inner membrane	C
GO:0005640	11	4.08E-02	1.00E+00	3.00E-02	1.00E+00	1.85E-01	1.00E+00	1.32E-01	1.00E+00	7.52E-02	1.00E+00	1.18E-01	1.00E+00	1.41E-02	4.39E-01	6.29E-02	1.00E+00	nuclear outer membrane	C
GO:0005643	56	1.53E-09	9.73E-04	1.42E-18	0.00E+00	4.38E-10	0.00E+00	3.86E-15	0.00E+00	8.37E-05	3.00E-03	4.77E-12	0.00E+00	2.57E-02	6.06E-01	4.20E-06	3.91E-03	nuclear pore	C
GO:0005654	519	2.80E-08	9.73E-04	6.21E-19	0.00E+00	2.47E-07	9.88E-04	2.56E-17	0.00E+00	2.15E-05	1.56E-03	9.50E-11	0.00E+00	3.72E-02	7.83E-01	2.54E-05	3.91E-03	nucleoplasm	C
GO:0005657	27	1.20E-02	9.83E-01	4.61E-02	1.00E+00	4.57E-02	1.00E+00	2.32E-01	1.00E+00	6.51E-02	1.00E+00	3.56E-02	1.00E+00	3.15E-02	7.53E-01	8.30E-02	1.00E+00	replication fork	C
GO:0005667	259	2.45E-01	1.00E+00	1.84E-03	1.62E-01	2.83E-01	1.00E+00	4.44E-03	1.42E-01	3.46E-01	1.00E+00	1.60E-02	1.00E+00	3.84E-01	1.00E+00	5.07E-02	1.00E+00	transcription factor complex	C
GO:0005669	19	1.29E-02	9.83E-01	2.72E-03	1.87E-01	6.09E-03	1.88E-01	6.39E-03	3.78E-01	8.63E-02	1.00E+00	9.42E-02	1.00E+00	3.16E-02	7.53E-01	3.70E-01	1.00E+00	transcription factor TFIID complex	C
GO:0005681	125	1.70E-05	5.00E-03	2.59E-11	2.66E-03	2.14E-04	1.61E-02	2.16E-08	0.00E+00	5.80E-03	1.65E-01	1.90E-07	1.75E-03	1.47E-01	1.00E+00	1.52E-02	9.40E-01	spliceosome complex	C
GO:0005689	14	2.99E-03	1.39E-01	9.76E-04	7.30E-02	2.09E-03	1.18E-01	2.68E-03	1.42E-01	1.94E-01	1.00E+00	4.01E-02	1.00E+00	5.67E-01	1.00E+00	1.21E-01	1.00E+00	minor (U12-dependent) spliceosome comple	C
GO:0005694	396	1.39E-10	6.62E-04	1.01E-13	0.00E+00	2.07E-10	0.00E+00	7.69E-13	0.00E+00	1.39E-07	0.00E+00	4.44E-06	2.00E-03	4.84E-02	1.00E+00	1.51E-03	4.40E-02	chromosome	C
GO:0005720	26	6.88E-04	5.20E-02	4.38E-04	4.30E-02	7.79E-04	3.00E-02	1.85E-03	4.40E-02	1.57E-03	4.80E-02	5.53E-03	2.02E-01	7.44E-02	1.00E+00	6.64E-02	1.00E+00	nuclear heterochromatin	C
GO:0005730	149	1.52E-05	5.00E-03	1.61E-06	2.66E-03	1.44E-06	9.88E-04	7.57E-08	0.00E+00	3.13E-03	1.35E-01	4.71E-05	2.00E-03	1.90E-01	1.00E+00	2.01E-01	1.00E+00	nucleolus	C
GO:0005732	14	3.11E-01	1.00E+00	5.08E-02	1.00E+00	2.21E-01	1.00E+00	1.67E-01	1.00E+00	4.88E-01	1.00E+00	7.30E-02	1.00E+00	9.44E-01	1.00E+00	2.02E-01	1.00E+00	small nucleolar ribonucleoprotein complex	C
GO:0005737	6029	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.14E-33	0.00E+00	0.00E+00	0.00E+00	6.46E-31	0.00E+00	1.11E-40	0.00E+00	1.87E-16	0.00E+00	1.00E-31	0.00E+00	cytoplasm	C
GO:0005739	952	4.90E-19	0.00E+00	1.37E-33	0.00E+00	1.85E-12	0.00E+00	3.73E-18	0.00E+00	2.10E-12	0.00E+00	2.26E-22	0.00E+00	4.41E-05	2.00E-03	4.74E-14	0.00E+00	mitochondrion	C
GO:0005740	395	5.50E-09	9.73E-04	2.48E-15	0.00E+00	6.22E-06	1.69E-03	1.57E-10	0.00E+00	2.69E-06	7.65E-04	6.23E-11	0.00E+00	3.24E-03	6.72E-02	9.30E-06	3.91E-03	mitochondrial envelope	C
GO:0005741	65	9.47E-04	9.30E-02	3.09E-04	4.20E-02	3.85E-02	1.00E+00	4.75E-04	1.31E-02	1.14E-03	4.40E-02	7.78E-03	3.55E-01	1.50E-01	1.00E+00	1.26E-02	9.40E-01	mitochondrial outer membrane	C
GO:0005743	295	1.57E-06	2.00E-03	2.94E-13	0.00E+00	4.17E-05	3.00E-03	7.64E-09	0.00E+00	2.74E-04	8.00E-03	5.76E-10	7.71E-04	1.32E-02	4.39E-01	8.63E-05	3.91E-03	mitochondrial inner membrane	C
GO:0005746	56	6.21E-03	3.64E-01	5.12E-08	2.66E-03	9.26E-03	4.69E-01	2.70E-05	2.00E-03	1.78E-01	1.00E+00	1.01E-04	5.36E-03	8.92E-02	1.00E+00	3.66E-03	2.16E-01	mitochondrial electron transport chain	C
GO:0005747	14	2.07E-02	1.00E+00	1.51E-03	7.50E-02	2.48E-02	1.00E+00	6.22E-04	2.70E-02	1.84E-01	1.00E+00	2.20E-02	1.00E+00	5.97E-02	1.00E+00	4.78E-02	1.00E+00	respiratory chain complex I (sensu Eukaryo	C
GO:0005758	24	1.83E-02	9.83E-01	1.76E-02	1.00E+00	6.48E-02	1.00E+00	5.37E-02	1.00E+00	3.91E-02	1.00E+00	4.53E-02	1.00E+00	5.82E-01	1.00E+00	6.88E-02	1.00E+00	mitochondrial intermembrane space	C
GO:0005759	153	4.48E-05	6.00E-03	4.53E-08	2.66E-03	1.54E-04	1.61E-02	1.66E-03	4.40E-02	6.86E-03	1.65E-01	1.99E-06	2.00E-03	7.80E-02	1.00E+00	1.37E-04	4.00E-03	mitochondrial matrix	C
GO:0005761	44	8.04E-03	6.18E-01	2.19E-03	1.62E-01	5.81E-03	1.88E-01	1.12E-01	1.00E+00	2.93E-01	1.00E+00	3.35E-03	1.43E-01	2.55E-01	1.00E+00	8.08E-02	1.00E+00	mitochondrial ribosome	C
GO:0005762	22	3.11E-01	1.00E+00	6.73E-02	1.00E+00	3.11E-01	1.00E+00	4.01E-01	1.00E+00	2.93E-01	1.00E+00	5.75E-02	1.00E+00	7.80E-01	1.00E+00	2.13E-01	1.00E+00	mitochondrial large ribosomal subunit	C
GO:0005763	14	3.80E-02	1.00E+00	1.36E-03	7.50E-02	7.90E-02	1.00E+00	4.27E-02	1.00E+00	3.88E-01	1.00E+00	1.66E-02	1.00E+00	2.38E-01	1.00E+00	4.62E-02	1.00E+00	mitochondrial small ribosomal subunit	C
GO:0005764	198	2.90E-03	1.39E-01	2.33E-04	2.80E-02	9.08E-02	1.00E+00	5.79E-02	1.00E+00	1.14E-01	1.00E+00	8.41E-02	1.00E+00	1.38E-02	4.39E-01	8.06E-05	3.91E-03	lysosome	C
GO:0005765	55	3.10E-01	1.00E+00	8.02E-04	7.30E-02	3.78E-01	1.00E+00	4.40E-02	1.00E+00	6.89E-01	1.00E+00	4.19E-02	1.00E+00	3.31E-01	1.00E+00	2.14E-03	6.30E-02	lysosomal membrane	C
GO:0005768	200	1.35E-03	9.30E-02	8.88E-04	7.30E-02	1.60E-02	8.10E-01	9.68E-04	3.60E-02	2.33E-02	1.00E+00	9.74E-02	1.00E+00	3.66E-02	7.83E-01	5.59E-03	2.58E-01	endosome	C
GO:0005769	59	5.68E-03	3.48E-01	1.78E-04	2.80E-02	5.31E-03	1.88E-01	3.95E-05	5.41E-03	2.42E-02	1.00E+00	3.82E-03	1.43E-01	1.19E-01	1.00E+00	3.56E-02	1.00E+00	early endosome	C
GO:0005770	59	3.10E-01	1.00E+00	9.89E-03	7.51E-01	3.10E-01	1.00E+00	3.34E-03	1.42E-01	7.59E-01	1.00E+00	4.57E-01	1.00E+00	4.41E-01	1.00E+00	5.08E-02	1.00E+00	late endosome	C
GO:0005771	11	9.20E-01	1.00E+00	1.22E-01	1.00E+00	5.23E-01	1.00E+00	2.31E-02	7.69E-01	9.99E-01	1.00E+00	8.42E-01	1.00E+00	9.82E-01	1.00E+00	2.65E-01	1.00E+00	multivesicular body	C
GO:0005773	219	1.42E-02	9.83E-01	6.76E-04	7.30E-02	1.91E-01	1.00E+00	5.64E-02	1.00E+00	2.28E-01	1.00E+00	1.79E-01	1.00E+00	3.22E-02	7.53E-01	1.19E-04	4.00E-03	vacuole	C
GO:0005774	67	6.08E-01	1.00E+00	8.07E-03	5.59E-01	6.38E-01	1.00E+00	9.43E-02	1.00E+00	8.81E-01	1.00E+00	8.92E-02	1.00E+00	4.98E-01	1.00E+00	9.79E-03	4.72E-01	vacuolar membrane	C
GO:0005777	99	5.30E-03	3.48E-01	9.95E-05	2.80E-02	2.88E-03	1.27E-01	1.49E-02	7.69E-01	1.33E-02	4.81E-01	2.04E-04	1.36E-02	1.48E-01	1.00E+00	2.11E-02	1.00E+00	peroxisome	C
GO:0005778	40	1.50E-03	9.30E-02	6.85E-03	5.59E-01	7.79E-03	3.43E-01	1.15E-01	1.00E+00	7.84E-03	3.18E-01	2.01E-02	1.00E+00	5.03E-02	1.00E+00	5.40E-02	1.00E+00	peroxisomal membrane	C
GO:0005783	834	1.25E-05	5.00E-03	2.58E-07	2.66E-03	7.65E-02	1.00E+00	2.10E-05	1.92E-03	3.73E-04	1.90E-02	2.28E-03	1.43E-01	3.40E-05	2.00E-03	7.50E-06	3.91E-03	endoplasmic reticulum	C
GO:0005788	60	8.79E-02	1.00E+00	5.87E-04	7.30E-02	4.31E-01	1.00E+00	6.41E-03	3.78E-01	9.77E-02	1.00E+00	2.24E-03	1.43E-01	1.13E-01	1.00E+00	4.83E-02	1.00E+00	endoplasmic reticulum lumen	C
GO:0005789	462	3.81E-04	5.20E-02	3.42E-04	4.20E-02	5.83E-02	1.00E+00	3.26E-03	1.42E-01	1.32E-03	4.80E-02	5.83E-02	1.00E+00	2.32E-03	5.54E-02	2.55E-03	8.70E-02	endoplasmic reticulum membrane	C
GO:0005791	16	2.55E-01	1.00E+00	2.28E-01	1.00E+00	4.08E-01	1.00E+00	6.36E-01	1.00E+00	7.29E-01	1.00E+00	2.43E-01	1.00E+00	8.07E-02	1.00E+00	1.87E-01	1.00E+00	rough endoplasmic reticulum	C
GO:0005792	172	8.31E-01	1.00E+00	5.00E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	3.30E-01	1.00E+00	5.85E-01	1.00E+00	1.29E-01	1.00E+00	9.10E-02	1.00E+00	microsome	C
GO:0005793	25	3.54E-01	1.00E+00	5.39E-02	1.00E+00	3.77E-01	1.00E+00	1.27E-02	3.78E-01	5.14E-01	1.00E+00	1.16E-01	1.00E+00	3.85E-01	1.00E+00	8.95E-01	1.00E+00	ER-Golgi intermediate compartment	C
GO:0005794	641	2.02E-06	2.00E-03	4.01E-09	2.66E-03	1.07E-02	4.74E-01	5.57E-07	1.00E-03	1.24E-04	8.00E-03	3.88E-04	2.00E-02	3.99E-04	1.89E-02	2.48E-06	3.91E-03	Golgi apparatus	C
GO:0005795	19	5.53E-02	1.00E+00	9.93E-02	1.00E+00	1.14E-01	1.00E+00	2.46E-02	7.69E-01	4.32E-02	1.00E+00	1.19E-01	1.00E+00	9.12E-01	1.00E+00	8.34E-01	1.00E+00	Golgi stack	C
GO:0005798	43	1.03E-04	1.90E-02	4.81E-04	4.30E-02	1.07E-02	4.74E-01	1.02E-03	3.60E-02	1.96E-04	8.00E-03	4.66E-03	2.02E-01	6.28E-03	2.01E-01	1.25E-01	1.00E+00	Golgi-associated vesicle	C
GO:0005801	12	1.10E-02	9.83E-01	5.78E-03	5.59E-01	1.93E-02	8.10E-01	2.11E-02	7.69E-01	1.19E-03	4.40E-02	1.09E-02	4.01E-01	5.01E-01	1.00E+00	2.20E-01	1.00E+00	Golgi cis face	C
GO:0005802	41	1.08E-03	9.30E-02	3.82E-04	4.30E-02	1.67E-02	8.10E-01	1.42E-04	5.80E-03	7.77E-02	1.00E+00	6.28E-03	3.17E-01	2.97E-03	5.54E-02	3.65E-02	1.00E+00	Golgi trans face	C
GO:0005811	12	3.49E-01	1.00E+00	6.95E-02	1.00E+00	5.81E-01	1.00E+00	3.17E-01	1.00E+00	1.99E-01	1.00E+00	1.67E-01	1.00E+00	6.49E-01	1.00E+00	2.12E-01	1.00E+00	lipid particle	C
GO:0005813	132	1.51E-06	2.00E-03	4.44E-09	2.66E-03	1.16E-06	9.88E-04	1.74E-05	1.92E-03	6.36E-06	9.62E-04	4.39E-07	2.00E-03	3.09E-02	7.53E-01	8.63E-04	3.30E-02	centrosome	C
GO:0005814	11	2.38E-01	1.00E+00	5.54E-03	5.59E-01	9.06E-02	1.00E+00	2.80E-02	1.00E+00	1.62E-01	1.00E+00	3.42E-02	1.00E+00	6.72E-01	1.00E+00	7.79E-02	1.00E+00	centriole	C
GO:0005815	150	2.16E-06	2.00E-03	5.87E-07	2.66E-03	2.75E-06	1.69E-03	7.93E-05	5.80E-03	2.03E-05	1.56E-03	1.45E-05	2.00E-03	3.01E-02	7.53E-01	5.25E-03	2.58E-01	microtubule organizing center	C

GO:0005819	85	3.18E-06	2.00E-03	1.54E-07	2.66E-03	7.63E-07	9.88E-04	1.26E-06	1.00E-03	2.22E-04	8.00E-03	5.25E-05	3.82E-03	7.27E-02	1.00E+00	8.53E-03	4.48E-01	spindle	C
GO:0005829	462	4.49E-07	2.00E-03	2.10E-06	2.86E-03	6.90E-06	1.69E-03	3.26E-05	5.41E-03	1.87E-03	5.40E-02	8.71E-05	5.36E-03	1.38E-03	3.80E-02	8.74E-03	4.48E-01	cytosol	C
GO:0005833	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	hemoglobin complex	C
GO:0005834	37	7.27E-01	1.00E+00	8.64E-01	1.00E+00	5.47E-01	1.00E+00	8.67E-01	1.00E+00	8.97E-01	1.00E+00	7.57E-01	1.00E+00	3.71E-01	1.00E+00	8.91E-01	1.00E+00	heterotrimeric G-protein complex	C
GO:0005839	18	2.61E-02	1.00E+00	9.83E-03	7.51E-01	6.92E-02	1.00E+00	2.12E-01	1.00E+00	2.28E-01	1.00E+00	4.78E-03	2.02E-01	2.08E-01	1.00E+00	1.11E-01	1.00E+00	proteasome core complex (sensu Eukaryota	C
GO:0005840	259	6.26E-01	1.00E+00	6.16E-03	5.59E-01	4.22E-01	1.00E+00	2.80E-03	1.42E-01	4.01E-01	1.00E+00	8.11E-02	1.00E+00	1.00E+00	1.00E+00	5.40E-01	1.00E+00	ribosome	C
GO:0005856	1035	1.36E-09	9.73E-04	4.26E-06	2.86E-03	5.21E-07	9.88E-04	2.20E-04	1.10E-02	2.74E-06	7.65E-04	6.77E-04	2.00E-02	1.71E-05	2.00E-03	6.59E-04	3.30E-02	cytoskeleton	C
GO:0005863	15	9.17E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.83E-01	1.00E+00	7.86E-01	1.00E+00	1.00E+00	1.00E+00	2.87E-01	1.00E+00	8.30E-01	1.00E+00	striated muscle thick filament	C
GO:0005865	12	2.84E-01	1.00E+00	9.89E-01	1.00E+00	3.36E-01	1.00E+00	1.00E+00	1.00E+00	1.53E-01	1.00E+00	9.31E-01	1.00E+00	5.88E-01	1.00E+00	9.73E-01	1.00E+00	striated muscle thin filament	C
GO:0005871	12	5.62E-03	3.48E-01	4.31E-02	1.00E+00	1.55E-02	8.10E-01	3.15E-02	1.00E+00	1.52E-01	1.00E+00	5.32E-02	1.00E+00	3.19E-01	1.00E+00	4.71E-01	1.00E+00	kinesin complex	C
GO:0005874	229	2.42E-10	9.73E-04	7.83E-09	2.66E-03	5.07E-08	0.00E+00	1.80E-06	1.00E-03	2.30E-06	7.65E-04	3.93E-05	2.00E-03	4.82E-05	2.00E-03	1.84E-04	7.00E-03	microtubule	C
GO:0005875	112	7.02E-06	5.00E-03	1.39E-05	7.00E-03	1.69E-04	1.61E-02	7.73E-04	2.70E-02	5.14E-05	1.56E-03	2.99E-04	1.36E-02	4.89E-03	7.75E-02	3.74E-02	1.00E+00	microtubule associated complex	C
GO:0005876	14	1.52E-05	5.00E-03	1.79E-04	2.80E-02	1.21E-06	9.88E-04	1.35E-03	4.40E-02	4.89E-05	1.56E-03	1.19E-02	1.00E+00	4.53E-02	8.34E-01	7.13E-03	2.58E-01	spindle microtubule	C
GO:0005882	92	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	9.99E-01	1.00E+00	9.16E-01	1.00E+00	9.82E-01	1.00E+00	intermediate filament	C
GO:0005884	35	2.02E-02	1.00E+00	2.24E-01	1.00E+00	1.54E-01	1.00E+00	7.22E-01	1.00E+00	1.09E-01	1.00E+00	4.39E-01	1.00E+00	2.28E-02	5.60E-01	1.59E-01	1.00E+00	actin filament	C
GO:0005886	2561	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.33E-02	8.34E-01	2.61E-01	1.00E+00	plasma membrane	C
GO:0005887	490	9.18E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	8.34E-01	1.00E+00	1.00E+00	1.00E+00	1.24E-01	1.00E+00	8.39E-01	1.00E+00	integral to plasma membrane	C
GO:0005891	27	7.56E-01	1.00E+00	9.33E-01	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	9.44E-01	1.00E+00	9.56E-01	1.00E+00	1.44E-01	1.00E+00	4.43E-01	1.00E+00	voltage-gated calcium channel complex	C
GO:0005892	13	3.69E-01	1.00E+00	9.00E-01	1.00E+00	6.66E-01	1.00E+00	9.66E-01	1.00E+00	9.87E-01	1.00E+00	8.74E-01	1.00E+00	2.13E-02	5.29E-01	4.99E-01	1.00E+00	nicotinic acetylcholine-gated receptor-chanr	C
GO:0005901	33	2.00E-02	1.00E+00	6.01E-02	1.00E+00	4.99E-02	1.00E+00	8.22E-02	1.00E+00	1.45E-01	1.00E+00	1.44E-01	1.00E+00	1.31E-02	4.39E-01	2.39E-01	1.00E+00	caveola	C
GO:0005902	18	5.28E-01	1.00E+00	6.46E-01	1.00E+00	6.10E-01	1.00E+00	6.17E-01	1.00E+00	4.71E-01	1.00E+00	7.93E-01	1.00E+00	2.95E-01	1.00E+00	8.21E-01	1.00E+00	microvillus	C
GO:0005903	28	2.38E-01	1.00E+00	6.12E-01	1.00E+00	1.85E-01	1.00E+00	8.71E-01	1.00E+00	4.14E-01	1.00E+00	4.19E-01	1.00E+00	2.50E-01	1.00E+00	4.23E-01	1.00E+00	brush border	C
GO:0005905	33	5.10E-02	1.00E+00	6.23E-02	1.00E+00	6.73E-02	1.00E+00	7.45E-02	1.00E+00	4.35E-01	1.00E+00	4.27E-01	1.00E+00	7.90E-02	1.00E+00	1.24E-01	1.00E+00	coated pit	C
GO:0005911	174	7.49E-01	1.00E+00	5.18E-01	1.00E+00	9.09E-01	1.00E+00	2.70E-01	1.00E+00	9.77E-01	1.00E+00	9.79E-01	1.00E+00	2.79E-02	6.06E-01	2.57E-01	1.00E+00	intercellular junction	C
GO:0005912	79	9.24E-02	1.00E+00	1.60E-01	1.00E+00	2.86E-01	1.00E+00	1.33E-01	1.00E+00	3.43E-01	1.00E+00	7.21E-01	1.00E+00	3.00E-02	7.53E-01	1.44E-01	1.00E+00	adherens junction	C
GO:0005913	30	6.77E-01	1.00E+00	3.94E-01	1.00E+00	7.30E-01	1.00E+00	1.44E-01	1.00E+00	6.85E-01	1.00E+00	6.38E-01	1.00E+00	3.97E-01	1.00E+00	6.54E-01	1.00E+00	cell-cell adherens junction	C
GO:0005921	28	6.27E-01	1.00E+00	5.63E-01	1.00E+00	9.67E-01	1.00E+00	4.29E-01	1.00E+00	4.25E-01	1.00E+00	6.49E-01	1.00E+00	3.10E-01	1.00E+00	7.53E-01	1.00E+00	gap junction	C
GO:0005922	22	9.21E-01	1.00E+00	7.21E-01	1.00E+00	1.00E+00	1.00E+00	5.61E-01	1.00E+00	5.99E-01	1.00E+00	8.91E-01	1.00E+00	6.10E-01	1.00E+00	7.87E-01	1.00E+00	connexon complex	C
GO:0005923	88	5.46E-01	1.00E+00	2.65E-01	1.00E+00	4.78E-01	1.00E+00	2.18E-01	1.00E+00	9.95E-01	1.00E+00	9.33E-01	1.00E+00	4.04E-02	8.34E-01	7.24E-02	1.00E+00	tight junction	C
GO:0005924	45	5.36E-02	1.00E+00	3.15E-01	1.00E+00	1.59E-01	1.00E+00	3.61E-01	1.00E+00	4.30E-01	1.00E+00	6.85E-01	1.00E+00	1.67E-02	4.71E-01	2.50E-01	1.00E+00	cell-substrate adherens junction	C
GO:0005925	41	1.02E-01	1.00E+00	6.31E-01	1.00E+00	3.78E-01	1.00E+00	8.49E-01	1.00E+00	3.55E-01	1.00E+00	9.74E-01	1.00E+00	1.84E-02	4.71E-01	1.53E-01	1.00E+00	focal adhesion	C
GO:0005929	96	4.12E-03	1.86E-01	4.54E-02	1.00E+00	1.15E-02	4.74E-01	2.78E-02	1.00E+00	8.76E-02	1.00E+00	7.84E-02	1.00E+00	4.84E-02	1.00E+00	2.32E-01	1.00E+00	cilium	C
GO:0005930	16	8.47E-01	1.00E+00	4.58E-01	1.00E+00	9.16E-01	1.00E+00	3.48E-01	1.00E+00	2.03E-01	1.00E+00	4.28E-01	1.00E+00	9.67E-01	1.00E+00	8.27E-01	1.00E+00	axoneme	C
GO:0005932	14	4.48E-01	1.00E+00	7.49E-01	1.00E+00	2.98E-01	1.00E+00	7.27E-01	1.00E+00	5.93E-01	1.00E+00	7.95E-01	1.00E+00	8.61E-01	1.00E+00	6.47E-01	1.00E+00	basal body	C
GO:0005938	90	3.16E-01	1.00E+00	1.63E-01	1.00E+00	5.09E-01	1.00E+00	1.50E-01	1.00E+00	9.31E-01	1.00E+00	6.12E-01	1.00E+00	7.96E-02	1.00E+00	1.36E-01	1.00E+00	cell cortex	C
GO:0005941	44	6.36E-02	1.00E+00	5.31E-01	1.00E+00	6.92E-02	1.00E+00	6.28E-01	1.00E+00	2.37E-01	1.00E+00	4.87E-01	1.00E+00	8.05E-02	1.00E+00	6.00E-01	1.00E+00	unlocalized protein complex	C
GO:0005942	18	2.93E-02	1.00E+00	3.45E-02	1.00E+00	1.88E-01	1.00E+00	9.84E-02	1.00E+00	1.38E-01	1.00E+00	9.65E-02	1.00E+00	3.07E-02	7.53E-01	3.22E-02	1.00E+00	phosphoinositide 3-kinase complex	C
GO:0005952	21	9.01E-01	1.00E+00	5.78E-01	1.00E+00	9.99E-01	1.00E+00	7.85E-01	1.00E+00	4.75E-01	1.00E+00	6.93E-01	1.00E+00	6.53E-01	1.00E+00	1.15E-01	1.00E+00	cAMP-dependent protein kinase complex	C
GO:0005964	15	1.70E-01	1.00E+00	9.09E-01	1.00E+00	3.00E-01	1.00E+00	9.89E-01	1.00E+00	1.12E-01	1.00E+00	5.48E-01	1.00E+00	3.61E-01	1.00E+00	8.73E-01	1.00E+00	phosphorylase kinase complex	C
GO:0005975	477	1.14E-02	9.83E-01	2.95E-02	1.00E+00	6.96E-02	1.00E+00	2.93E-01	1.00E+00	5.52E-02	1.00E+00	1.88E-02	1.00E+00	5.20E-02	1.00E+00	5.42E-02	1.00E+00	carbohydrate metabolism	P
GO:0005976	76	2.69E-01	1.00E+00	9.19E-01	1.00E+00	4.93E-01	1.00E+00	9.85E-01	1.00E+00	1.19E-01	1.00E+00	7.19E-01	1.00E+00	3.93E-01	1.00E+00	6.76E-01	1.00E+00	polysaccharide metabolism	P
GO:0005977	46	7.29E-02	1.00E+00	8.57E-01	1.00E+00	3.14E-01	1.00E+00	8.87E-01	1.00E+00	3.83E-02	1.00E+00	7.76E-01	1.00E+00	9.73E-02	1.00E+00	6.03E-01	1.00E+00	glycogen metabolism	P
GO:0005978	26	1.06E-01	1.00E+00	9.63E-01	1.00E+00	2.81E-01	1.00E+00	9.97E-01	1.00E+00	6.33E-02	1.00E+00	7.33E-01	1.00E+00	1.51E-01	1.00E+00	6.33E-01	1.00E+00	glycogen biosynthesis	P
GO:0005996	182	3.58E-02	1.00E+00	1.59E-01	1.00E+00	2.12E-01	1.00E+00	6.36E-01	1.00E+00	7.97E-02	1.00E+00	8.84E-02	1.00E+00	6.53E-02	1.00E+00	3.29E-01	1.00E+00	monosaccharide metabolism	P
GO:0006006	137	6.68E-02	1.00E+00	3.14E-01	1.00E+00	4.88E-01	1.00E+00	8.55E-01	1.00E+00	1.42E-01	1.00E+00	1.09E-01	1.00E+00	3.72E-02	7.83E-01	5.72E-01	1.00E+00	glucose metabolism	P
GO:0006007	67	1.00E-02	9.83E-01	1.33E-01	1.00E+00	4.44E-02	1.00E+00	3.48E-01	1.00E+00	1.01E-01	1.00E+00	4.42E-02	1.00E+00	2.39E-02	5.60E-01	4.65E-01	1.00E+00	glucose catabolism	P
GO:0006013	10	1.38E-01	1.00E+00	1.18E-02	7.51E-01	1.20E-01	1.00E+00	1.48E-02	7.69E-01	2.76E-01	1.00E+00	1.13E-01	1.00E+00	3.07E-01	1.00E+00	5.90E-02	1.00E+00	mannose metabolism	P
GO:0006020	12	4.57E-01	1.00E+00	2.99E-01	1.00E+00	1.50E-01	1.00E+00	4.93E-01	1.00E+00	4.83E-01	1.00E+00	3.46E-01	1.00E+00	9.32E-01	1.00E+00	4.35E-01	1.00E+00	myo-inositol metabolism	P
GO:0006022	29	7.19E-01	1.00E+00	5.94E-01	1.00E+00	8.77E-01	1.00E+00	6.46E-01	1.00E+00	2.70E-01	1.00E+00	8.25E-01	1.00E+00	9.40E-01	1.00E+00	3.95E-01	1.00E+00	aminoglycan metabolism	P
GO:0006023	14	4.98E-01	1.00E+00	3.83E-01	1.00E+00	7.32E-01	1.00E+00	3.63E-01	1.00E+00	2.28E-01	1.00E+00	7.23E-01	1.00E+00	8.38E-01	1.00E+00	3.53E-01	1.00E+00	aminoglycan biosynthesis	P
GO:0006024	14	4.98E-01	1.00E+00	3.83E-01	1.00E+00	7.32E-01	1.00E+00	3.63E-01	1.00E+00	2.28E-01	1.00E+00	7.23E-01	1.00E+00	8.38E-01	1.00E+00	3.53E-01	1.00E+00	glycosaminoglycan biosynthesis	P
GO:0006029	27	9.90E-01	1.00E+00	7.65E-01	1.00E+00	9.96E-01	1.00E+00	9.09E-01	1.00E+00	6.24E-01	1.00E+00	8.30E-01	1.00E+00	9.60E-01	1.00E+00	3.62E-01	1.00E+00	proteoglycan metabolism	P
GO:0006030	12	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	chitin metabolism	P
GO:0006032	10	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.79E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	chitin catabolism	P
GO:0006040	33	7.27E-01	1.00E+00	5.26E-01	1.00E+00	5.58E-01	1.00E+00	3.98E-01	1.00E+00	9.33E-01	1.00E+00	7.58E-01	1.00E+00	5.70E-01	1.00E+00	3.95E-01	1.00E+00	amino sugar metabolism	P
GO:0006041	26	7.99E-01	1.00E+00	4.31E-01	1.00E+00	2.90E-01	1.00E+00	2.30E-01	1.00E+00	9.50E-01	1.00E+00	7.47E-01	1.00E+00	9.09E-01	1.00E+00	4.51E-01	1.00E+00	glucosamine metabolism	P
GO:0006043	11	1.00E+00	1.00E+00	8.65E-01	1.00E+00	9.80E-01	1.00E+00	8.34E-01	1.00E+00	9.90E-01	1.00E+00	8.82E-01	1.00E+00	1.00E+00	1.00E+00	6.65E-01	1.00E+00	glucosamine catabolism	P
GO:0006044	26	7.99E-01	1.00E+00	4.31E-01	1.00E+00	2.90E-01	1.00E+00	2.30E-01	1.00E+00	9.50E-01	1.00E+00	7.47E-01	1.00E+00	9.09E-01	1.00E+00	4.51E-01	1.00E+00	N-acetylglucosamine metabolism	P
GO:0006046	10	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.79E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	N-acetylglucosamine catabolism	P
GO:0006066	382	5.69E-02	1.00E+00	2.96E-01	1.00E+00	2.62E-01	1.00E+00	6.71E-01	1.00E+00	2.68E-01	1.00E+00	1.96E-01	1.00E+00	4.78E-02	1.00E+00	5.18E-01	1.00E+00	alcohol metabolism	P
GO:0006071	32	2.79E-02	1.00E+00	1.63E-01	1.00E+00	5.18E-02	1.00E+00	5.71E-02	1.00E+00	3.93E-01	1.00E+00	4.23E-01	1.00E+00	6.57E-02	1.00E+00	3.44E-01	1.00E+00	glycerol metabolism	P
GO:0006072	17	2.99E-01	1.00E+00	3.27E-01	1.00E+00	4.27E-01	1.00E+00	2.85E-01	1.00E+00	5.09E-01	1.00E+00	5.38E-01	1.00E+00	2.68E-01	1.00E+00	4.96E-01	1.00E+00	glycerol-3-phosphate metabolism	P
GO:0006073	46	7.29E-02	1.00E+00	8.57E-01	1.00E+00	3.14E-01	1.00E+00	8.87E-01	1.00E+00	3.83E-02	1.00E+00	7.76E-01	1.00E+00	9.73E-02	1.00E+00	6.03E-01	1.00E+00	glucan metabolism	P
GO:0006081	16	5.64E-01	1.00E+00	1.14E-01	1.00E+00	5.55E-01	1.00E+00	4.96E-01	1.00E+00	6.36E-01	1.00E+00	7.87E-02	1.00E+00	3.45E-01	1.00E+00	1.04E-01	1.00E+00	aldehyde metabolism	P
GO:0006082	633	2.79E-03	1.39E-01	1.26E-03	7.50E-02	5.66E-02	1.00E+00	5.11E-02	1.00E+00	3.24E-02	1.00E+00	2.23E-03	1.43E-01	3.45E-03	6.72E-02	4.81E-04	2.10E-02	organic acid metabolism	P
GO:0006084	33	1.33E-01	1.00E+00	9.85E-02	1.00E+00	6.07E-02	1.00E+00	6.45E-02	1.00E+00	3.48E-01	1.00E+00	2.99E-01	1.00E+00	2.78E-01	1.00E+00	6.16E-02	1.00E+00	acetyl-CoA metabolism	P
GO:0006090	30	2.23E-01	1.00E+00	7.33E-01	1.00E+00	7.74E-01	1.00E+00	8.02E-01	1.00E+00	3.01E-01	1.00E+00	9.35E-01	1.00E+00	7.45E-02	1.00E+00	3.60E-01	1.00E+00	pyruvate metabolism	P
GO:0006091	236	1.34E-04	1.90E-02	2.86E-02	1.00E+00	7.75E-02	1.00E+00	1.84E-01	1.00E+00	2.50E-03	1.35E-01	3.50E-02	1.00E+00	2.42E-03	5.54E-02	8.42E-02	1.00E+00	generation of precursor metabolites and ene	P
GO:0006092	116	1.23E-03	9.30E-02	4.28E-02	1.00E+00	1.76E-02	8.10E-01	1.24E-01	1.00E+00	3.46E-02	1.00E+00	4.11E-02	1.00E+00	7.15E-03	2.01E-01	1.24E-01	1.00E+00	main pathways of carbohydrate metabolism	P
GO:0006094	24	1.15E-01	1.00E+00	5.61E-01	1.00E+00	7.05E-01	1.00E+00	5.91E-01	1.00E+00	2.02E-01	1.00E+00	8.42E-01	1.00E+00	4.29E-02	8.34E-01	3.20E-01	1.00E+00	gluconeogenesis	P
GO:0006096	59	4.48E-02	1.00E+00	3.66E-01	1.00E+00	8.52E-02	1.00E+00	7.32E-01	1.00E+00	2.08E-01	1.00E+00	1.23E-01	1.00E+00	5.19E-02	1.00E+00	5.61E-01	1.00E+00	glycolysis	P
GO:0006099	23	2.40E-02	1.00E+00	4.14E-02	1.00E+00	2.45E-02	1.00E+00	8.84E-03	3.78E-01	1.86E-01	1.00E+00	2.10E-01	1.00E+00	8.21E-02	1.00E+00	5.02E-02	1.00E+00	tricarboxylic acid cycle	P
GO:0006100	19	1.80E-01	1.00E+00	1.35E-01	1.00E+00	2.77E-01	1.00E+00	3.56E-01	1.00E+00	1.03E-01	1.00E+00	2.80E-01	1.00E+00	3.57E-01	1.00E+00	4.18E-02	1.00E+00	tricarboxylic acid cycle intermediate metabo	P
GO:0006109	13	2.61E-01	1.00E+00	3.33E-01	1.00E+00	9.14E-01	1.00E+00	7.56E-01	1.00E+00	3.79E-01	1.00E+00	7.89E-01	1.00E+00	7.34E-02	1.00E+00	5.12E-02	1.00E+00	regulation of carbohydrate metabolism	P
GO:0006112	50	7.07E-02	1.00E+00	9.27E-01	1.00E+00	3.45E-01	1.00E+00	9.13E-01	1.00E+00	2.83E-02	1.00E+00	8.20E-01	1.00E+00	8.60E-02	1.00E+00	7.63E-01	1.00E+00	energy reserve metabolism	P

GO:0006118	30	1.34E-02	9.83E-01	6.23E-03	5.59E-01	2.08E-01	1.00E+00	2.47E-02	7.69E-01	4.85E-02	1.00E+00	4.60E-02	1.00E+00	7.52E-02	1.00E+00	3.42E-02	1.00E+00	electron transport	P
GO:0006119	55	1.31E-01	1.00E+00	6.14E-02	1.00E+00	7.74E-01	1.00E+00	2.60E-01	1.00E+00	1.72E-01	1.00E+00	1.26E-01	1.00E+00	1.33E-01	1.00E+00	1.18E-01	1.00E+00	oxidative phosphorylation	P
GO:0006120	11	4.87E-02	1.00E+00	1.75E-01	1.00E+00	3.53E-01	1.00E+00	3.27E-01	1.00E+00	1.94E-01	1.00E+00	3.66E-01	1.00E+00	7.98E-02	1.00E+00	1.23E-01	1.00E+00	mitochondrial electron transport, NADH to u	P
GO:0006139	3589	9.47E-12	6.62E-04	1.17E-32	0.00E+00	4.59E-12	0.00E+00	1.01E-31	0.00E+00	3.57E-10	0.00E+00	5.92E-21	0.00E+00	2.63E-01	1.00E+00	5.35E-03	2.58E-01	nucleobase, nucleoside, nucleotide and nuc	P
GO:0006140	18	2.08E-01	1.00E+00	6.57E-01	1.00E+00	7.24E-01	1.00E+00	9.94E-01	1.00E+00	2.43E-01	1.00E+00	4.34E-01	1.00E+00	2.93E-01	1.00E+00	8.29E-01	1.00E+00	regulation of nucleotide metabolism	P
GO:0006163	82	8.80E-02	1.00E+00	1.15E-02	7.51E-01	5.79E-01	1.00E+00	1.62E-02	7.69E-01	3.68E-02	1.00E+00	2.45E-02	1.00E+00	4.39E-01	1.00E+00	1.04E-01	1.00E+00	purine nucleotide metabolism	P
GO:0006164	66	1.47E-01	1.00E+00	3.23E-02	1.00E+00	6.43E-01	1.00E+00	4.60E-02	1.00E+00	5.08E-02	1.00E+00	8.08E-02	1.00E+00	5.37E-01	1.00E+00	1.36E-01	1.00E+00	purine nucleotide biosynthesis	P
GO:0006171	20	8.67E-01	1.00E+00	9.91E-01	1.00E+00	9.95E-01	1.00E+00	9.01E-01	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	9.36E-01	1.00E+00	9.51E-01	1.00E+00	cAMP biosynthesis	P
GO:0006182	13	8.12E-01	1.00E+00	9.90E-01	1.00E+00	9.57E-01	1.00E+00	9.74E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.82E-01	1.00E+00	9.87E-01	1.00E+00	cGMP biosynthesis	P
GO:0006183	12	1.03E-01	1.00E+00	6.66E-02	1.00E+00	8.81E-02	1.00E+00	7.37E-02	1.00E+00	6.99E-02	1.00E+00	8.10E-02	1.00E+00	4.91E-01	1.00E+00	2.76E-01	1.00E+00	GTP biosynthesis	P
GO:0006206	10	4.30E-01	1.00E+00	2.18E-01	1.00E+00	9.26E-02	1.00E+00	1.60E-01	1.00E+00	4.96E-01	1.00E+00	2.59E-01	1.00E+00	9.76E-01	1.00E+00	3.60E-01	1.00E+00	pyrimidine base metabolism	P
GO:0006220	23	8.14E-02	1.00E+00	2.17E-02	1.00E+00	6.23E-02	1.00E+00	4.83E-02	1.00E+00	6.34E-02	1.00E+00	1.35E-02	1.00E+00	3.27E-01	1.00E+00	1.57E-01	1.00E+00	pyrimidine nucleotide metabolism	P
GO:0006221	20	4.61E-02	1.00E+00	1.14E-02	7.51E-01	2.95E-02	1.00E+00	2.46E-02	7.69E-01	4.10E-02	1.00E+00	1.53E-02	1.00E+00	3.16E-01	1.00E+00	7.57E-02	1.00E+00	pyrimidine nucleotide biosynthesis	P
GO:0006228	11	1.04E-01	1.00E+00	1.02E-01	1.00E+00	5.89E-02	1.00E+00	1.63E-01	1.00E+00	5.18E-02	1.00E+00	9.12E-02	1.00E+00	7.68E-01	1.00E+00	2.83E-01	1.00E+00	UTP biosynthesis	P
GO:0006241	12	9.92E-02	1.00E+00	7.31E-02	1.00E+00	4.69E-02	1.00E+00	1.04E-01	1.00E+00	6.29E-02	1.00E+00	6.78E-02	1.00E+00	7.71E-01	1.00E+00	2.86E-01	1.00E+00	CTP biosynthesis	P
GO:0006259	705	2.21E-20	0.00E+00	4.59E-26	0.00E+00	4.24E-18	0.00E+00	7.75E-20	0.00E+00	2.98E-13	0.00E+00	9.13E-14	0.00E+00	2.55E-04	1.70E-02	1.49E-08	0.00E+00	DNA metabolism	P
GO:0006260	166	2.04E-09	9.73E-04	2.22E-11	2.66E-03	3.77E-08	0.00E+00	4.47E-08	0.00E+00	9.37E-06	1.56E-03	1.98E-09	7.71E-04	1.80E-03	5.54E-02	1.37E-04	4.00E-03	DNA replication	P
GO:0006261	73	2.83E-04	1.90E-02	3.75E-05	2.80E-02	1.19E-02	4.74E-01	1.07E-03	3.60E-02	9.83E-04	4.40E-02	9.67E-04	4.80E-02	1.17E-02	4.39E-01	6.83E-03	2.58E-01	DNA-dependent DNA replication	P
GO:0006265	22	1.15E-01	1.00E+00	8.22E-02	1.00E+00	6.36E-02	1.00E+00	4.50E-01	1.00E+00	2.58E-01	1.00E+00	5.21E-02	1.00E+00	3.88E-01	1.00E+00	5.53E-01	1.00E+00	DNA topological change	P
GO:0006268	11	5.09E-02	1.00E+00	1.24E-02	7.51E-01	4.87E-01	1.00E+00	2.54E-02	7.69E-01	1.50E-02	4.81E-01	4.07E-02	1.00E+00	2.47E-01	1.00E+00	2.16E-01	1.00E+00	DNA unwinding during replication	P
GO:0006270	20	1.88E-02	9.83E-01	1.08E-02	7.51E-01	7.89E-02	1.00E+00	8.58E-03	3.78E-01	6.86E-03	1.65E-01	1.03E-01	1.00E+00	5.72E-01	1.00E+00	3.33E-02	1.00E+00	DNA replication initiation	P
GO:0006275	30	9.03E-03	9.83E-01	1.23E-01	1.00E+00	5.35E-02	1.00E+00	3.45E-01	1.00E+00	4.56E-02	1.00E+00	2.33E-01	1.00E+00	5.19E-02	1.00E+00	8.01E-02	1.00E+00	regulation of DNA replication	P
GO:0006281	238	6.78E-09	9.73E-04	1.15E-12	0.00E+00	2.57E-07	9.88E-04	4.70E-08	0.00E+00	5.43E-07	7.65E-04	9.20E-11	0.00E+00	7.17E-03	2.01E-01	2.24E-03	6.30E-02	DNA repair	P
GO:0006284	23	2.72E-01	1.00E+00	2.22E-01	1.00E+00	8.95E-02	1.00E+00	5.57E-01	1.00E+00	3.87E-01	1.00E+00	9.80E-02	1.00E+00	5.55E-01	1.00E+00	6.90E-01	1.00E+00	base-excision repair	P
GO:0006289	32	8.11E-03	6.18E-01	2.00E-02	1.00E+00	1.26E-03	7.90E-02	7.40E-02	1.00E+00	6.34E-02	1.00E+00	1.10E-01	1.00E+00	7.15E-01	1.00E+00	4.88E-02	1.00E+00	nucleotide-excision repair	P
GO:0006298	14	2.54E-02	1.00E+00	3.21E-03	2.13E-01	8.07E-02	1.00E+00	1.10E-02	3.78E-01	3.48E-02	1.00E+00	6.97E-03	3.55E-01	3.69E-02	7.83E-01	3.79E-02	1.00E+00	mismatch repair	P
GO:0006302	31	1.91E-03	1.02E-01	5.65E-04	7.30E-02	3.56E-02	1.00E+00	2.24E-03	4.50E-02	4.02E-03	1.35E-01	1.46E-03	5.10E-02	9.02E-02	1.00E+00	5.50E-03	2.58E-01	double-strand break repair	P
GO:0006304	34	4.86E-01	1.00E+00	6.97E-01	1.00E+00	6.90E-01	1.00E+00	8.46E-01	1.00E+00	1.50E-01	1.00E+00	6.88E-01	1.00E+00	5.14E-01	1.00E+00	2.90E-01	1.00E+00	DNA modification	P
GO:0006305	33	5.11E-01	1.00E+00	6.87E-01	1.00E+00	6.86E-01	1.00E+00	8.16E-01	1.00E+00	1.60E-01	1.00E+00	7.12E-01	1.00E+00	5.83E-01	1.00E+00	2.85E-01	1.00E+00	DNA alkylation	P
GO:0006306	33	5.11E-01	1.00E+00	6.87E-01	1.00E+00	6.86E-01	1.00E+00	8.16E-01	1.00E+00	1.60E-01	1.00E+00	7.12E-01	1.00E+00	5.83E-01	1.00E+00	2.85E-01	1.00E+00	DNA methylation	P
GO:0006308	17	2.13E-01	1.00E+00	3.33E-01	1.00E+00	2.51E-01	1.00E+00	3.65E-01	1.00E+00	3.24E-01	1.00E+00	8.08E-01	1.00E+00	1.64E-01	1.00E+00	7.08E-01	1.00E+00	DNA catabolism	P
GO:0006310	85	2.18E-05	5.00E-03	2.93E-06	2.86E-03	2.39E-03	1.18E-01	1.04E-06	1.00E-03	4.70E-03	1.35E-01	1.60E-03	5.10E-02	6.92E-03	2.01E-01	7.06E-04	3.30E-02	DNA recombination	P
GO:0006323	281	1.63E-08	9.73E-04	9.08E-13	0.00E+00	1.74E-08	0.00E+00	4.75E-11	0.00E+00	3.93E-05	1.56E-03	6.40E-06	2.00E-03	1.63E-01	1.00E+00	2.63E-05	3.91E-03	DNA packaging	P
GO:0006325	279	3.08E-08	9.73E-04	9.58E-13	0.00E+00	3.87E-08	0.00E+00	4.82E-11	0.00E+00	3.84E-05	1.56E-03	7.29E-06	2.00E-03	2.02E-01	1.00E+00	2.73E-05	3.91E-03	establishment and/or maintenance of chrom	P
GO:0006333	134	1.10E-03	9.30E-02	1.74E-04	2.80E-02	1.38E-03	7.90E-02	7.50E-04	2.70E-02	2.94E-02	1.00E+00	1.09E-02	4.01E-01	2.15E-01	1.00E+00	5.22E-02	1.00E+00	chromatin assembly or disassembly	P
GO:0006334	88	5.42E-02	1.00E+00	9.48E-02	1.00E+00	6.68E-02	1.00E+00	1.13E-02	3.78E-01	1.05E-01	1.00E+00	1.51E-01	1.00E+00	7.88E-01	1.00E+00	8.84E-01	1.00E+00	nucleosome assembly	P
GO:0006338	47	1.22E-04	1.90E-02	1.27E-09	2.66E-03	4.18E-05	3.00E-03	3.39E-05	5.41E-03	5.85E-03	1.65E-01	1.10E-05	2.00E-03	2.22E-01	1.00E+00	7.54E-04	3.30E-02	chromatin remodeling	P
GO:0006342	15	6.59E-02	1.00E+00	3.09E-04	4.20E-02	8.87E-02	1.00E+00	5.02E-02	1.00E+00	1.49E-01	1.00E+00	1.09E-02	4.01E-01	2.26E-01	1.00E+00	4.04E-03	2.16E-01	chromatin silencing	P
GO:0006350	2465	2.66E-01	1.00E+00	7.32E-08	2.66E-03	2.13E-02	1.00E+00	5.19E-11	0.00E+00	1.83E-01	1.00E+00	1.53E-05	2.00E-03	9.82E-01	1.00E+00	6.11E-01	1.00E+00	transcription	P
GO:0006351	2286	3.39E-01	1.00E+00	2.78E-07	2.66E-03	5.18E-02	1.00E+00	1.20E-09	0.00E+00	1.87E-01	1.00E+00	1.19E-05	2.00E-03	9.82E-01	1.00E+00	6.15E-01	1.00E+00	transcription, DNA-dependent	P
GO:0006352	50	1.10E-04	1.90E-02	4.91E-06	2.86E-03	2.62E-05	3.00E-03	3.77E-05	5.41E-03	6.57E-02	1.00E+00	4.86E-03	2.02E-01	2.49E-02	5.60E-01	1.27E-01	1.00E+00	transcription initiation	P
GO:0006354	11	3.48E-02	1.00E+00	1.58E-03	7.50E-02	5.99E-02	1.00E+00	4.54E-03	1.42E-01	6.72E-01	1.00E+00	2.00E-02	1.00E+00	3.11E-02	7.53E-01	4.05E-01	1.00E+00	RNA elongation	P
GO:0006355	2255	4.28E-01	1.00E+00	2.53E-06	2.86E-03	9.40E-02	1.00E+00	7.32E-09	0.00E+00	2.31E-01	1.00E+00	8.66E-05	5.36E-03	9.81E-01	1.00E+00	6.93E-01	1.00E+00	regulation of transcription, DNA-dependent	P
GO:0006357	502	9.43E-01	1.00E+00	8.24E-01	1.00E+00	9.77E-01	1.00E+00	3.31E-01	1.00E+00	9.74E-01	1.00E+00	9.82E-01	1.00E+00	8.60E-01	1.00E+00	8.64E-01	1.00E+00	regulation of transcription from RNA polyme	P
GO:0006360	10	2.13E-01	1.00E+00	4.10E-01	1.00E+00	3.15E-01	1.00E+00	1.22E-01	1.00E+00	3.17E-01	1.00E+00	8.96E-01	1.00E+00	3.99E-01	1.00E+00	9.67E-01	1.00E+00	transcription from RNA polymerase I promot	P
GO:0006364	65	1.96E-03	1.02E-01	7.76E-04	7.30E-02	4.81E-02	1.00E+00	9.80E-05	5.80E-03	5.92E-03	1.65E-01	4.17E-02	1.00E+00	1.21E-01	1.00E+00	6.66E-01	1.00E+00	rRNA processing	P
GO:0006366	549	6.98E-01	1.00E+00	4.17E-01	1.00E+00	6.35E-01	1.00E+00	7.70E-02	1.00E+00	8.44E-01	1.00E+00	8.55E-01	1.00E+00	8.54E-01	1.00E+00	8.08E-01	1.00E+00	transcription from RNA polymerase II promo	P
GO:0006367	23	1.53E-03	9.30E-02	2.05E-04	2.80E-02	1.84E-03	1.18E-01	1.08E-03	3.60E-02	3.72E-02	1.00E+00	6.01E-02	1.00E+00	2.19E-01	1.00E+00	1.13E-01	1.00E+00	transcription initiation from RNA polymerase	P
GO:0006376	10	5.35E-01	1.00E+00	4.11E-01	1.00E+00	8.99E-01	1.00E+00	3.20E-01	1.00E+00	3.31E-01	1.00E+00	4.09E-01	1.00E+00	3.21E-01	1.00E+00	5.82E-01	1.00E+00	mRNA splice site selection	P
GO:0006396	392	6.97E-11	6.62E-04	2.90E-26	0.00E+00	1.99E-08	0.00E+00	2.58E-20	0.00E+00	1.15E-06	7.65E-04	3.02E-16	0.00E+00	8.79E-02	1.00E+00	6.54E-04	3.30E-02	RNA processing	P
GO:0006397	235	1.28E-08	9.73E-04	4.95E-18	0.00E+00	1.85E-06	9.88E-04	6.10E-16	0.00E+00	1.52E-04	8.00E-03	6.76E-12	0.00E+00	1.04E-01	1.00E+00	4.38E-02	1.00E+00	mRNA processing	P
GO:0006399	124	2.84E-04	1.90E-02	7.37E-07	2.66E-03	1.31E-03	7.90E-02	2.17E-05	1.92E-03	6.82E-04	4.40E-02	1.99E-04	1.36E-02	1.08E-01	1.00E+00	2.27E-03	6.30E-02	tRNA metabolism	P
GO:0006400	11	3.58E-01	1.00E+00	2.32E-02	1.00E+00	1.06E-01	1.00E+00	1.88E-01	1.00E+00	1.25E-01	1.00E+00	4.58E-02	1.00E+00	1.00E+00	1.00E+00	5.41E-02	1.00E+00	tRNA modification	P
GO:0006401	33	1.24E-02	9.83E-01	2.38E-02	1.00E+00	3.72E-02	1.00E+00	2.51E-02	7.69E-01	6.24E-02	1.00E+00	4.40E-01	1.00E+00	1.76E-02	4.71E-01	1.27E-01	1.00E+00	RNA catabolism	P
GO:0006402	27	5.06E-02	1.00E+00	1.05E-01	1.00E+00	5.09E-02	1.00E+00	6.45E-02	1.00E+00	1.60E-01	1.00E+00	7.60E-01	1.00E+00	1.54E-01	1.00E+00	2.49E-01	1.00E+00	mRNA catabolism	P
GO:0006403	60	1.23E-05	5.00E-03	2.98E-08	2.66E-03	1.54E-05	1.69E-03	6.47E-08	0.00E+00	8.06E-04	4.40E-02	2.09E-06	2.00E-03	1.96E-01	1.00E+00	2.28E-01	1.00E+00	RNA localization	P
GO:0006405	20	4.18E-03	1.86E-01	1.76E-03	1.62E-01	4.41E-03	1.88E-01	1.23E-04	5.80E-03	2.98E-02	1.00E+00	3.52E-02	1.00E+00	2.08E-01	1.00E+00	3.53E-01	1.00E+00	RNA export from nucleus	P
GO:0006406	15	1.05E-01	1.00E+00	1.90E-02	1.00E+00	1.82E-02	8.10E-01	1.46E-04	5.80E-03	1.55E-01	1.00E+00	1.04E-01	1.00E+00	8.91E-01	1.00E+00	5.68E-01	1.00E+00	mRNA export from nucleus	P
GO:0006412	689	5.57E-02	1.00E+00	3.74E-07	2.66E-03	5.72E-03	1.88E-01	1.14E-05	1.77E-03	9.75E-02	1.00E+00	7.06E-05	5.36E-03	9.83E-01	1.00E+00	4.97E-02	1.00E+00	protein biosynthesis	P
GO:0006413	60	2.84E-03	1.39E-01	5.26E-06	3.00E-03	1.25E-02	4.74E-01	3.86E-02	1.00E+00	3.70E-04	1.90E-02	7.99E-08	7.71E-04	7.55E-01	1.00E+00	2.57E-01	1.00E+00	translational initiation	P
GO:0006414	21	7.52E-01	1.00E+00	4.31E-02	1.00E+00	3.60E-01	1.00E+00	4.62E-02	1.00E+00	5.46E-01	1.00E+00	4.62E-01	1.00E+00	1.00E+00	1.00E+00	1.96E-01	1.00E+00	translational elongation	P
GO:0006417	154	1.37E-01	1.00E+00	1.14E-01	1.00E+00	4.65E-02	1.00E+00	1.18E-01	1.00E+00	3.22E-01	1.00E+00	1.10E-01	1.00E+00	4.84E-01	1.00E+00	3.07E-01	1.00E+00	regulation of protein biosynthesis	P
GO:0006418	67	2.01E-03	1.02E-01	1.09E-04	2.80E-02	7.30E-03	2.83E-01	1.05E-04	5.80E-03	4.65E-03	1.35E-01	3.49E-03	1.43E-01	8.33E-02	1.00E+00	8.97E-02	1.00E+00	tRNA aminoacylation for protein translation	P
GO:0006445	31	9.74E-03	9.83E-01	2.54E-04	2.80E-02	2.67E-02	1.00E+00	2.43E-04	1.15E-02	9.15E-03	3.69E-01	2.75E-03	1.43E-01	7.61E-01	1.00E+00	1.12E-01	1.00E+00	regulation of translation	P
GO:0006446	22	2.55E-03	1.39E-01	8.30E-04	7.30E-02	4.64E-03	1.88E-01	1.49E-03	4.40E-02	3.76E-03	1.35E-01	1.02E-03	4.80E-02	8.42E-01	1.00E+00	9.28E-02	1.00E+00	regulation of translational initiation	P
GO:0006457	143	2.31E-04	1.90E-02	4.37E-09	2.66E-03	1.49E-02	8.10E-01	7.36E-06	1.77E-03	9.44E-04	4.40E-02	5.42E-06	2.00E-03	1.77E-01	1.00E+00	6.12E-03	2.58E-01	protein folding	P
GO:0006461	282	3.35E-03	1.86E-01	2.44E-02	1.00E+00	3.48E-02	1.00E+00	1.85E-02	7.69E-01	1.30E-02	4.81E-01	1.45E-01	1.00E+00	5.99E-01	1.00E+00	2.34E-01	1.00E+00	protein complex assembly	P
GO:0006464	1738	3.24E-12	6.62E-04	1.17E-23	0.00E+00	4.90E-09	0.00E+00	2.78E-14	0.00E+00	5.50E-09	0.00E+00	6.66E-15	0.00E+00	8.76E-04	2.40E-02	3.39E-13	0.00E+00	protein modification	P
GO:0006468	728	9.87E-02	1.00E+00	1.04E-02	7.51E-01	4.63E-01	1.00E+00	2.25E-01	1.00E+00	1.93E-01	1.00E+00	1.88E-02	1.00E+00	3.22E-02	7.53E-01	1.00E-02	4.72E-01	protein amino acid phosphorylation	P
GO:0006469	50	2.51E-01	1.00E+00	3.11E-01	1.00E+00	3.48E-01	1.00E+00	6.97E-02	1.00E+00	6.51E-01	1.00E+00	8.96E-01	1.00E+00	1.20E-01	1.00E+00	7.11E-01	1.00E+00	negative regulation of protein kinase activity	P
GO:0006470	133	4.25E-02	1.00E+00	9.04E-03	5.59E-01	2.17E-01	1.00E+00	8.55E-02	1.00E+00	5.29E-02	1.00E+00	7.71E-02	1.00E+00	3.76E-02	7.83E-01	3.02E-03	2.16E-01	protein amino acid dephosphorylation	P
GO:0006471	16	3.92E-01	1.00E+00	1.37E-01	1.00E+00	4.19E-01	1.00E+00	4.65E-02	1.00E+00	7.35E-01	1.00E+00	5.39E-01	1.00E+00	1.53E-01	1.00E+00	2.95E-01	1.00E+00	protein amino acid ADP-ribosylation	P
GO:0006473	16	3.68E-02	1.00E+00	4.05E-02	1.00E+00	4.60E-02	1.00E+00	5.58E-02	1.00E+00	1.40E-01	1.00E+00	2.21E-02	1.00E+00	2.39E-01	1.00E+00	1.16E-01	1.00E+00	protein amino acid acetylation	P
GO:0006476	18	1.18E-02	9.83E-01	8.46E-03	5.59E-01	4.99E-02	1.00E+00	2.19E-02	7.69E-01	1.68E-02	7.19E-01	6.79E-02	1.00E+00	2.36E-01	1.00E+00	3.31E-02	1.00E+00	protein amino acid deacetylation	P
GO:0006479	35	1.96E-03	1.02E-01	3.02E-04	4.20E-02	5.56E-03	1.88E-01	3.20E-03	1.42E-01	3.52E-03	1.35E-01	5.25E-04	2.00E-02	7.97E-02	1.00E+00	1.61E-02	9.40E-01	protein amino acid methylation	P

GO:0006486	83	6.13E-01	1.00E+00	4.25E-02	1.00E+00	5.92E-01	1.00E+00	1.61E-01	1.00E+00	9.55E-01	1.00E+00	1.35E-01	1.00E+00	1.41E-01	1.00E+00	4.07E-03	2.16E-01	protein amino acid glycosylation	P
GO:0006487	21	3.28E-01	1.00E+00	1.65E-03	7.50E-02	2.21E-01	1.00E+00	3.24E-02	1.00E+00	6.48E-01	1.00E+00	3.54E-03	1.43E-01	3.28E-01	1.00E+00	6.35E-04	3.30E-02	protein amino acid N-linked glycosylation	P
GO:0006493	15	4.66E-01	1.00E+00	3.19E-01	1.00E+00	4.73E-01	1.00E+00	3.15E-01	1.00E+00	2.39E-01	1.00E+00	3.88E-01	1.00E+00	8.75E-01	1.00E+00	3.23E-01	1.00E+00	protein amino acid O-linked glycosylation	P
GO:0006497	47	1.85E-01	1.00E+00	5.13E-02	1.00E+00	3.80E-02	1.00E+00	5.12E-02	1.00E+00	3.32E-01	1.00E+00	1.61E-01	1.00E+00	8.37E-01	1.00E+00	1.90E-01	1.00E+00	protein amino acid lipidation	P
GO:0006505	27	7.88E-02	1.00E+00	1.69E-02	1.00E+00	2.20E-02	1.00E+00	2.80E-02	1.00E+00	2.36E-01	1.00E+00	6.06E-02	1.00E+00	4.51E-01	1.00E+00	2.80E-01	1.00E+00	GPI anchor metabolism	P
GO:0006506	23	4.73E-02	1.00E+00	3.39E-03	2.13E-01	1.11E-02	4.74E-01	1.30E-02	3.78E-01	1.69E-01	1.00E+00	3.48E-02	1.00E+00	4.96E-01	1.00E+00	1.74E-01	1.00E+00	GPI anchor biosynthesis	P
GO:0006508	799	1.18E-01	1.00E+00	1.09E-02	7.51E-01	2.66E-01	1.00E+00	1.88E-01	1.00E+00	5.60E-01	1.00E+00	2.10E-01	1.00E+00	2.25E-02	5.60E-01	2.24E-04	1.70E-02	proteolysis	P
GO:0006509	13	6.63E-01	1.00E+00	8.13E-01	1.00E+00	6.13E-01	1.00E+00	9.84E-01	1.00E+00	9.93E-01	1.00E+00	9.73E-01	1.00E+00	2.25E-01	1.00E+00	8.32E-01	1.00E+00	membrane protein ectodomain proteolysis	P
GO:0006511	152	1.74E-06	2.00E-03	3.96E-11	2.66E-03	1.88E-05	3.00E-03	2.01E-08	0.00E+00	1.29E-06	7.65E-04	2.22E-07	1.75E-03	2.52E-01	1.00E+00	1.05E-04	4.00E-03	ubiquitin-dependent protein catabolism	P
GO:0006512	529	5.83E-14	6.62E-04	3.62E-24	0.00E+00	7.01E-13	0.00E+00	1.93E-17	0.00E+00	3.82E-14	0.00E+00	1.17E-17	0.00E+00	6.40E-02	1.00E+00	7.89E-09	0.00E+00	ubiquitin cycle	P
GO:0006515	12	8.18E-02	1.00E+00	1.13E-03	7.30E-02	4.50E-02	1.00E+00	8.59E-04	2.70E-02	2.55E-01	1.00E+00	3.97E-02	1.00E+00	6.79E-01	1.00E+00	2.49E-02	1.00E+00	misfolded or incompletely synthesized prote	P
GO:0006516	10	5.10E-01	1.00E+00	7.74E-03	5.59E-01	1.78E-01	1.00E+00	6.27E-02	1.00E+00	7.55E-01	1.00E+00	1.01E-01	1.00E+00	5.37E-01	1.00E+00	3.06E-02	1.00E+00	glycoprotein catabolism	P
GO:0006518	14	5.01E-01	1.00E+00	5.97E-01	1.00E+00	1.00E+00	1.00E+00	6.35E-01	1.00E+00	1.78E-01	1.00E+00	4.92E-01	1.00E+00	7.57E-01	1.00E+00	5.10E-01	1.00E+00	peptide metabolism	P
GO:0006519	454	6.08E-02	1.00E+00	6.68E-02	1.00E+00	2.26E-01	1.00E+00	1.42E-01	1.00E+00	3.75E-01	1.00E+00	1.08E-01	1.00E+00	3.87E-02	7.83E-01	9.78E-02	1.00E+00	amino acid and derivative metabolism	P
GO:0006520	368	5.20E-02	1.00E+00	2.94E-02	1.00E+00	9.19E-02	1.00E+00	1.32E-01	1.00E+00	1.85E-01	1.00E+00	2.42E-02	1.00E+00	8.38E-02	1.00E+00	1.03E-01	1.00E+00	amino acid metabolism	P
GO:0006521	96	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.21E-01	1.00E+00	6.76E-01	1.00E+00	regulation of amino acid metabolism	P
GO:0006536	10	1.25E-01	1.00E+00	2.65E-01	1.00E+00	6.99E-01	1.00E+00	1.77E-01	1.00E+00	2.23E-01	1.00E+00	3.04E-01	1.00E+00	1.53E-01	1.00E+00	4.75E-01	1.00E+00	glutamate metabolism	P
GO:0006541	17	3.92E-01	1.00E+00	1.96E-02	1.00E+00	3.60E-01	1.00E+00	3.22E-02	1.00E+00	3.58E-01	1.00E+00	9.26E-02	1.00E+00	7.26E-01	1.00E+00	3.84E-02	1.00E+00	glutamine metabolism	P
GO:0006544	12	3.42E-01	1.00E+00	4.13E-02	1.00E+00	1.52E-01	1.00E+00	1.41E-01	1.00E+00	4.71E-01	1.00E+00	9.05E-03	3.55E-01	6.42E-01	1.00E+00	1.25E-01	1.00E+00	glycine metabolism	P
GO:0006547	11	8.98E-01	1.00E+00	6.00E-01	1.00E+00	8.25E-01	1.00E+00	4.47E-01	1.00E+00	9.82E-01	1.00E+00	7.67E-01	1.00E+00	3.76E-01	1.00E+00	3.74E-01	1.00E+00	histidine metabolism	P
GO:0006548	11	8.98E-01	1.00E+00	6.00E-01	1.00E+00	8.25E-01	1.00E+00	4.47E-01	1.00E+00	9.82E-01	1.00E+00	7.67E-01	1.00E+00	3.76E-01	1.00E+00	3.74E-01	1.00E+00	histidine catabolism	P
GO:0006570	14	6.90E-01	1.00E+00	7.05E-01	1.00E+00	5.09E-01	1.00E+00	8.66E-01	1.00E+00	9.19E-01	1.00E+00	5.89E-01	1.00E+00	6.80E-01	1.00E+00	4.58E-01	1.00E+00	tyrosine metabolism	P
GO:0006575	153	1.88E-01	1.00E+00	5.41E-01	1.00E+00	5.82E-01	1.00E+00	4.63E-01	1.00E+00	7.58E-01	1.00E+00	6.59E-01	1.00E+00	6.36E-02	1.00E+00	4.80E-01	1.00E+00	amino acid derivative metabolism	P
GO:0006576	86	6.41E-01	1.00E+00	9.31E-01	1.00E+00	9.85E-01	1.00E+00	5.69E-01	1.00E+00	8.28E-01	1.00E+00	9.93E-01	1.00E+00	2.52E-01	1.00E+00	6.45E-01	1.00E+00	biogenic amine metabolism	P
GO:0006582	10	5.20E-01	1.00E+00	8.62E-01	1.00E+00	3.93E-01	1.00E+00	9.18E-01	1.00E+00	7.72E-01	1.00E+00	7.07E-01	1.00E+00	4.82E-01	1.00E+00	7.57E-01	1.00E+00	melanin metabolism	P
GO:0006584	36	9.69E-01	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	9.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	9.06E-01	1.00E+00	catecholamine metabolism	P
GO:0006586	11	2.03E-01	1.00E+00	4.60E-01	1.00E+00	7.62E-01	1.00E+00	9.35E-01	1.00E+00	1.76E-01	1.00E+00	4.99E-01	1.00E+00	3.16E-02	7.53E-01	1.29E-01	1.00E+00	indolalkylamine metabolism	P
GO:0006595	19	2.08E-01	1.00E+00	1.18E-01	1.00E+00	4.72E-01	1.00E+00	1.98E-02	7.69E-01	3.15E-01	1.00E+00	5.74E-01	1.00E+00	7.66E-01	1.00E+00	6.21E-01	1.00E+00	polyamine metabolism	P
GO:0006596	10	5.60E-02	1.00E+00	2.32E-01	1.00E+00	3.70E-01	1.00E+00	2.58E-01	1.00E+00	1.18E-01	1.00E+00	4.24E-01	1.00E+00	8.70E-02	1.00E+00	1.76E-01	1.00E+00	polyamine biosynthesis	P
GO:0006605	221	9.72E-04	9.30E-02	9.85E-08	2.66E-03	4.91E-03	1.88E-01	1.40E-05	1.77E-03	3.81E-03	1.35E-01	1.89E-05	2.00E-03	8.06E-02	1.00E+00	2.09E-03	6.30E-02	protein targeting	P
GO:0006606	81	2.51E-02	1.00E+00	4.23E-05	2.80E-02	6.59E-02	1.00E+00	7.08E-04	2.70E-02	9.82E-02	1.00E+00	3.91E-04	2.00E-02	1.37E-01	1.00E+00	7.27E-03	2.58E-01	protein import into nucleus	P
GO:0006611	18	1.41E-03	9.30E-02	2.42E-03	1.87E-01	4.99E-03	1.88E-01	2.07E-02	7.69E-01	4.63E-02	1.00E+00	4.17E-02	1.00E+00	3.74E-02	7.83E-01	4.30E-02	1.00E+00	protein export from nucleus	P
GO:0006612	29	2.24E-02	1.00E+00	6.52E-04	7.30E-02	3.82E-02	1.00E+00	1.97E-03	4.40E-02	4.07E-03	1.35E-01	4.35E-03	1.52E-01	2.46E-01	1.00E+00	2.07E-01	1.00E+00	protein targeting to membrane	P
GO:0006613	19	1.37E-01	1.00E+00	5.66E-03	5.59E-01	1.94E-01	1.00E+00	1.15E-02	3.78E-01	6.28E-02	1.00E+00	1.21E-02	1.00E+00	6.92E-01	1.00E+00	4.18E-01	1.00E+00	cotranslational protein targeting to membrar	P
GO:0006614	16	2.41E-01	1.00E+00	1.29E-02	7.51E-01	3.46E-01	1.00E+00	1.12E-02	3.78E-01	1.49E-01	1.00E+00	1.98E-02	1.00E+00	6.57E-01	1.00E+00	5.44E-01	1.00E+00	SRP-dependent cotranslational protein targ	P
GO:0006625	10	2.77E-01	1.00E+00	1.96E-01	1.00E+00	2.51E-01	1.00E+00	2.65E-01	1.00E+00	2.56E-01	1.00E+00	3.73E-01	1.00E+00	6.18E-01	1.00E+00	1.29E-01	1.00E+00	protein targeting to peroxisome	P
GO:0006626	10	1.52E-01	1.00E+00	3.15E-02	1.00E+00	6.52E-01	1.00E+00	2.24E-02	7.69E-01	1.43E-01	1.00E+00	3.82E-01	1.00E+00	2.59E-01	1.00E+00	3.13E-01	1.00E+00	protein targeting to mitochondrion	P
GO:0006629	742	7.00E-03	3.64E-01	2.44E-02	1.00E+00	8.23E-03	3.43E-01	2.48E-01	1.00E+00	3.01E-01	1.00E+00	7.32E-02	1.00E+00	9.25E-03	2.17E-01	2.08E-03	6.30E-02	lipid metabolism	P
GO:0006631	186	2.72E-02	1.00E+00	2.54E-03	1.87E-01	1.25E-01	1.00E+00	3.37E-02	1.00E+00	7.73E-02	1.00E+00	4.04E-03	1.52E-01	8.93E-02	1.00E+00	1.77E-03	6.30E-02	fatty acid metabolism	P
GO:0006633	83	3.76E-01	1.00E+00	3.88E-01	1.00E+00	9.34E-01	1.00E+00	7.29E-01	1.00E+00	2.95E-01	1.00E+00	3.60E-01	1.00E+00	1.11E-01	1.00E+00	1.15E-01	1.00E+00	fatty acid biosynthesis	P
GO:0006635	16	5.47E-02	1.00E+00	1.48E-03	7.50E-02	4.74E-02	1.00E+00	6.25E-03	3.78E-01	6.40E-02	1.00E+00	2.59E-02	1.00E+00	5.00E-01	1.00E+00	6.31E-03	2.58E-01	fatty acid beta-oxidation	P
GO:0006637	15	7.93E-01	1.00E+00	7.49E-02	1.00E+00	2.87E-01	1.00E+00	2.65E-01	1.00E+00	7.48E-01	1.00E+00	3.39E-02	1.00E+00	6.70E-01	1.00E+00	6.08E-02	1.00E+00	acyl-CoA metabolism	P
GO:0006638	36	2.37E-01	1.00E+00	7.61E-01	1.00E+00	7.69E-01	1.00E+00	8.62E-01	1.00E+00	9.08E-01	1.00E+00	9.79E-01	1.00E+00	2.76E-02	6.06E-01	4.05E-01	1.00E+00	neutral lipid metabolism	P
GO:0006639	35	2.76E-01	1.00E+00	8.04E-01	1.00E+00	8.14E-01	1.00E+00	9.25E-01	1.00E+00	9.40E-01	1.00E+00	9.89E-01	1.00E+00	2.91E-02	6.06E-01	3.90E-01	1.00E+00	acylglycerol metabolism	P
GO:0006641	30	2.38E-01	1.00E+00	8.13E-01	1.00E+00	8.20E-01	1.00E+00	8.88E-01	1.00E+00	9.32E-01	1.00E+00	9.87E-01	1.00E+00	1.56E-02	4.39E-01	4.91E-01	1.00E+00	triacylglycerol metabolism	P
GO:0006643	201	2.54E-04	1.90E-02	1.76E-04	2.80E-02	3.98E-04	1.61E-02	5.98E-04	2.70E-02	9.24E-02	1.00E+00	1.55E-02	1.00E+00	8.15E-03	2.17E-01	9.09E-03	4.48E-01	membrane lipid metabolism	P
GO:0006644	160	5.06E-04	5.20E-02	5.37E-03	5.59E-01	2.15E-04	1.61E-02	8.25E-03	3.78E-01	1.17E-01	1.00E+00	3.95E-02	1.00E+00	1.35E-02	4.39E-01	3.87E-02	1.00E+00	phospholipid metabolism	P
GO:0006650	84	1.09E-04	1.90E-02	8.28E-06	3.00E-03	1.03E-04	1.61E-02	7.78E-04	2.70E-02	2.05E-02	7.19E-01	3.18E-04	1.36E-02	7.81E-03	2.01E-01	1.26E-03	4.40E-02	glycerophospholipid metabolism	P
GO:0006662	37	1.70E-01	1.00E+00	6.82E-01	1.00E+00	7.44E-01	1.00E+00	9.24E-01	1.00E+00	6.53E-01	1.00E+00	9.77E-01	1.00E+00	2.99E-02	7.53E-01	2.23E-01	1.00E+00	glycerol ether metabolism	P
GO:0006664	17	7.68E-02	1.00E+00	9.09E-02	1.00E+00	1.05E-01	1.00E+00	4.27E-02	1.00E+00	7.29E-01	1.00E+00	6.54E-01	1.00E+00	2.84E-01	1.00E+00	4.44E-02	1.00E+00	glycolipid metabolism	P
GO:0006665	54	3.17E-02	1.00E+00	1.12E-03	7.30E-02	8.47E-02	1.00E+00	1.91E-03	4.40E-02	2.43E-01	1.00E+00	8.05E-02	1.00E+00	1.67E-01	1.00E+00	5.28E-02	1.00E+00	sphingolipid metabolism	P
GO:0006672	30	2.23E-02	1.00E+00	4.50E-04	4.30E-02	6.22E-02	1.00E+00	3.58E-03	1.42E-01	2.58E-01	1.00E+00	4.74E-02	1.00E+00	1.84E-01	1.00E+00	5.82E-02	1.00E+00	ceramide metabolism	P
GO:0006684	10	8.09E-02	1.00E+00	3.86E-01	1.00E+00	1.80E-02	8.10E-01	2.04E-01	1.00E+00	6.23E-01	1.00E+00	4.23E-01	1.00E+00	3.28E-01	1.00E+00	5.52E-01	1.00E+00	sphingomyelin metabolism	P
GO:0006687	11	3.45E-03	1.86E-01	1.43E-01	1.00E+00	4.31E-02	1.00E+00	2.52E-02	7.69E-01	5.86E-01	1.00E+00	7.82E-01	1.00E+00	1.46E-01	1.00E+00	9.02E-02	1.00E+00	glycosphingolipid metabolism	P
GO:0006690	33	6.10E-01	1.00E+00	7.63E-01	1.00E+00	7.63E-01	1.00E+00	5.55E-01	1.00E+00	4.38E-01	1.00E+00	9.77E-01	1.00E+00	5.51E-01	1.00E+00	3.54E-01	1.00E+00	icosanoid metabolism	P
GO:0006691	19	7.27E-01	1.00E+00	9.58E-01	1.00E+00	6.33E-01	1.00E+00	8.87E-01	1.00E+00	7.29E-01	1.00E+00	9.86E-01	1.00E+00	5.21E-01	1.00E+00	4.77E-01	1.00E+00	leukotriene metabolism	P
GO:0006692	14	3.58E-01	1.00E+00	3.05E-01	1.00E+00	7.81E-01	1.00E+00	1.58E-01	1.00E+00	1.34E-01	1.00E+00	7.50E-01	1.00E+00	5.56E-01	1.00E+00	3.00E-01	1.00E+00	prostanoid metabolism	P
GO:0006693	14	3.58E-01	1.00E+00	3.05E-01	1.00E+00	7.81E-01	1.00E+00	1.58E-01	1.00E+00	1.34E-01	1.00E+00	7.50E-01	1.00E+00	5.56E-01	1.00E+00	3.00E-01	1.00E+00	prostaglandin metabolism	P
GO:0006694	93	7.55E-01	1.00E+00	7.38E-01	1.00E+00	6.71E-01	1.00E+00	9.31E-01	1.00E+00	6.18E-01	1.00E+00	3.68E-01	1.00E+00	6.42E-01	1.00E+00	8.07E-01	1.00E+00	steroid biosynthesis	P
GO:0006695	29	5.39E-01	1.00E+00	2.12E-01	1.00E+00	4.77E-01	1.00E+00	2.33E-01	1.00E+00	7.95E-01	1.00E+00	1.31E-01	1.00E+00	3.97E-01	1.00E+00	8.02E-01	1.00E+00	cholesterol biosynthesis	P
GO:0006700	15	9.65E-01	1.00E+00	1.00E+00	1.00E+00	8.07E-01	1.00E+00	9.57E-01	1.00E+00	8.91E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	C21-steroid hormone biosynthesis	P
GO:0006706	10	1.28E-01	1.00E+00	2.18E-01	1.00E+00	3.80E-01	1.00E+00	6.65E-01	1.00E+00	1.27E-01	1.00E+00	5.30E-01	1.00E+00	9.99E-02	1.00E+00	1.36E-01	1.00E+00	steroid catabolism	P
GO:0006720	36	1.25E-01	1.00E+00	3.14E-01	1.00E+00	6.64E-01	1.00E+00	4.00E-01	1.00E+00	3.57E-01	1.00E+00	2.77E-01	1.00E+00	8.93E-02	1.00E+00	7.54E-01	1.00E+00	isoprenoid metabolism	P
GO:0006725	174	1.97E-01	1.00E+00	6.11E-01	1.00E+00	4.05E-01	1.00E+00	8.15E-01	1.00E+00	6.51E-01	1.00E+00	4.46E-01	1.00E+00	1.37E-01	1.00E+00	4.30E-01	1.00E+00	aromatic compound metabolism	P
GO:0006730	118	1.74E-02	9.83E-01	1.23E-02	7.51E-01	2.34E-02	1.00E+00	1.44E-01	1.00E+00	1.18E-02	4.21E-01	9.02E-03	3.55E-01	3.73E-01	1.00E+00	1.85E-02	9.40E-01	one-carbon compound metabolism	P
GO:0006732	174	1.87E-02	9.83E-01	5.61E-03	5.59E-01	1.99E-01	1.00E+00	2.57E-02	7.69E-01	5.69E-02	1.00E+00	3.49E-02	1.00E+00	4.62E-02	8.34E-01	1.44E-02	9.40E-01	coenzyme metabolism	P
GO:0006733	35	3.68E-03	1.86E-01	1.46E-01	1.00E+00	1.41E-02	8.10E-01	1.36E-01	1.00E+00	1.87E-02	7.19E-01	4.13E-01	1.00E+00	1.98E-02	4.71E-01	2.10E-01	1.00E+00	oxidoreduction coenzyme metabolism	P
GO:0006739	14	2.40E-02	1.00E+00	3.46E-01	1.00E+00	9.09E-02	1.00E+00	2.72E-01	1.00E+00	1.17E-01	1.00E+00	3.89E-01	1.00E+00	8.53E-02	1.00E+00	6.80E-01	1.00E+00	NADP metabolism	P
GO:0006749	26	4.98E-01	1.00E+00	3.34E-01	1.00E+00	9.33E-01	1.00E+00	4.61E-01	1.00E+00	2.09E-01	1.00E+00	1.42E-01	1.00E+00	5.20E-01	1.00E+00	8.50E-01	1.00E+00	glutathione metabolism	P
GO:0006752	62	2.58E-01	1.00E+00	1.13E-01	1.00E+00	8.27E-01	1.00E+00	3.93E-01	1.00E+00	1.40E-01	1.00E+00	2.75E-01	1.00E+00	2.99E-01	1.00E+00	1.11E-01	1.00E+00	group transfer coenzyme metabolism	P
GO:0006753	34	6.22E-01	1.00E+00	7.15E-01	1.00E+00	9.97E-01	1.00E+00	8.51E-01	1.00E+00	2.50E-01	1.00E+00	8.53E-01	1.00E+00	7.20E-01	1.00E+00	6.02E-01	1.00E+00	nucleoside phosphate metabolism	P
GO:0006754	34	6.22E-01	1.00E+00	7.15E-01	1.00E+00	9.97E-01	1.00E+00	8.51E-01	1.00E+00	2.50E-01	1.00E+00	8.53E-01	1.00E+00	7.20E-01	1.00E+00	6.02E-01	1.00E+00	ATP biosynthesis	P
GO:0006760	16	1.27E-01	1.00E+00	2.26E-03	1.62E-01	3.23E-01	1.00E+00	5.98E-02	1.00E+00	9.85E-02	1.00E+00	5.66E-03	2.02E-01	7.19E-02	1.00E+00	6.41E-03	2.58E-01	folic acid and derivative metabolism	P
GO:0006766	78	2.56E-01	1.00E+00	1.52E-01	1.00E+00	3.45E-01	1.00E+00	9.00E-02	1.00E+00	5.36E-01	1.00E+00	4.07E-01	1.00E+00	1.03E-01	1.00E+00	4.73E-01	1.00E+00	vitamin metabolism	P
GO:0006767	49	3.66E-02	1.00E+00	1.42E-01	1.00E+00	8.15E-02	1.00E+00	1.29E-01	1.00E+00	1.41E-01	1.00E+00	2.50E-01	1.00E+00	4.27E-02	8.34E-01	5.49E-01	1.00E+00	water-soluble vitamin metabolism	P

GO:0006769	23	3.82E-02	1.00E+00	3.40E-01	1.00E+00	1.00E-01	1.00E+00	3.00E-01	1.00E+00	1.42E-01	1.00E+00	5.82E-01	1.00E+00	7.04E-02	1.00E+00	3.47E-01	1.00E+00	nicotinamide metabolism	P
GO:0006775	28	9.80E-01	1.00E+00	4.02E-01	1.00E+00	9.90E-01	1.00E+00	2.34E-01	1.00E+00	9.79E-01	1.00E+00	8.01E-01	1.00E+00	6.37E-01	1.00E+00	4.12E-01	1.00E+00	fat-soluble vitamin metabolism	P
GO:0006776	22	9.90E-01	1.00E+00	7.28E-01	1.00E+00	1.00E+00	1.00E+00	5.77E-01	1.00E+00	9.28E-01	1.00E+00	7.55E-01	1.00E+00	8.30E-01	1.00E+00	6.75E-01	1.00E+00	vitamin A metabolism	P
GO:0006778	26	4.04E-02	1.00E+00	7.72E-02	1.00E+00	1.14E-01	1.00E+00	8.05E-02	1.00E+00	3.64E-02	1.00E+00	5.06E-01	1.00E+00	9.52E-02	1.00E+00	1.10E-01	1.00E+00	porphyrin metabolism	P
GO:0006779	20	7.32E-02	1.00E+00	2.29E-01	1.00E+00	3.28E-01	1.00E+00	1.13E-01	1.00E+00	1.91E-02	7.19E-01	7.93E-01	1.00E+00	1.17E-01	1.00E+00	1.76E-01	1.00E+00	porphyrin biosynthesis	P
GO:0006783	13	7.05E-02	1.00E+00	3.55E-01	1.00E+00	3.55E-01	1.00E+00	2.24E-01	1.00E+00	1.89E-02	7.19E-01	6.95E-01	1.00E+00	1.15E-01	1.00E+00	3.23E-01	1.00E+00	heme biosynthesis	P
GO:0006790	85	4.16E-01	1.00E+00	1.76E-01	1.00E+00	9.64E-01	1.00E+00	5.68E-01	1.00E+00	1.71E-01	1.00E+00	1.08E-01	1.00E+00	5.19E-01	1.00E+00	2.03E-01	1.00E+00	sulfur metabolism	P
GO:0006793	977	1.36E-02	9.83E-01	3.21E-05	2.80E-02	3.23E-01	1.00E+00	1.94E-02	7.69E-01	5.17E-02	1.00E+00	1.88E-03	1.43E-01	6.80E-03	2.01E-01	4.10E-05	3.91E-03	phosphorus metabolism	P
GO:0006796	977	1.36E-02	9.83E-01	3.21E-05	2.80E-02	3.23E-01	1.00E+00	1.94E-02	7.69E-01	5.17E-02	1.00E+00	1.88E-03	1.43E-01	6.80E-03	2.01E-01	4.10E-05	3.91E-03	phosphate metabolism	P
GO:0006800	131	2.44E-03	1.02E-01	9.06E-05	2.80E-02	1.69E-02	8.10E-01	2.39E-03	6.52E-02	2.46E-01	1.00E+00	7.95E-03	3.55E-01	1.78E-03	5.54E-02	1.25E-03	4.40E-02	oxygen and reactive oxygen species metab	P
GO:0006801	19	4.20E-01	1.00E+00	2.12E-01	1.00E+00	8.67E-01	1.00E+00	4.91E-01	1.00E+00	6.51E-01	1.00E+00	2.33E-01	1.00E+00	8.21E-02	1.00E+00	2.12E-02	1.00E+00	superoxide metabolism	P
GO:0006805	13	2.10E-01	1.00E+00	5.51E-01	1.00E+00	4.17E-01	1.00E+00	9.86E-01	1.00E+00	2.30E-01	1.00E+00	3.11E-01	1.00E+00	1.45E-01	1.00E+00	2.20E-01	1.00E+00	xenobiotic metabolism	P
GO:0006807	559	7.36E-02	1.00E+00	1.12E-01	1.00E+00	2.83E-01	1.00E+00	1.89E-01	1.00E+00	4.63E-01	1.00E+00	2.18E-01	1.00E+00	3.26E-02	7.53E-01	7.70E-02	1.00E+00	nitrogen compound metabolism	P
GO:0006809	23	5.23E-01	1.00E+00	9.05E-01	1.00E+00	5.54E-01	1.00E+00	7.87E-01	1.00E+00	9.18E-01	1.00E+00	9.48E-01	1.00E+00	1.24E-01	1.00E+00	5.96E-01	1.00E+00	nitric oxide biosynthesis	P
GO:0006810	2901	7.72E-09	9.73E-04	6.15E-08	2.66E-03	2.09E-02	1.00E+00	2.65E-06	1.00E-03	8.61E-04	4.40E-02	9.13E-03	3.55E-01	1.58E-09	0.00E+00	1.14E-06	3.91E-03	transport	P
GO:0006811	922	8.00E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	1.08E-03	2.40E-02	7.67E-01	1.00E+00	ion transport	P
GO:0006812	655	4.78E-01	1.00E+00	9.91E-01	1.00E+00	9.96E-01	1.00E+00	9.15E-01	1.00E+00	7.40E-01	1.00E+00	1.00E+00	1.00E+00	5.09E-03	9.40E-02	4.70E-01	1.00E+00	cation transport	P
GO:0006813	277	5.08E-01	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	9.84E-01	1.00E+00	8.87E-01	1.00E+00	1.00E+00	1.00E+00	5.44E-02	1.00E+00	9.92E-01	1.00E+00	potassium ion transport	P
GO:0006814	137	8.25E-01	1.00E+00	9.99E-01	1.00E+00	9.62E-01	1.00E+00	9.94E-01	1.00E+00	8.76E-01	1.00E+00	1.00E+00	1.00E+00	1.70E-01	1.00E+00	7.45E-01	1.00E+00	sodium ion transport	P
GO:0006816	163	4.29E-01	1.00E+00	8.82E-01	1.00E+00	9.86E-01	1.00E+00	8.57E-01	1.00E+00	7.86E-01	1.00E+00	9.99E-01	1.00E+00	6.96E-04	2.40E-02	6.77E-02	1.00E+00	calcium ion transport	P
GO:0006817	89	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.79E-01	1.00E+00	8.82E-01	1.00E+00	phosphate transport	P
GO:0006818	74	2.30E-01	1.00E+00	1.68E-01	1.00E+00	9.87E-01	1.00E+00	4.01E-01	1.00E+00	2.05E-01	1.00E+00	1.53E-01	1.00E+00	7.67E-02	1.00E+00	3.11E-01	1.00E+00	hydrogen transport	P
GO:0006820	216	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.91E-01	1.00E+00	1.00E+00	1.00E+00	3.35E-01	1.00E+00	9.53E-01	1.00E+00	anion transport	P
GO:0006821	74	8.20E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.15E-01	1.00E+00	4.47E-01	1.00E+00	9.94E-01	1.00E+00	3.98E-01	1.00E+00	9.99E-01	1.00E+00	chloride transport	P
GO:0006825	11	4.14E-02	1.00E+00	5.90E-01	1.00E+00	2.38E-01	1.00E+00	4.22E-01	1.00E+00	6.55E-02	1.00E+00	9.29E-01	1.00E+00	2.92E-01	1.00E+00	3.34E-01	1.00E+00	copper ion transport	P
GO:0006826	27	3.17E-01	1.00E+00	2.91E-01	1.00E+00	4.15E-01	1.00E+00	2.04E-01	1.00E+00	4.28E-01	1.00E+00	3.12E-01	1.00E+00	2.45E-01	1.00E+00	7.50E-01	1.00E+00	iron ion transport	P
GO:0006829	22	5.37E-01	1.00E+00	1.05E-01	1.00E+00	2.70E-01	1.00E+00	1.24E-01	1.00E+00	4.08E-01	1.00E+00	5.10E-01	1.00E+00	8.83E-01	1.00E+00	1.89E-01	1.00E+00	zinc ion transport	P
GO:0006833	11	7.14E-01	1.00E+00	6.63E-01	1.00E+00	7.32E-01	1.00E+00	3.64E-01	1.00E+00	8.18E-01	1.00E+00	8.15E-01	1.00E+00	4.39E-01	1.00E+00	6.54E-01	1.00E+00	water transport	P
GO:0006835	57	5.64E-01	1.00E+00	9.94E-01	1.00E+00	5.44E-01	1.00E+00	9.83E-01	1.00E+00	7.76E-01	1.00E+00	9.98E-01	1.00E+00	4.86E-01	1.00E+00	8.99E-01	1.00E+00	dicarboxylic acid transport	P
GO:0006836	62	9.65E-01	1.00E+00	9.92E-01	1.00E+00	9.81E-01	1.00E+00	9.96E-01	1.00E+00	6.00E-01	1.00E+00	9.80E-01	1.00E+00	9.52E-01	1.00E+00	8.06E-01	1.00E+00	neurotransmitter transport	P
GO:0006839	46	4.87E-02	1.00E+00	8.08E-04	7.30E-02	1.90E-01	1.00E+00	1.00E-03	3.60E-02	4.36E-02	1.00E+00	3.00E-02	1.00E+00	1.74E-01	1.00E+00	4.00E-02	1.00E+00	mitochondrial transport	P
GO:0006857	10	1.15E-01	1.00E+00	4.35E-01	1.00E+00	8.16E-01	1.00E+00	8.21E-01	1.00E+00	2.84E-01	1.00E+00	1.96E-01	1.00E+00	1.71E-02	4.71E-01	3.65E-01	1.00E+00	oligopeptide transport	P
GO:0006865	71	6.56E-01	1.00E+00	2.66E-01	1.00E+00	8.27E-01	1.00E+00	5.59E-01	1.00E+00	8.78E-01	1.00E+00	3.46E-01	1.00E+00	4.44E-01	1.00E+00	4.43E-02	1.00E+00	amino acid transport	P
GO:0006869	103	5.30E-02	1.00E+00	1.61E-01	1.00E+00	4.70E-02	1.00E+00	3.56E-01	1.00E+00	8.46E-02	1.00E+00	2.97E-01	1.00E+00	1.99E-01	1.00E+00	1.27E-01	1.00E+00	lipid transport	P
GO:0006873	151	1.17E-01	1.00E+00	9.32E-01	1.00E+00	2.73E-01	1.00E+00	5.74E-01	1.00E+00	2.08E-01	1.00E+00	9.97E-01	1.00E+00	1.29E-01	1.00E+00	8.58E-01	1.00E+00	cell ion homeostasis	P
GO:0006874	86	1.82E-01	1.00E+00	9.22E-01	1.00E+00	6.03E-01	1.00E+00	7.97E-01	1.00E+00	3.88E-01	1.00E+00	9.99E-01	1.00E+00	3.48E-02	7.53E-01	4.86E-01	1.00E+00	calcium ion homeostasis	P
GO:0006875	133	9.84E-02	1.00E+00	9.23E-01	1.00E+00	2.06E-01	1.00E+00	5.70E-01	1.00E+00	1.49E-01	1.00E+00	9.96E-01	1.00E+00	1.16E-01	1.00E+00	9.05E-01	1.00E+00	metal ion homeostasis	P
GO:0006879	25	6.29E-02	1.00E+00	5.10E-01	1.00E+00	3.21E-02	1.00E+00	3.17E-01	1.00E+00	6.58E-02	1.00E+00	3.99E-01	1.00E+00	4.99E-01	1.00E+00	9.98E-01	1.00E+00	iron ion homeostasis	P
GO:0006885	34	9.15E-01	1.00E+00	9.79E-01	1.00E+00	9.76E-01	1.00E+00	9.39E-01	1.00E+00	8.54E-01	1.00E+00	9.90E-01	1.00E+00	8.91E-01	1.00E+00	7.65E-01	1.00E+00	regulation of pH	P
GO:0006886	509	7.80E-10	9.73E-04	1.05E-16	0.00E+00	4.49E-06	1.69E-03	2.40E-12	0.00E+00	2.42E-07	0.00E+00	1.22E-10	7.71E-04	5.40E-04	1.89E-02	1.36E-05	3.91E-03	intracellular protein transport	P
GO:0006887	100	1.75E-01	1.00E+00	8.12E-01	1.00E+00	2.96E-01	1.00E+00	6.17E-01	1.00E+00	4.03E-01	1.00E+00	9.98E-01	1.00E+00	9.17E-02	1.00E+00	1.97E-01	1.00E+00	exocytosis	P
GO:0006888	28	1.45E-01	1.00E+00	8.25E-03	5.59E-01	1.22E-01	1.00E+00	3.24E-02	1.00E+00	3.62E-01	1.00E+00	7.97E-03	3.55E-01	3.76E-01	1.00E+00	3.55E-01	1.00E+00	ER to Golgi vesicle-mediated transport	P
GO:0006891	11	3.13E-02	1.00E+00	1.12E-02	7.51E-01	1.27E-01	1.00E+00	6.03E-03	3.78E-01	7.57E-02	1.00E+00	6.75E-02	1.00E+00	1.58E-01	1.00E+00	1.93E-01	1.00E+00	intra-Golgi vesicle-mediated transport	P
GO:0006892	15	5.51E-03	3.48E-01	1.81E-01	1.00E+00	1.35E-01	1.00E+00	1.42E-01	1.00E+00	8.02E-02	1.00E+00	3.04E-01	1.00E+00	5.10E-02	1.00E+00	5.05E-01	1.00E+00	post-Golgi vesicle-mediated transport	P
GO:0006897	197	3.81E-03	1.86E-01	6.03E-02	1.00E+00	1.01E-01	1.00E+00	1.69E-01	1.00E+00	2.96E-01	1.00E+00	4.49E-01	1.00E+00	3.45E-04	1.89E-02	2.19E-02	1.00E+00	endocytosis	P
GO:0006898	25	4.47E-01	1.00E+00	6.20E-02	1.00E+00	4.95E-01	1.00E+00	2.59E-02	7.69E-01	8.25E-01	1.00E+00	1.65E-01	1.00E+00	2.57E-01	1.00E+00	2.23E-01	1.00E+00	receptor mediated endocytosis	P
GO:0006904	18	4.12E-01	1.00E+00	2.07E-01	1.00E+00	5.02E-01	1.00E+00	3.15E-01	1.00E+00	5.02E-01	1.00E+00	4.79E-01	1.00E+00	2.34E-01	1.00E+00	5.22E-02	1.00E+00	vesicle docking during exocytosis	P
GO:0006909	50	5.89E-01	1.00E+00	9.94E-01	1.00E+00	7.20E-01	1.00E+00	9.80E-01	1.00E+00	7.30E-01	1.00E+00	9.99E-01	1.00E+00	3.07E-01	1.00E+00	9.69E-01	1.00E+00	phagocytosis	P
GO:0006910	12	7.28E-01	1.00E+00	4.89E-01	1.00E+00	7.39E-01	1.00E+00	5.02E-01	1.00E+00	8.87E-01	1.00E+00	4.08E-01	1.00E+00	4.69E-01	1.00E+00	7.91E-01	1.00E+00	phagocytosis, recognition	P
GO:0006911	14	9.90E-01	1.00E+00	9.48E-01	1.00E+00	9.39E-01	1.00E+00	9.08E-01	1.00E+00	8.08E-01	1.00E+00	8.57E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	phagocytosis, engulfment	P
GO:0006913	230	2.11E-05	5.00E-03	5.38E-09	2.66E-03	2.31E-04	1.61E-02	2.11E-07	9.57E-04	6.29E-04	4.40E-02	1.93E-06	2.00E-03	3.30E-02	7.53E-01	4.40E-04	2.10E-02	nucleocytoplasmic transport	P
GO:0006914	30	4.19E-02	1.00E+00	7.78E-03	5.59E-01	8.39E-02	1.00E+00	9.41E-02	1.00E+00	1.67E-01	1.00E+00	1.49E-01	1.00E+00	4.85E-02	1.00E+00	2.37E-02	1.00E+00	autophagy	P
GO:0006915	758	3.65E-03	1.86E-01	3.32E-02	1.00E+00	3.52E-02	1.00E+00	3.62E-02	1.00E+00	9.82E-03	3.69E-01	1.92E-01	1.00E+00	6.03E-02	1.00E+00	1.01E-01	1.00E+00	apoptosis	P
GO:0006916	105	3.05E-01	1.00E+00	5.79E-01	1.00E+00	5.38E-01	1.00E+00	3.76E-01	1.00E+00	5.06E-01	1.00E+00	8.01E-01	1.00E+00	4.41E-01	1.00E+00	5.15E-01	1.00E+00	anti-apoptosis	P
GO:0006917	185	8.29E-03	6.18E-01	2.43E-02	1.00E+00	9.49E-02	1.00E+00	2.84E-02	1.00E+00	8.13E-02	1.00E+00	1.22E-01	1.00E+00	2.65E-03	5.54E-02	9.16E-02	1.00E+00	induction of apoptosis	P
GO:0006919	35	2.84E-03	1.39E-01	5.88E-02	1.00E+00	6.60E-03	2.83E-01	7.64E-02	1.00E+00	3.09E-02	1.00E+00	7.24E-02	1.00E+00	1.63E-02	4.71E-01	1.32E-01	1.00E+00	caspase activation	P
GO:0006921	12	4.56E-02	1.00E+00	6.67E-02	1.00E+00	1.23E-01	1.00E+00	3.79E-02	1.00E+00	1.04E-01	1.00E+00	2.32E-01	1.00E+00	1.72E-01	1.00E+00	3.11E-01	1.00E+00	disassembly of cell structures during apoptc	P
GO:0006928	433	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.34E-01	1.00E+00	9.10E-01	1.00E+00	cell motility	P
GO:0006935	157	9.94E-01	1.00E+00	9.03E-01	1.00E+00	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	9.65E-01	1.00E+00	7.23E-01	1.00E+00	7.80E-02	1.00E+00	chemotaxis	P
GO:0006936	73	2.33E-01	1.00E+00	9.31E-01	1.00E+00	6.00E-01	1.00E+00	6.99E-01	1.00E+00	2.07E-01	1.00E+00	9.99E-01	1.00E+00	1.07E-01	1.00E+00	6.94E-01	1.00E+00	muscle contraction	P
GO:0006937	28	2.02E-01	1.00E+00	9.88E-01	1.00E+00	2.17E-01	1.00E+00	9.88E-01	1.00E+00	5.31E-01	1.00E+00	9.98E-01	1.00E+00	1.93E-01	1.00E+00	6.19E-01	1.00E+00	regulation of muscle contraction	P
GO:0006939	22	3.32E-01	1.00E+00	9.68E-01	1.00E+00	5.81E-01	1.00E+00	5.89E-01	1.00E+00	2.41E-01	1.00E+00	1.00E+00	1.00E+00	4.75E-01	1.00E+00	8.04E-01	1.00E+00	smooth muscle contraction	P
GO:0006940	16	4.34E-01	1.00E+00	1.00E+00	1.00E+00	4.46E-01	1.00E+00	1.00E+00	1.00E+00	4.84E-01	1.00E+00	1.00E+00	1.00E+00	5.40E-01	1.00E+00	6.61E-01	1.00E+00	regulation of smooth muscle contraction	P
GO:0006941	28	6.91E-01	1.00E+00	9.18E-01	1.00E+00	9.69E-01	1.00E+00	7.07E-01	1.00E+00	5.10E-01	1.00E+00	1.00E+00	1.00E+00	1.34E-01	1.00E+00	7.28E-01	1.00E+00	striated muscle contraction	P
GO:0006944	23	1.60E-01	1.00E+00	7.71E-01	1.00E+00	9.08E-02	1.00E+00	6.27E-01	1.00E+00	6.94E-01	1.00E+00	8.70E-01	1.00E+00	1.62E-01	1.00E+00	6.00E-01	1.00E+00	membrane fusion	P
GO:0006950	1202	1.01E-01	1.00E+00	5.78E-02	1.00E+00	1.33E-01	1.00E+00	1.86E-02	7.69E-01	2.84E-01	1.00E+00	2.71E-01	1.00E+00	2.36E-01	1.00E+00	3.44E-01	1.00E+00	response to stress	P
GO:0006952	551	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.57E-01	1.00E+00	1.00E+00	1.00E+00	defense response	P
GO:0006953	29	9.89E-01	1.00E+00	9.83E-01	1.00E+00	8.67E-01	1.00E+00	9.92E-01	1.00E+00	9.69E-01	1.00E+00	9.98E-01	1.00E+00	9.65E-01	1.00E+00	4.38E-01	1.00E+00	acute-phase response	P
GO:0006954	291	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	9.82E-01	1.00E+00	inflammatory response	P
GO:0006955	553	9.67E-01	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.19E-02	1.00E+00	8.78E-01	1.00E+00	immune response	P
GO:0006956	37	9.88E-01	1.00E+00	9.98E-01	1.00E+00	8.33E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	5.78E-01	1.00E+00	9.61E-01	1.00E+00	complement activation	P
GO:0006957	10	7.77E-01	1.00E+00	1.00E+00	1.00E+00	6.47E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.97E-01	1.00E+00	9.54E-01	1.00E+00	complement activation, alternative pathway	P
GO:0006958	29	9.85E-01	1.00E+00	9.68E-01	1.00E+00	8.98E-01	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	8.05E-01	1.00E+00	6.25E-01	1.00E+00	9.15E-01	1.00E+00	complement activation, classical pathway	P
GO:0006959	55	9.69E-01	1.00E+00	1.00E+00	1.00E+00	8.86E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	4.20E-01	1.00E+00	9.84E-01	1.00E+00	humoral immune response	P
GO:0006968	12	5.81E-01	1.00E+00	9.54E-01	1.00E+00	2.82E-01	1.00E+00	8.74E-01	1.00E+00	5.88E-01	1.00E+00	9.53E-01	1.00E+00	9.36E-01	1.00E+00	5.63E-01	1.00E+00	cellular defense response	P

GO:0006970	16	1.70E-01	1.00E+00	6.84E-02	1.00E+00	4.08E-01	1.00E+00	1.17E-01	1.00E+00	1.90E-01	1.00E+00	1.46E-01	1.00E+00	3.31E-01	1.00E+00	1.63E-01	1.00E+00	response to osmotic stress	P
GO:0006974	303	5.21E-10	9.73E-04	1.25E-15	0.00E+00	3.07E-08	0.00E+00	4.41E-11	0.00E+00	2.56E-07	0.00E+00	2.48E-11	0.00E+00	8.93E-03	2.17E-01	3.79E-05	3.91E-03	response to DNA damage stimulus	P
GO:0006979	100	6.56E-03	3.64E-01	5.70E-04	7.30E-02	3.20E-02	1.00E+00	7.13E-03	3.78E-01	1.52E-01	1.00E+00	8.37E-03	3.55E-01	2.91E-02	6.06E-01	3.35E-02	1.00E+00	response to oxidative stress	P
GO:0006984	23	4.74E-02	1.00E+00	2.54E-01	1.00E+00	8.95E-02	1.00E+00	2.09E-01	1.00E+00	1.29E-01	1.00E+00	2.31E-01	1.00E+00	2.48E-01	1.00E+00	6.92E-01	1.00E+00	ER-nuclear signaling pathway	P
GO:0006986	48	1.44E-03	9.30E-02	2.87E-01	1.00E+00	4.73E-03	1.88E-01	1.21E-01	1.00E+00	1.49E-02	4.81E-01	4.29E-01	1.00E+00	4.58E-02	8.34E-01	8.66E-01	1.00E+00	response to unfolded protein	P
GO:0006996	1070	2.60E-22	0.00E+00	3.34E-25	0.00E+00	4.97E-16	0.00E+00	4.67E-20	0.00E+00	8.16E-16	0.00E+00	4.54E-11	0.00E+00	4.68E-05	2.00E-03	7.43E-09	0.00E+00	organelle organization and biogenesis	P
GO:0006997	15	8.33E-02	1.00E+00	2.09E-02	1.00E+00	2.32E-02	1.00E+00	2.97E-02	1.00E+00	6.28E-02	1.00E+00	3.38E-02	1.00E+00	7.85E-01	1.00E+00	3.82E-01	1.00E+00	nuclear organization and biogenesis	P
GO:0007001	303	2.96E-09	9.73E-04	7.45E-14	0.00E+00	8.27E-09	0.00E+00	2.01E-12	0.00E+00	3.08E-06	7.65E-04	4.87E-06	2.00E-03	1.07E-01	1.00E+00	7.04E-06	3.91E-03	chromosome organization and biogenesis (s	P
GO:0007005	53	1.40E-02	9.83E-01	1.62E-03	7.50E-02	1.82E-01	1.00E+00	3.43E-03	1.42E-01	3.63E-03	1.35E-01	3.13E-02	1.00E+00	4.30E-01	1.00E+00	9.55E-02	1.00E+00	mitochondrion organization and biogenesis	P
GO:0007006	25	4.43E-02	1.00E+00	2.39E-03	1.87E-01	2.65E-01	1.00E+00	4.39E-03	1.42E-01	3.58E-02	1.00E+00	1.20E-01	1.00E+00	6.81E-01	1.00E+00	2.05E-01	1.00E+00	mitochondrial membrane organization and b	P
GO:0007009	11	2.92E-01	1.00E+00	8.94E-01	1.00E+00	2.85E-01	1.00E+00	9.69E-01	1.00E+00	4.19E-01	1.00E+00	7.47E-01	1.00E+00	2.80E-01	1.00E+00	8.33E-01	1.00E+00	plasma membrane organization and biogen	P
GO:0007010	488	2.26E-07	9.73E-04	1.09E-04	2.80E-02	2.02E-05	3.00E-03	1.34E-03	4.40E-02	1.16E-04	6.00E-03	7.85E-03	3.55E-01	9.70E-04	2.40E-02	8.27E-03	4.48E-01	cytoskeleton organization and biogenesis	P
GO:0007015	55	1.28E-01	1.00E+00	2.68E-01	1.00E+00	1.78E-01	1.00E+00	3.47E-01	1.00E+00	2.41E-01	1.00E+00	5.58E-01	1.00E+00	4.10E-01	1.00E+00	3.19E-01	1.00E+00	actin filament organization	P
GO:0007017	214	2.53E-07	9.73E-04	1.35E-05	7.00E-03	2.72E-06	1.69E-03	1.32E-04	5.80E-03	8.24E-05	3.00E-03	6.93E-04	2.00E-02	2.99E-03	5.54E-02	2.99E-02	1.00E+00	microtubule-based process	P
GO:0007018	116	1.32E-04	1.90E-02	2.89E-03	1.87E-01	4.66E-04	1.61E-02	1.34E-02	3.78E-01	1.45E-03	4.80E-02	1.78E-02	1.00E+00	4.11E-02	8.34E-01	5.03E-02	1.00E+00	microtubule-based movement	P
GO:0007019	17	2.62E-02	1.00E+00	2.79E-01	1.00E+00	2.20E-01	1.00E+00	2.28E-01	1.00E+00	3.67E-02	1.00E+00	3.25E-01	1.00E+00	2.86E-02	6.06E-01	5.88E-01	1.00E+00	microtubule depolymerization	P
GO:0007026	16	6.06E-02	1.00E+00	1.73E-01	1.00E+00	1.59E-01	1.00E+00	1.73E-01	1.00E+00	7.50E-02	1.00E+00	2.16E-01	1.00E+00	6.31E-02	1.00E+00	4.61E-01	1.00E+00	negative regulation of microtubule depolyme	P
GO:0007028	118	2.64E-04	1.90E-02	3.76E-06	2.86E-03	2.64E-02	1.00E+00	1.84E-06	1.00E-03	1.41E-03	4.80E-02	5.27E-03	2.02E-01	1.23E-01	1.00E+00	2.01E-01	1.00E+00	cytoplasm organization and biogenesis	P
GO:0007030	12	7.58E-02	1.00E+00	1.41E-01	1.00E+00	1.36E-01	1.00E+00	8.75E-02	1.00E+00	3.32E-02	1.00E+00	1.77E-01	1.00E+00	4.03E-01	1.00E+00	4.67E-01	1.00E+00	Golgi organization and biogenesis	P
GO:0007031	20	3.00E-02	1.00E+00	1.82E-02	1.00E+00	5.34E-02	1.00E+00	1.47E-01	1.00E+00	6.25E-02	1.00E+00	6.08E-02	1.00E+00	1.38E-01	1.00E+00	2.02E-02	1.00E+00	peroxisome organization and biogenesis	P
GO:0007033	31	4.14E-01	1.00E+00	1.46E-01	1.00E+00	2.14E-01	1.00E+00	2.59E-01	1.00E+00	6.92E-01	1.00E+00	2.49E-01	1.00E+00	7.61E-01	1.00E+00	1.22E-01	1.00E+00	vacuole organization and biogenesis	P
GO:0007034	22	1.45E-01	1.00E+00	4.53E-02	1.00E+00	1.15E-01	1.00E+00	1.21E-01	1.00E+00	2.26E-01	1.00E+00	1.50E-01	1.00E+00	2.93E-01	1.00E+00	3.67E-02	1.00E+00	vacuolar transport	P
GO:0007040	27	4.81E-01	1.00E+00	1.23E-01	1.00E+00	2.43E-01	1.00E+00	2.13E-01	1.00E+00	7.70E-01	1.00E+00	2.24E-01	1.00E+00	8.18E-01	1.00E+00	1.16E-01	1.00E+00	lysosome organization and biogenesis	P
GO:0007041	12	3.75E-01	1.00E+00	1.98E-01	1.00E+00	1.80E-01	1.00E+00	4.32E-01	1.00E+00	5.39E-01	1.00E+00	1.87E-01	1.00E+00	5.87E-01	1.00E+00	1.74E-01	1.00E+00	lysosomal transport	P
GO:0007046	66	2.20E-03	1.02E-01	4.55E-04	4.30E-02	5.02E-02	1.00E+00	7.23E-05	5.80E-03	6.28E-03	1.65E-01	2.64E-02	1.00E+00	1.24E-01	1.00E+00	6.54E-01	1.00E+00	ribosome biogenesis	P
GO:0007049	671	2.54E-13	6.62E-04	2.91E-23	0.00E+00	1.35E-14	0.00E+00	2.58E-19	0.00E+00	1.53E-08	0.00E+00	6.31E-14	0.00E+00	9.49E-03	2.17E-01	3.73E-08	0.00E+00	cell cycle	P
GO:0007050	61	1.49E-01	1.00E+00	6.57E-01	1.00E+00	2.22E-01	1.00E+00	1.87E-01	1.00E+00	9.78E-02	1.00E+00	6.80E-01	1.00E+00	4.69E-01	1.00E+00	8.19E-01	1.00E+00	cell cycle arrest	P
GO:0007051	18	1.47E-02	9.83E-01	4.07E-02	1.00E+00	1.72E-02	8.10E-01	5.57E-02	1.00E+00	1.24E-01	1.00E+00	1.08E-01	1.00E+00	3.56E-02	7.53E-01	3.88E-01	1.00E+00	spindle organization and biogenesis	P
GO:0007059	55	5.95E-03	3.64E-01	1.43E-05	7.00E-03	1.50E-02	8.10E-01	2.35E-05	1.92E-03	7.47E-03	3.18E-01	1.28E-04	1.36E-02	5.33E-01	1.00E+00	5.57E-02	1.00E+00	chromosome segregation	P
GO:0007067	186	1.21E-10	6.62E-04	6.94E-20	0.00E+00	1.08E-10	0.00E+00	2.12E-14	0.00E+00	4.14E-08	0.00E+00	1.61E-12	0.00E+00	7.63E-03	2.01E-01	5.14E-09	0.00E+00	mitosis	P
GO:0007076	14	7.76E-02	1.00E+00	1.06E-01	1.00E+00	7.31E-02	1.00E+00	5.73E-02	1.00E+00	4.11E-02	1.00E+00	1.63E-01	1.00E+00	7.19E-01	1.00E+00	5.16E-01	1.00E+00	mitotic chromosome condensation	P
GO:0007088	44	6.48E-02	1.00E+00	5.99E-03	5.59E-01	3.27E-02	1.00E+00	4.89E-03	1.42E-01	2.82E-02	1.00E+00	3.75E-02	1.00E+00	3.71E-01	1.00E+00	2.49E-02	1.00E+00	regulation of mitosis	P
GO:0007090	11	1.31E-01	1.00E+00	3.62E-01	1.00E+00	3.00E-01	1.00E+00	2.67E-01	1.00E+00	1.22E-01	1.00E+00	3.09E-01	1.00E+00	4.22E-01	1.00E+00	7.20E-01	1.00E+00	regulation of S phase of mitotic cell cycle	P
GO:0007093	13	2.70E-03	1.39E-01	4.27E-06	2.86E-03	7.19E-03	2.83E-01	1.18E-05	1.77E-03	1.24E-02	4.81E-01	1.42E-03	5.10E-02	2.74E-01	1.00E+00	5.09E-03	2.58E-01	mitotic checkpoint	P
GO:0007098	12	2.34E-02	1.00E+00	5.50E-03	5.59E-01	3.93E-03	1.88E-01	1.58E-02	7.69E-01	1.81E-01	1.00E+00	3.69E-02	1.00E+00	2.93E-01	1.00E+00	1.17E-01	1.00E+00	centrosome cycle	P
GO:0007126	83	3.23E-04	3.25E-02	4.46E-07	2.66E-03	5.17E-05	3.00E-03	2.15E-04	1.10E-02	3.18E-02	1.00E+00	1.28E-04	1.36E-02	1.26E-01	1.00E+00	8.71E-04	3.30E-02	meiosis	P
GO:0007127	29	2.01E-03	1.02E-01	1.53E-04	2.80E-02	2.63E-04	1.61E-02	9.49E-04	3.60E-02	7.60E-02	1.00E+00	4.48E-05	2.00E-03	1.83E-01	1.00E+00	3.38E-02	1.00E+00	meiosis I	P
GO:0007129	11	1.08E-02	9.83E-01	5.66E-04	7.30E-02	9.02E-03	4.69E-01	3.77E-03	1.42E-01	7.03E-02	1.00E+00	1.36E-03	5.10E-02	1.37E-01	1.00E+00	2.80E-02	1.00E+00	synapsis	P
GO:0007143	11	6.73E-01	1.00E+00	1.22E-01	1.00E+00	4.67E-01	1.00E+00	1.96E-01	1.00E+00	6.09E-01	1.00E+00	1.60E-01	1.00E+00	8.68E-01	1.00E+00	1.37E-01	1.00E+00	female meiosis	P
GO:0007154	3405	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.01E-01	1.00E+00	5.12E-01	1.00E+00	cell communication	P
GO:0007155	681	9.56E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	8.75E-02	1.00E+00	9.44E-01	1.00E+00	cell adhesion	P
GO:0007156	83	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.01E-01	1.00E+00	9.97E-01	1.00E+00	homophilic cell adhesion	P
GO:0007157	35	8.60E-01	1.00E+00	6.43E-01	1.00E+00	9.03E-01	1.00E+00	4.72E-01	1.00E+00	8.43E-01	1.00E+00	9.92E-01	1.00E+00	6.01E-01	1.00E+00	4.04E-01	1.00E+00	heterophilic cell adhesion	P
GO:0007159	18	4.30E-01	1.00E+00	2.23E-01	1.00E+00	3.96E-01	1.00E+00	3.81E-01	1.00E+00	3.36E-01	1.00E+00	5.53E-01	1.00E+00	6.98E-01	1.00E+00	9.69E-02	1.00E+00	leukocyte adhesion	P
GO:0007160	87	2.68E-01	1.00E+00	2.13E-01	1.00E+00	1.18E-01	1.00E+00	4.56E-01	1.00E+00	5.39E-01	1.00E+00	4.83E-01	1.00E+00	4.95E-01	1.00E+00	9.65E-02	1.00E+00	cell-matrix adhesion	P
GO:0007162	16	3.96E-01	1.00E+00	8.60E-01	1.00E+00	5.69E-01	1.00E+00	9.49E-01	1.00E+00	6.79E-01	1.00E+00	7.67E-01	1.00E+00	1.68E-01	1.00E+00	7.61E-01	1.00E+00	negative regulation of cell adhesion	P
GO:0007163	25	4.00E-01	1.00E+00	4.04E-01	1.00E+00	3.79E-01	1.00E+00	4.57E-01	1.00E+00	5.15E-01	1.00E+00	7.88E-01	1.00E+00	6.08E-01	1.00E+00	1.64E-01	1.00E+00	establishment and/or maintenance of cell po	P
GO:0007165	3094	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	4.79E-01	1.00E+00	signal transduction	P
GO:0007166	1751	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.91E-01	1.00E+00	cell surface receptor linked signal transducti	P
GO:0007167	295	9.81E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.31E-01	1.00E+00	9.46E-01	1.00E+00	5.25E-01	1.00E+00	6.64E-01	1.00E+00	enzyme linked receptor protein signaling pa	P
GO:0007169	187	8.48E-01	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	7.95E-01	1.00E+00	8.72E-01	1.00E+00	2.39E-01	1.00E+00	7.78E-01	1.00E+00	transmembrane receptor protein tyrosine kir	P
GO:0007172	13	2.97E-01	1.00E+00	8.35E-01	1.00E+00	6.18E-01	1.00E+00	9.83E-01	1.00E+00	2.59E-01	1.00E+00	5.88E-01	1.00E+00	1.66E-01	1.00E+00	4.81E-01	1.00E+00	signal complex formation	P
GO:0007173	20	2.55E-01	1.00E+00	4.56E-01	1.00E+00	4.18E-01	1.00E+00	9.92E-01	1.00E+00	1.90E-01	1.00E+00	8.48E-02	1.00E+00	2.51E-01	1.00E+00	4.54E-01	1.00E+00	epidermal growth factor receptor signaling p	P
GO:0007178	104	9.89E-01	1.00E+00	9.77E-01	1.00E+00	9.96E-01	1.00E+00	9.94E-01	1.00E+00	9.37E-01	1.00E+00	9.43E-01	1.00E+00	9.63E-01	1.00E+00	7.31E-01	1.00E+00	transmembrane receptor protein serine/thre	P
GO:0007179	63	8.62E-01	1.00E+00	9.03E-01	1.00E+00	8.94E-01	1.00E+00	8.71E-01	1.00E+00	8.50E-01	1.00E+00	9.65E-01	1.00E+00	8.04E-01	1.00E+00	5.31E-01	1.00E+00	transforming growth factor beta receptor sig	P
GO:0007186	1117	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	G-protein coupled receptor protein signaling	P
GO:0007187	61	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.65E-01	1.00E+00	8.73E-01	1.00E+00	G-protein signaling, coupled to cyclic nucle	P
GO:0007188	57	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	8.67E-01	1.00E+00	G-protein signaling, coupled to cAMP nucle	P
GO:0007189	34	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	G-protein signaling, adenylate cyclase activ	P
GO:0007190	14	9.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.93E-01	1.00E+00	adenylate cyclase activation	P
GO:0007193	15	8.14E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	8.30E-01	1.00E+00	7.62E-01	1.00E+00	1.77E-01	1.00E+00	2.90E-01	1.00E+00	G-protein signaling, adenylate cyclase inhib	P
GO:0007200	44	8.61E-01	1.00E+00	6.84E-01	1.00E+00	9.05E-01	1.00E+00	5.43E-01	1.00E+00	4.11E-01	1.00E+00	7.38E-01	1.00E+00	9.25E-01	1.00E+00	6.37E-01	1.00E+00	G-protein signaling, coupled to IP3 second r	P
GO:0007204	37	2.76E-01	1.00E+00	8.99E-01	1.00E+00	3.91E-01	1.00E+00	8.78E-01	1.00E+00	5.85E-01	1.00E+00	9.93E-01	1.00E+00	7.95E-02	1.00E+00	3.91E-01	1.00E+00	elevation of cytosolic calcium ion concentrat	P
GO:0007205	21	7.80E-01	1.00E+00	8.29E-01	1.00E+00	4.51E-01	1.00E+00	7.46E-01	1.00E+00	8.44E-01	1.00E+00	7.10E-01	1.00E+00	8.81E-01	1.00E+00	9.47E-01	1.00E+00	protein kinase C activation	P
GO:0007212	14	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.10E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	9.79E-01	1.00E+00	dopamine receptor signaling pathway	P
GO:0007214	31	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	8.25E-01	1.00E+00	1.00E+00	1.00E+00	gamma-aminobutyric acid signaling pathwa	P
GO:0007215	13	1.70E-01	1.00E+00	2.25E-01	1.00E+00	4.27E-01	1.00E+00	2.03E-01	1.00E+00	3.77E-01	1.00E+00	2.63E-01	1.00E+00	7.61E-02	1.00E+00	2.06E-01	1.00E+00	glutamate signaling pathway	P
GO:0007218	96	9.93E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	7.58E-01	1.00E+00	1.00E+00	1.00E+00	6.72E-01	1.00E+00	5.87E-01	1.00E+00	neuropeptide signaling pathway	P
GO:0007219	55	7.10E-01	1.00E+00	3.85E-01	1.00E+00	7.72E-01	1.00E+00	2.05E-01	1.00E+00	8.19E-01	1.00E+00	9.85E-01	1.00E+00	4.77E-01	1.00E+00	5.32E-01	1.00E+00	Notch signaling pathway	P
GO:0007223	20	9.96E-01	1.00E+00	9.86E-01	1.00E+00	9.99E-01	1.00E+00	9.21E-01	1.00E+00	9.92E-01	1.00E+00	9.82E-01	1.00E+00	7.16E-01	1.00E+00	8.80E-01	1.00E+00	frizzled-2 signaling pathway	P
GO:0007224	30	4.61E-01	1.00E+00	6.22E-01	1.00E+00	9.69E-01	1.00E+00	8.99E-01	1.00E+00	7.00E-01	1.00E+00	7.70E-01	1.00E+00	2.68E-02	6.06E-01	1.51E-01	1.00E+00	smoothened signaling pathway	P
GO:0007229	90	7.08E-01	1.00E+00	9.64E-01	1.00E+00	3.77E-01	1.00E+00	8.36E-01	1.00E+00	9.52E-01	1.00E+00	9.56E-01	1.00E+00	3.11E-01	1.00E+00	9.17E-01	1.00E+00	integrin-mediated signaling pathway	P
GO:0007242	1211	1.17E-02	9.83E-01	9.36E-04	7.30E-02	4.29E-02	1.00E+00	1.20E-02	3.78E-01	8.80E-02	1.00E+00	2.26E-02	1.00E+00	9.11E-02	1.00E+00	2.88E-03	2.16E-01	intracellular signaling cascade	P
GO:0007243	352	5.45E-01	1.00E+00	1.99E-02	1.00E+00	8.68E-01	1.00E+00	6.86E-02	1.00E+00	9.24E-01	1.00E+00	1.36E-01	1.00E+00	2.14E-01	1.00E+00	6.55E-03	2.58E-01	protein kinase cascade	P
GO:0007249	104	1.97E-01	1.00E+00	1.26E-02	7.51E-01	2.24E-01	1.00E+00	7.32E-03	3.78E-01	8.07E-01	1.00E+00	1.61E-01	1.00E+00	9.96E-02	1.00E+00	9.08E-02	1.00E+00	I-kappaB kinase/NF-kappaB cascade	P

GO:0007254	50	8.85E-01	1.00E+00	9.63E-01	1.00E+00	9.72E-01	1.00E+00	9.74E-01	1.00E+00	9.07E-01	1.00E+00	7.80E-01	1.00E+00	4.83E-01	1.00E+00	9.26E-01	1.00E+00	JNK cascade	P
GO:0007257	12	4.67E-01	1.00E+00	4.11E-01	1.00E+00	9.26E-01	1.00E+00	5.06E-01	1.00E+00	1.43E-01	1.00E+00	4.23E-01	1.00E+00	2.70E-01	1.00E+00	3.75E-01	1.00E+00	activation of JNK activity	P
GO:0007259	42	4.38E-01	1.00E+00	2.76E-01	1.00E+00	5.10E-01	1.00E+00	4.63E-01	1.00E+00	8.57E-01	1.00E+00	4.02E-01	1.00E+00	2.22E-01	1.00E+00	2.88E-01	1.00E+00	JAK-STAT cascade	P
GO:0007260	19	9.48E-01	1.00E+00	9.62E-01	1.00E+00	9.55E-01	1.00E+00	5.59E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.04E-01	1.00E+00	6.05E-01	1.00E+00	tyrosine phosphorylation of STAT protein	P
GO:0007264	419	2.32E-03	1.02E-01	2.61E-03	1.87E-01	1.03E-02	4.74E-01	2.49E-02	7.69E-01	2.46E-03	1.35E-01	8.30E-03	3.55E-01	1.92E-01	1.00E+00	7.12E-02	1.00E+00	small GTPase mediated signal transduction	P
GO:0007265	34	7.14E-02	1.00E+00	3.42E-01	1.00E+00	1.31E-01	1.00E+00	1.02E-01	1.00E+00	1.13E-01	1.00E+00	5.03E-01	1.00E+00	3.28E-01	1.00E+00	7.93E-01	1.00E+00	Ras protein signal transduction	P
GO:0007266	96	9.09E-02	1.00E+00	1.59E-01	1.00E+00	3.65E-01	1.00E+00	7.32E-01	1.00E+00	3.65E-01	1.00E+00	1.70E-01	1.00E+00	3.00E-02	7.53E-01	3.79E-02	1.00E+00	Rho protein signal transduction	P
GO:0007267	391	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	9.08E-01	1.00E+00	9.02E-01	1.00E+00	cell-cell signaling	P
GO:0007268	239	9.79E-01	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	4.45E-01	1.00E+00	8.59E-01	1.00E+00	synaptic transmission	P
GO:0007269	70	9.00E-01	1.00E+00	1.00E+00	1.00E+00	7.85E-01	1.00E+00	9.99E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	6.99E-01	1.00E+00	9.48E-01	1.00E+00	neurotransmitter secretion	P
GO:0007270	51	7.57E-01	1.00E+00	9.61E-01	1.00E+00	9.39E-01	1.00E+00	9.80E-01	1.00E+00	4.82E-01	1.00E+00	9.54E-01	1.00E+00	6.44E-01	1.00E+00	7.94E-01	1.00E+00	nerve-nerve synaptic transmission	P
GO:0007271	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.10E-01	1.00E+00	8.15E-01	1.00E+00	synaptic transmission, cholinergic	P
GO:0007272	38	3.52E-01	1.00E+00	5.42E-01	1.00E+00	4.42E-01	1.00E+00	6.72E-01	1.00E+00	3.81E-01	1.00E+00	7.02E-01	1.00E+00	4.09E-01	1.00E+00	1.70E-01	1.00E+00	ensheathment of neurons	P
GO:0007274	13	6.95E-01	1.00E+00	6.65E-01	1.00E+00	8.86E-01	1.00E+00	8.56E-01	1.00E+00	8.98E-01	1.00E+00	4.43E-01	1.00E+00	2.06E-01	1.00E+00	9.25E-01	1.00E+00	neuromuscular synaptic transmission	P
GO:0007275	2606	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.69E-01	1.00E+00	development	P
GO:0007276	384	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	7.87E-01	1.00E+00	9.77E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gametogenesis	P
GO:0007281	40	2.84E-01	1.00E+00	7.25E-02	1.00E+00	3.84E-01	1.00E+00	1.41E-01	1.00E+00	4.65E-01	1.00E+00	1.76E-01	1.00E+00	3.25E-01	1.00E+00	1.10E-01	1.00E+00	germ cell development	P
GO:0007283	213	6.74E-03	3.64E-01	2.62E-03	1.87E-01	1.04E-02	4.74E-01	1.86E-03	4.40E-02	4.44E-02	1.00E+00	2.34E-02	1.00E+00	2.89E-01	1.00E+00	2.58E-01	1.00E+00	spermatogenesis	P
GO:0007286	42	2.55E-01	1.00E+00	9.96E-03	7.51E-01	6.90E-02	1.00E+00	4.56E-02	1.00E+00	8.56E-01	1.00E+00	2.01E-02	1.00E+00	7.47E-01	1.00E+00	2.25E-01	1.00E+00	spermatid development	P
GO:0007292	42	1.86E-01	1.00E+00	1.23E-01	1.00E+00	1.50E-01	1.00E+00	1.71E-01	1.00E+00	4.70E-01	1.00E+00	5.52E-01	1.00E+00	1.73E-01	1.00E+00	4.33E-02	1.00E+00	female gamete generation	P
GO:0007338	45	6.72E-01	1.00E+00	4.00E-01	1.00E+00	4.00E-01	1.00E+00	2.41E-01	1.00E+00	9.98E-01	1.00E+00	6.98E-01	1.00E+00	3.90E-01	1.00E+00	6.38E-01	1.00E+00	fertilization (sensu Metazoa)	P
GO:0007339	19	7.62E-01	1.00E+00	6.19E-01	1.00E+00	4.78E-01	1.00E+00	5.67E-01	1.00E+00	9.99E-01	1.00E+00	6.40E-01	1.00E+00	5.14E-01	1.00E+00	5.74E-01	1.00E+00	binding of sperm to zona pellucida	P
GO:0007340	11	6.12E-01	1.00E+00	3.30E-01	1.00E+00	6.45E-01	1.00E+00	3.69E-01	1.00E+00	8.23E-01	1.00E+00	2.26E-01	1.00E+00	3.77E-01	1.00E+00	4.41E-01	1.00E+00	acrosome reaction	P
GO:0007346	35	1.54E-01	1.00E+00	1.11E-01	1.00E+00	3.63E-01	1.00E+00	7.33E-02	1.00E+00	1.68E-02	7.19E-01	2.43E-01	1.00E+00	7.59E-01	1.00E+00	6.59E-01	1.00E+00	regulation of progression through mitotic cel	P
GO:0007368	35	9.50E-01	1.00E+00	7.27E-01	1.00E+00	9.65E-01	1.00E+00	7.35E-01	1.00E+00	8.47E-01	1.00E+00	7.30E-01	1.00E+00	9.86E-01	1.00E+00	5.99E-01	1.00E+00	determination of left/right symmetry	P
GO:0007369	66	9.30E-01	1.00E+00	1.02E-01	1.00E+00	9.78E-01	1.00E+00	1.50E-01	1.00E+00	7.10E-01	1.00E+00	2.89E-01	1.00E+00	7.12E-01	1.00E+00	1.18E-01	1.00E+00	gastrulation	P
GO:0007389	241	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	pattern specification	P
GO:0007398	131	9.97E-01	1.00E+00	9.64E-01	1.00E+00	9.56E-01	1.00E+00	5.61E-01	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.11E-01	1.00E+00	ectoderm development	P
GO:0007399	720	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	nervous system development	P
GO:0007405	26	3.09E-01	1.00E+00	5.29E-01	1.00E+00	3.70E-01	1.00E+00	7.82E-01	1.00E+00	1.94E-01	1.00E+00	6.68E-01	1.00E+00	6.42E-01	1.00E+00	4.37E-01	1.00E+00	neuroblast proliferation	P
GO:0007409	172	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.22E-01	1.00E+00	9.99E-01	1.00E+00	axonogenesis	P
GO:0007411	91	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	axon guidance	P
GO:0007416	19	9.85E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.43E-01	1.00E+00	9.20E-01	1.00E+00	synaptogenesis	P
GO:0007417	313	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	central nervous system development	P
GO:0007420	241	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.93E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	brain development	P
GO:0007422	26	9.99E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.50E-01	1.00E+00	9.82E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.43E-01	1.00E+00	peripheral nervous system development	P
GO:0007423	162	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.95E-01	1.00E+00	sensory organ development	P
GO:0007431	12	9.42E-01	1.00E+00	9.71E-01	1.00E+00	9.96E-01	1.00E+00	9.95E-01	1.00E+00	7.24E-01	1.00E+00	9.34E-01	1.00E+00	7.29E-01	1.00E+00	7.84E-01	1.00E+00	salivary gland development	P
GO:0007439	10	7.71E-01	1.00E+00	7.01E-01	1.00E+00	9.93E-01	1.00E+00	9.24E-01	1.00E+00	4.06E-01	1.00E+00	9.36E-01	1.00E+00	3.94E-01	1.00E+00	1.32E-01	1.00E+00	ectodermal gut development	P
GO:0007492	21	8.94E-01	1.00E+00	6.70E-01	1.00E+00	9.90E-01	1.00E+00	4.02E-01	1.00E+00	9.18E-01	1.00E+00	9.84E-01	1.00E+00	3.85E-01	1.00E+00	8.44E-01	1.00E+00	endoderm development	P
GO:0007498	55	7.32E-01	1.00E+00	1.78E-01	1.00E+00	7.93E-01	1.00E+00	3.13E-01	1.00E+00	6.28E-01	1.00E+00	3.45E-01	1.00E+00	7.25E-01	1.00E+00	6.42E-02	1.00E+00	mesoderm development	P
GO:0007507	162	7.06E-01	1.00E+00	2.92E-01	1.00E+00	9.58E-01	1.00E+00	1.91E-01	1.00E+00	4.56E-01	1.00E+00	8.84E-01	1.00E+00	5.12E-01	1.00E+00	1.81E-01	1.00E+00	heart development	P
GO:0007512	13	7.92E-01	1.00E+00	9.95E-01	1.00E+00	8.32E-01	1.00E+00	8.88E-01	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	4.28E-01	1.00E+00	7.32E-01	1.00E+00	adult heart development	P
GO:0007517	204	9.21E-01	1.00E+00	1.00E+00	1.00E+00	6.27E-01	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	6.74E-01	1.00E+00	9.90E-01	1.00E+00	muscle development	P
GO:0007519	148	7.62E-01	1.00E+00	9.96E-01	1.00E+00	6.26E-01	1.00E+00	9.06E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	5.17E-01	1.00E+00	9.08E-01	1.00E+00	striated muscle development	P
GO:0007528	23	8.72E-01	1.00E+00	7.29E-01	1.00E+00	8.37E-01	1.00E+00	9.36E-01	1.00E+00	9.04E-01	1.00E+00	5.78E-01	1.00E+00	4.26E-01	1.00E+00	5.18E-01	1.00E+00	neuromuscular junction development	P
GO:0007530	20	7.62E-01	1.00E+00	1.00E+00	1.00E+00	7.13E-01	1.00E+00	9.95E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	3.87E-01	1.00E+00	8.71E-01	1.00E+00	sex determination	P
GO:0007548	96	9.74E-01	1.00E+00	6.20E-01	1.00E+00	8.64E-01	1.00E+00	7.01E-01	1.00E+00	9.58E-01	1.00E+00	6.77E-01	1.00E+00	9.85E-01	1.00E+00	6.50E-01	1.00E+00	sex differentiation	P
GO:0007565	45	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	6.59E-01	1.00E+00	pregnancy	P
GO:0007566	15	9.16E-01	1.00E+00	6.41E-01	1.00E+00	8.32E-01	1.00E+00	6.63E-01	1.00E+00	9.90E-01	1.00E+00	9.84E-01	1.00E+00	6.53E-01	1.00E+00	2.20E-01	1.00E+00	embryo implantation	P
GO:0007568	53	4.07E-01	1.00E+00	5.56E-01	1.00E+00	4.55E-01	1.00E+00	8.50E-01	1.00E+00	5.13E-01	1.00E+00	2.58E-01	1.00E+00	5.31E-01	1.00E+00	8.55E-01	1.00E+00	aging	P
GO:0007569	28	5.26E-01	1.00E+00	6.56E-01	1.00E+00	6.64E-01	1.00E+00	5.15E-01	1.00E+00	4.17E-01	1.00E+00	6.08E-01	1.00E+00	9.01E-01	1.00E+00	9.31E-01	1.00E+00	cell aging	P
GO:0007582	11603	4.23E-32	0.00E+00	0.00E+00	0.00E+00	1.14E-16	0.00E+00	7.51E-37	0.00E+00	8.57E-18	0.00E+00	3.78E-29	0.00E+00	1.62E-09	0.00E+00	1.79E-18	0.00E+00	physiological process	P
GO:0007584	42	6.06E-03	3.64E-01	2.02E-01	1.00E+00	3.79E-03	1.88E-01	1.23E-01	1.00E+00	1.40E-01	1.00E+00	2.44E-01	1.00E+00	8.87E-02	1.00E+00	4.39E-01	1.00E+00	response to nutrient	P
GO:0007585	28	5.75E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	4.68E-01	1.00E+00	1.00E+00	1.00E+00	2.12E-01	1.00E+00	1.00E+00	1.00E+00	respiratory gaseous exchange	P
GO:0007586	34	7.38E-02	1.00E+00	5.98E-01	1.00E+00	1.29E-01	1.00E+00	8.50E-01	1.00E+00	2.20E-01	1.00E+00	4.56E-01	1.00E+00	6.48E-02	1.00E+00	3.55E-01	1.00E+00	digestion	P
GO:0007588	17	9.70E-01	1.00E+00	7.95E-01	1.00E+00	9.95E-01	1.00E+00	9.26E-01	1.00E+00	6.42E-01	1.00E+00	6.42E-01	1.00E+00	9.27E-01	1.00E+00	5.85E-01	1.00E+00	excretion	P
GO:0007595	25	9.68E-01	1.00E+00	8.93E-01	1.00E+00	9.94E-01	1.00E+00	9.93E-01	1.00E+00	9.21E-01	1.00E+00	8.68E-01	1.00E+00	4.38E-01	1.00E+00	7.58E-01	1.00E+00	lactation	P
GO:0007596	112	9.87E-01	1.00E+00	9.85E-01	1.00E+00	8.40E-01	1.00E+00	9.98E-01	1.00E+00	9.81E-01	1.00E+00	9.96E-01	1.00E+00	9.38E-01	1.00E+00	4.99E-01	1.00E+00	blood coagulation	P
GO:0007599	114	9.86E-01	1.00E+00	9.79E-01	1.00E+00	8.37E-01	1.00E+00	9.89E-01	1.00E+00	9.68E-01	1.00E+00	9.98E-01	1.00E+00	9.53E-01	1.00E+00	4.71E-01	1.00E+00	hemostasis	P
GO:0007600	263	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	5.85E-01	1.00E+00	7.82E-01	1.00E+00	sensory perception	P
GO:0007601	117	4.52E-01	1.00E+00	8.75E-01	1.00E+00	6.01E-01	1.00E+00	9.52E-01	1.00E+00	7.08E-01	1.00E+00	7.55E-01	1.00E+00	1.65E-01	1.00E+00	5.38E-01	1.00E+00	visual perception	P
GO:0007602	22	1.98E-01	1.00E+00	1.52E-01	1.00E+00	1.77E-01	1.00E+00	2.39E-01	1.00E+00	1.59E-01	1.00E+00	3.19E-01	1.00E+00	2.81E-01	1.00E+00	2.88E-01	1.00E+00	phototransduction	P
GO:0007605	74	9.97E-01	1.00E+00	9.72E-01	1.00E+00	9.99E-01	1.00E+00	9.70E-01	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	8.47E-01	1.00E+00	5.89E-01	1.00E+00	sensory perception of sound	P
GO:0007606	47	9.51E-01	1.00E+00	8.04E-01	1.00E+00	8.69E-01	1.00E+00	5.54E-01	1.00E+00	7.39E-01	1.00E+00	9.51E-01	1.00E+00	9.06E-01	1.00E+00	4.53E-01	1.00E+00	sensory perception of chemical stimulus	P
GO:0007608	28	9.86E-01	1.00E+00	7.95E-01	1.00E+00	7.77E-01	1.00E+00	4.16E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	9.67E-01	1.00E+00	5.93E-01	1.00E+00	sensory perception of smell	P
GO:0007610	406	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.81E-01	1.00E+00	1.36E-01	1.00E+00	behavior	P
GO:0007611	81	3.71E-01	1.00E+00	5.97E-01	1.00E+00	7.44E-01	1.00E+00	5.27E-01	1.00E+00	6.80E-01	1.00E+00	8.60E-01	1.00E+00	7.12E-02	1.00E+00	1.29E-01	1.00E+00	learning and/or memory	P
GO:0007612	53	8.75E-01	1.00E+00	7.30E-01	1.00E+00	9.69E-01	1.00E+00	5.07E-01	1.00E+00	7.78E-01	1.00E+00	7.67E-01	1.00E+00	4.52E-01	1.00E+00	8.03E-01	1.00E+00	learning	P
GO:0007613	25	2.47E-01	1.00E+00	8.41E-01	1.00E+00	5.86E-01	1.00E+00	7.02E-01	1.00E+00	4.93E-01	1.00E+00	9.10E-01	1.00E+00	1.07E-01	1.00E+00	3.38E-01	1.00E+00	memory	P
GO:0007617	14	9.71E-01	1.00E+00	9.93E-01	1.00E+00	9.34E-01	1.00E+00	9.80E-01	1.00E+00	8.32E-01	1.00E+00	9.74E-01	1.00E+00	7.76E-01	1.00E+00	9.63E-01	1.00E+00	mating behavior	P
GO:0007623	34	8.91E-01	1.00E+00	8.44E-01	1.00E+00	9.79E-01	1.00E+00	9.67E-01	1.00E+00	9.97E-01	1.00E+00	7.39E-01	1.00E+00	3.45E-01	1.00E+00	5.44E-01	1.00E+00	circadian rhythm	P
GO:0007626	267	9.96E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	6.11E-01	1.00E+00	2.34E-01	1.00E+00	locomotory behavior	P
GO:0007628	24	8.71E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	7.01E-01	1.00E+00	1.00E+00	1.00E+00	7.00E-01	1.00E+00	9.93E-01	1.00E+00	adult walking behavior	P
GO:0007631	45	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.81E-01	1.00E+00	1.00E+00	1.00E+00	9.47E-01	1.00E+00	4.42E-01	1.00E+00	feeding behavior	P

GO:0007632	27	5.05E-01	1.00E+00	9.68E-01	1.00E+00	8.60E-01	1.00E+00	8.28E-01	1.00E+00	2.75E-01	1.00E+00	9.96E-01	1.00E+00	3.76E-01	1.00E+00	9.72E-01	1.00E+00	visual behavior	P
GO:0008009	55	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.87E-01	1.00E+00	chemokine activity	F
GO:0008013	16	4.89E-03	3.48E-01	9.51E-03	7.51E-01	2.40E-03	1.18E-01	2.78E-02	1.00E+00	5.03E-03	1.35E-01	8.66E-02	1.00E+00	2.70E-02	6.06E-01	3.56E-02	1.00E+00	beta-catenin binding	F
GO:0008015	130	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	circulation	P
GO:0008016	43	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.00E-01	1.00E+00	9.26E-01	1.00E+00	regulation of heart contraction	P
GO:0008017	58	6.19E-06	5.00E-03	7.15E-06	3.00E-03	3.05E-04	1.61E-02	5.71E-03	3.78E-01	4.30E-05	1.56E-03	1.58E-04	1.36E-02	5.29E-03	9.40E-02	5.78E-03	2.58E-01	microtubule binding	F
GO:0008021	72	2.26E-01	1.00E+00	9.59E-01	1.00E+00	5.81E-01	1.00E+00	9.92E-01	1.00E+00	4.33E-01	1.00E+00	9.35E-01	1.00E+00	4.05E-02	8.34E-01	6.20E-01	1.00E+00	synaptic vesicle	C
GO:0008022	68	2.39E-02	1.00E+00	1.66E-02	1.00E+00	5.61E-03	1.88E-01	1.11E-02	3.78E-01	1.20E-01	1.00E+00	1.23E-01	1.00E+00	2.91E-01	1.00E+00	3.58E-02	1.00E+00	protein C-terminus binding	F
GO:0008026	98	7.07E-05	7.00E-03	6.59E-07	2.66E-03	2.40E-06	1.00E-03	3.89E-06	1.00E-03	7.87E-04	4.40E-02	1.74E-04	1.36E-02	7.47E-02	1.00E+00	8.96E-04	3.30E-02	ATP-dependent helicase activity	F
GO:0008028	16	2.22E-01	1.00E+00	7.45E-01	1.00E+00	1.99E-01	1.00E+00	4.65E-01	1.00E+00	4.46E-01	1.00E+00	9.42E-01	1.00E+00	6.80E-01	1.00E+00	3.63E-01	1.00E+00	monocarboxylic acid transporter activity	F
GO:0008033	57	4.57E-02	1.00E+00	1.54E-03	7.50E-02	5.34E-02	1.00E+00	3.94E-02	1.00E+00	5.43E-02	1.00E+00	1.06E-02	4.01E-01	3.36E-01	1.00E+00	9.03E-03	4.48E-01	tRNA processing	P
GO:0008034	23	3.26E-01	1.00E+00	6.02E-01	1.00E+00	1.24E-01	1.00E+00	9.00E-01	1.00E+00	5.13E-01	1.00E+00	5.90E-01	1.00E+00	5.70E-01	1.00E+00	8.35E-01	1.00E+00	lipoprotein binding	F
GO:0008037	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.95E-01	1.00E+00	8.27E-01	1.00E+00	8.85E-01	1.00E+00	cell recognition	P
GO:0008038	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.05E-01	1.00E+00	9.97E-01	1.00E+00	neuron recognition	P
GO:0008045	13	9.57E-01	1.00E+00	1.00E+00	1.00E+00	8.99E-01	1.00E+00	1.00E+00	1.00E+00	8.41E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	motor axon guidance	P
GO:0008047	266	4.16E-03	1.86E-01	6.38E-03	5.59E-01	6.85E-03	2.83E-01	1.20E-01	1.00E+00	8.55E-03	3.69E-01	6.63E-02	1.00E+00	2.63E-01	1.00E+00	2.40E-03	6.30E-02	enzyme activator activity	F
GO:0008060	23	2.21E-02	1.00E+00	1.47E-01	1.00E+00	4.92E-02	1.00E+00	2.90E-01	1.00E+00	2.38E-01	1.00E+00	1.91E-01	1.00E+00	2.84E-02	6.06E-01	9.23E-02	1.00E+00	ARF GTPase activator activity	F
GO:0008064	51	5.97E-02	1.00E+00	3.38E-02	1.00E+00	2.26E-01	1.00E+00	3.43E-02	1.00E+00	1.71E-01	1.00E+00	2.47E-01	1.00E+00	4.95E-02	1.00E+00	3.17E-02	1.00E+00	regulation of actin polymerization and/or de	P
GO:0008066	63	9.91E-01	1.00E+00	9.78E-01	1.00E+00	9.40E-01	1.00E+00	8.81E-01	1.00E+00	9.94E-01	1.00E+00	9.87E-01	1.00E+00	6.13E-01	1.00E+00	7.61E-01	1.00E+00	glutamate receptor activity	F
GO:0008067	45	9.91E-01	1.00E+00	8.64E-01	1.00E+00	8.36E-01	1.00E+00	8.02E-01	1.00E+00	9.98E-01	1.00E+00	8.71E-01	1.00E+00	9.04E-01	1.00E+00	5.85E-01	1.00E+00	metabotropic glutamate, GABA-B-like recep	F
GO:0008076	133	3.87E-01	1.00E+00	9.92E-01	1.00E+00	6.70E-01	1.00E+00	9.34E-01	1.00E+00	4.61E-01	1.00E+00	1.00E+00	1.00E+00	5.53E-01	1.00E+00	9.69E-01	1.00E+00	voltage-gated potassium channel complex	C
GO:0008080	52	1.91E-01	1.00E+00	2.86E-02	1.00E+00	8.48E-02	1.00E+00	2.62E-02	7.69E-01	4.69E-01	1.00E+00	2.64E-01	1.00E+00	7.20E-01	1.00E+00	1.07E-01	1.00E+00	N-acetyltransferase activity	F
GO:0008081	75	6.83E-02	1.00E+00	2.82E-01	1.00E+00	7.75E-03	3.43E-01	5.17E-01	1.00E+00	7.42E-01	1.00E+00	9.73E-02	1.00E+00	8.11E-02	1.00E+00	3.20E-01	1.00E+00	phosphoric diester hydrolase activity	F
GO:0008083	165	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	6.61E-01	1.00E+00	growth factor activity	F
GO:0008088	11	2.31E-02	1.00E+00	4.44E-02	1.00E+00	2.82E-02	1.00E+00	2.17E-02	7.69E-01	3.71E-02	1.00E+00	2.08E-02	1.00E+00	6.89E-01	1.00E+00	3.44E-01	1.00E+00	axon cargo transport	P
GO:0008092	436	8.31E-07	2.00E-03	1.93E-04	2.80E-02	2.30E-03	1.18E-01	3.42E-02	1.00E+00	2.67E-05	1.56E-03	1.05E-02	4.01E-01	4.87E-06	2.00E-03	1.36E-04	4.00E-03	cytoskeletal protein binding	F
GO:0008094	33	5.56E-05	7.00E-03	8.97E-07	2.66E-03	3.97E-03	1.88E-01	2.59E-04	1.15E-02	2.68E-03	1.35E-01	3.30E-05	2.00E-03	6.24E-04	2.40E-02	5.86E-05	3.91E-03	DNA-dependent ATPase activity	F
GO:0008104	929	1.04E-14	0.00E+00	1.08E-23	0.00E+00	2.48E-09	0.00E+00	2.43E-17	0.00E+00	1.59E-10	0.00E+00	3.06E-13	0.00E+00	4.25E-05	2.00E-03	3.95E-09	0.00E+00	protein localization	P
GO:0008105	10	9.37E-01	1.00E+00	8.86E-01	1.00E+00	1.00E+00	1.00E+00	8.85E-01	1.00E+00	5.24E-01	1.00E+00	7.95E-01	1.00E+00	8.42E-01	1.00E+00	9.86E-01	1.00E+00	asymmetric protein localization	P
GO:0008121	12	9.75E-02	1.00E+00	2.66E-02	1.00E+00	5.09E-01	1.00E+00	2.51E-01	1.00E+00	2.15E-01	1.00E+00	1.12E-01	1.00E+00	2.28E-01	1.00E+00	8.44E-02	1.00E+00	ubiquinol-cytochrome-c reductase activity	F
GO:0008134	290	6.27E-04	5.20E-02	1.71E-05	7.00E-03	2.22E-04	1.61E-02	4.20E-04	1.30E-02	2.86E-02	1.00E+00	3.15E-03	1.43E-01	1.76E-01	1.00E+00	2.41E-02	1.00E+00	transcription factor binding	F
GO:0008135	129	4.73E-05	6.00E-03	1.36E-07	2.66E-03	1.01E-04	1.61E-02	1.11E-04	5.80E-03	6.03E-05	1.56E-03	8.94E-07	2.00E-03	3.76E-01	1.00E+00	3.75E-02	1.00E+00	translation factor activity, nucleic acid bindin	F
GO:0008137	30	2.95E-02	1.00E+00	1.87E-03	1.62E-01	7.40E-02	1.00E+00	2.35E-03	6.52E-02	4.13E-01	1.00E+00	2.43E-02	1.00E+00	6.35E-02	1.00E+00	6.78E-02	1.00E+00	NADH dehydrogenase (ubiquinone) activity	F
GO:0008138	44	5.33E-01	1.00E+00	2.08E-01	1.00E+00	8.10E-01	1.00E+00	6.73E-01	1.00E+00	3.52E-01	1.00E+00	1.56E-01	1.00E+00	2.00E-01	1.00E+00	9.12E-02	1.00E+00	protein tyrosine/serine/threonine phosphata	F
GO:0008144	14	3.30E-01	1.00E+00	5.32E-01	1.00E+00	3.16E-01	1.00E+00	6.91E-01	1.00E+00	5.54E-01	1.00E+00	4.79E-01	1.00E+00	1.69E-01	1.00E+00	3.83E-01	1.00E+00	drug binding	F
GO:0008146	56	9.99E-01	1.00E+00	9.32E-01	1.00E+00	9.96E-01	1.00E+00	9.90E-01	1.00E+00	8.32E-01	1.00E+00	9.76E-01	1.00E+00	9.68E-01	1.00E+00	4.38E-01	1.00E+00	sulfotransferase activity	F
GO:0008150	13777	6.38E-17	0.00E+00	8.88E-36	0.00E+00	1.32E-07	9.88E-04	1.93E-21	0.00E+00	2.15E-09	0.00E+00	3.85E-15	0.00E+00	5.81E-06	2.00E-03	1.91E-13	0.00E+00	biological_process	P
GO:0008152	8007	1.01E-25	0.00E+00	0.00E+00	0.00E+00	1.25E-18	0.00E+00	1.38E-39	0.00E+00	2.88E-17	0.00E+00	8.16E-37	0.00E+00	1.62E-04	6.45E-03	5.53E-16	0.00E+00	metabolism	P
GO:0008154	68	1.01E-01	1.00E+00	4.04E-02	1.00E+00	3.00E-01	1.00E+00	6.68E-02	1.00E+00	2.12E-01	1.00E+00	2.79E-01	1.00E+00	1.06E-01	1.00E+00	1.85E-02	9.40E-01	actin polymerization and/or depolymerizatio	P
GO:0008156	12	1.80E-04	1.90E-02	8.82E-02	1.00E+00	1.23E-02	4.74E-01	1.02E-01	1.00E+00	1.91E-02	7.19E-01	1.57E-01	1.00E+00	4.54E-02	8.34E-01	2.46E-01	1.00E+00	negative regulation of DNA replication	P
GO:0008168	183	5.95E-07	2.00E-03	1.56E-08	2.66E-03	1.17E-05	1.69E-03	1.42E-04	5.80E-03	4.48E-06	9.62E-04	1.40E-07	1.75E-03	4.41E-01	1.00E+00	4.11E-04	2.10E-02	methyltransferase activity	F
GO:0008170	57	1.21E-02	9.83E-01	1.69E-02	1.00E+00	2.94E-02	1.00E+00	8.35E-02	1.00E+00	4.20E-03	1.35E-01	1.25E-02	1.00E+00	9.29E-01	1.00E+00	3.89E-02	1.00E+00	N-methyltransferase activity	F
GO:0008173	20	1.01E-01	1.00E+00	7.93E-03	5.59E-01	9.92E-02	1.00E+00	1.08E-01	1.00E+00	4.93E-02	1.00E+00	3.73E-02	1.00E+00	5.96E-01	1.00E+00	1.10E-01	1.00E+00	RNA methyltransferase activity	F
GO:0008180	10	4.65E-02	1.00E+00	1.46E-01	1.00E+00	3.75E-02	1.00E+00	1.91E-01	1.00E+00	4.70E-01	1.00E+00	8.15E-01	1.00E+00	4.83E-01	1.00E+00	8.58E-02	1.00E+00	signalosome complex	C
GO:0008188	123	9.99E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	6.58E-01	1.00E+00	4.01E-01	1.00E+00	neuropeptide receptor activity	F
GO:0008194	95	7.75E-01	1.00E+00	7.69E-01	1.00E+00	8.23E-01	1.00E+00	6.05E-01	1.00E+00	7.28E-01	1.00E+00	6.28E-01	1.00E+00	5.98E-01	1.00E+00	5.23E-01	1.00E+00	UDP-glycosyltransferase activity	F
GO:0008199	13	9.03E-01	1.00E+00	6.63E-01	1.00E+00	7.81E-01	1.00E+00	2.93E-01	1.00E+00	7.28E-01	1.00E+00	6.33E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	ferric iron binding	F
GO:0008201	67	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.74E-01	1.00E+00	8.93E-01	1.00E+00	heparin binding	F
GO:0008202	176	5.38E-01	1.00E+00	8.75E-01	1.00E+00	6.46E-01	1.00E+00	9.97E-01	1.00E+00	5.00E-01	1.00E+00	6.97E-01	1.00E+00	3.99E-01	1.00E+00	4.07E-01	1.00E+00	steroid metabolism	P
GO:0008203	75	5.34E-01	1.00E+00	5.11E-01	1.00E+00	5.64E-01	1.00E+00	7.79E-01	1.00E+00	7.84E-01	1.00E+00	3.99E-01	1.00E+00	3.21E-01	1.00E+00	5.03E-01	1.00E+00	cholesterol metabolism	P
GO:0008206	14	2.15E-01	1.00E+00	7.58E-01	1.00E+00	3.78E-01	1.00E+00	9.95E-01	1.00E+00	1.56E-01	1.00E+00	6.77E-01	1.00E+00	7.06E-01	1.00E+00	1.30E-02	9.40E-01	bile acid metabolism	P
GO:0008207	20	9.60E-01	1.00E+00	1.00E+00	1.00E+00	8.54E-01	1.00E+00	9.85E-01	1.00E+00	7.78E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.37E-01	1.00E+00	C21-steroid hormone metabolism	P
GO:0008211	11	7.23E-01	1.00E+00	1.00E+00	1.00E+00	4.92E-01	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	1.00E+00	1.00E+00	8.89E-01	1.00E+00	9.34E-01	1.00E+00	glucocorticoid metabolism	P
GO:0008213	35	1.96E-03	1.02E-01	3.02E-04	4.20E-02	5.56E-03	1.88E-01	3.20E-03	1.42E-01	3.52E-03	1.35E-01	5.25E-04	2.00E-02	7.97E-02	1.00E+00	1.61E-02	9.40E-01	protein amino acid alkylation	P
GO:0008217	60	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	9.98E-01	1.00E+00	blood pressure regulation	P
GO:0008219	793	5.09E-03	3.48E-01	6.02E-02	1.00E+00	3.98E-02	1.00E+00	6.36E-02	1.00E+00	2.76E-02	1.00E+00	2.57E-01	1.00E+00	4.83E-02	1.00E+00	1.16E-01	1.00E+00	cell death	P
GO:0008227	116	3.92E-01	1.00E+00	2.45E-01	1.00E+00	6.48E-01	1.00E+00	1.74E-01	1.00E+00	5.96E-01	1.00E+00	4.87E-01	1.00E+00	3.58E-01	1.00E+00	1.92E-01	1.00E+00	amine receptor activity	F
GO:0008233	756	3.15E-01	1.00E+00	2.39E-01	1.00E+00	6.19E-01	1.00E+00	5.80E-01	1.00E+00	8.66E-01	1.00E+00	6.30E-01	1.00E+00	1.67E-02	4.71E-01	6.81E-03	2.58E-01	peptidase activity	F
GO:0008234	172	5.47E-02	1.00E+00	1.68E-02	1.00E+00	1.60E-01	1.00E+00	3.58E-03	1.42E-01	1.54E-01	1.00E+00	2.76E-01	1.00E+00	4.46E-02	8.34E-01	2.67E-02	1.00E+00	cysteine-type peptidase activity	F
GO:0008235	61	2.66E-01	1.00E+00	3.90E-01	1.00E+00	1.09E-01	1.00E+00	2.14E-01	1.00E+00	3.72E-01	1.00E+00	3.28E-01	1.00E+00	5.05E-01	1.00E+00	9.43E-01	1.00E+00	metalloexopeptidase activity	F
GO:0008236	257	9.38E-01	1.00E+00	7.80E-01	1.00E+00	9.30E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	1.88E-01	1.00E+00	4.00E-03	2.16E-01	serine-type peptidase activity	F
GO:0008237	217	2.86E-01	1.00E+00	5.95E-01	1.00E+00	2.57E-01	1.00E+00	6.11E-01	1.00E+00	3.76E-01	1.00E+00	4.83E-01	1.00E+00	1.40E-01	1.00E+00	8.38E-01	1.00E+00	metallopeptidase activity	F
GO:0008238	105	6.19E-01	1.00E+00	4.34E-01	1.00E+00	3.92E-01	1.00E+00	1.92E-01	1.00E+00	6.11E-01	1.00E+00	7.38E-01	1.00E+00	8.35E-01	1.00E+00	5.94E-01	1.00E+00	exopeptidase activity	F
GO:0008239	12	5.17E-02	1.00E+00	1.93E-01	1.00E+00	5.28E-02	1.00E+00	5.31E-01	1.00E+00	3.41E-01	1.00E+00	1.63E-01	1.00E+00	5.54E-02	1.00E+00	3.29E-01	1.00E+00	dipeptidyl-peptidase activity	F
GO:0008252	10	1.62E-01	1.00E+00	3.71E-01	1.00E+00	3.58E-01	1.00E+00	3.67E-01	1.00E+00	1.26E-01	1.00E+00	4.09E-01	1.00E+00	9.69E-02	1.00E+00	6.90E-01	1.00E+00	nucleotidase activity	F
GO:0008270	2140	2.19E-08	9.73E-04	1.43E-19	0.00E+00	9.49E-10	0.00E+00	2.03E-16	0.00E+00	2.13E-07	0.00E+00	2.80E-14	0.00E+00	7.85E-02	1.00E+00	5.56E-04	2.10E-02	zinc ion binding	F
GO:0008271	11	2.01E-01	1.00E+00	9.79E-01	1.00E+00	2.81E-01	1.00E+00	9.70E-01	1.00E+00	1.05E-01	1.00E+00	8.79E-01	1.00E+00	3.36E-01	1.00E+00	9.94E-01	1.00E+00	sulfate porter activity	F
GO:0008272	16	1.43E-01	1.00E+00	8.69E-01	1.00E+00	3.26E-01	1.00E+00	6.37E-01	1.00E+00	9.16E-02	1.00E+00	9.13E-01	1.00E+00	1.88E-01	1.00E+00	8.42E-01	1.00E+00	sulfate transport	P
GO:0008276	43	3.29E-05	6.00E-03	3.10E-07	2.66E-03	2.05E-04	1.61E-02	5.74E-05	5.80E-03	2.85E-04	8.00E-03	7.28E-06	2.00E-03	9.89E-02	1.00E+00	2.56E-04	1.70E-02	protein methyltransferase activity	F
GO:0008277	20	8.81E-01	1.00E+00	3.42E-01	1.00E+00	4.52E-01	1.00E+00	7.15E-01	1.00E+00	8.05E-01	1.00E+00	1.85E-01	1.00E+00	9.83E-01	1.00E+00	2.47E-01	1.00E+00	regulation of G-protein coupled receptor pro	P
GO:0008283	636	9.96E-01	1.00E+00	9.96E-01	1.00E+00	9.90E-01	1.00E+00	7.77E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	9.33E-01	1.00E+00	9.97E-01	1.00E+00	cell proliferation	P
GO:0008284	250	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.97E-01	1.00E+00	6.74E-01	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	9.88E-01	1.00E+00	9.98E-01	1.00E+00	positive regulation of cell proliferation	P
GO:0008285	196	9.92E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	6.20E-01	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	5.16E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of cell proliferation	P
GO:0008286	30	2.10E-01	1.00E+00	1.75E-01	1.00E+00	3.74E-01	1.00E+00	1.09E-01	1.00E+00	3.79E-01	1.00E+00	4.57E-01	1.00E+00	1.14E-01	1.00E+00	1.58E-01	1.00E+00	insulin receptor signaling pathway	P
GO:0008287	40	3.55E-02	1.00E+00	2.08E-01	1.00E+00	3.92E-02	1.00E+00	1.92E-01	1.00E+00	1.68E-01	1.00E+00	4.21E-01	1.00E+00	4.77E-01	1.00E+00	3.14E-01	1.00E+00	protein serine/threonine phosphatase comp	C

GO:0008289	324	1.95E-01	1.00E+00	4.90E-02	1.00E+00	4.72E-01	1.00E+00	7.50E-01	1.00E+00	3.61E-01	1.00E+00	1.37E-01	1.00E+00	9.44E-02	1.00E+00	7.02E-03	2.58E-01	lipid binding	F
GO:0008299	19	4.46E-02	1.00E+00	3.20E-01	1.00E+00	1.35E-01	1.00E+00	2.40E-01	1.00E+00	3.58E-01	1.00E+00	2.64E-01	1.00E+00	1.33E-01	1.00E+00	9.66E-01	1.00E+00	isoprenoid biosynthesis	P
GO:0008305	34	6.40E-02	1.00E+00	2.93E-01	1.00E+00	4.77E-02	1.00E+00	5.03E-01	1.00E+00	1.61E-01	1.00E+00	2.56E-01	1.00E+00	2.32E-01	1.00E+00	3.39E-01	1.00E+00	integrin complex	C
GO:0008306	13	6.64E-01	1.00E+00	7.92E-01	1.00E+00	5.90E-01	1.00E+00	6.77E-01	1.00E+00	6.26E-01	1.00E+00	6.81E-01	1.00E+00	8.19E-01	1.00E+00	8.87E-01	1.00E+00	associative learning	P
GO:0008307	10	1.69E-01	1.00E+00	8.76E-01	1.00E+00	3.41E-01	1.00E+00	8.79E-01	1.00E+00	8.15E-01	1.00E+00	8.18E-01	1.00E+00	7.25E-02	1.00E+00	5.41E-01	1.00E+00	structural constituent of muscle	F
GO:0008312	13	1.98E-01	1.00E+00	4.51E-03	3.82E-01	3.57E-01	1.00E+00	1.23E-02	3.78E-01	1.05E-01	1.00E+00	8.59E-03	3.55E-01	6.42E-01	1.00E+00	2.16E-01	1.00E+00	7S RNA binding	F
GO:0008318	12	6.79E-01	1.00E+00	4.49E-01	1.00E+00	6.36E-01	1.00E+00	2.25E-01	1.00E+00	6.74E-01	1.00E+00	6.18E-01	1.00E+00	6.22E-01	1.00E+00	3.71E-01	1.00E+00	protein prenyltransferase activity	F
GO:0008324	694	9.64E-02	1.00E+00	8.45E-01	1.00E+00	8.79E-01	1.00E+00	9.70E-01	1.00E+00	3.76E-01	1.00E+00	9.78E-01	1.00E+00	4.28E-03	7.75E-02	1.94E-01	1.00E+00	cation transporter activity	F
GO:0008344	52	4.18E-01	1.00E+00	9.97E-01	1.00E+00	4.19E-01	1.00E+00	9.74E-01	1.00E+00	3.53E-01	1.00E+00	9.99E-01	1.00E+00	6.12E-01	1.00E+00	9.57E-01	1.00E+00	adult locomotory behavior	P
GO:0008360	51	3.46E-02	1.00E+00	4.82E-02	1.00E+00	4.95E-02	1.00E+00	1.11E-01	1.00E+00	2.48E-01	1.00E+00	2.06E-01	1.00E+00	5.75E-02	1.00E+00	6.66E-02	1.00E+00	regulation of cell shape	P
GO:0008361	161	3.73E-01	1.00E+00	7.74E-01	1.00E+00	5.82E-01	1.00E+00	4.40E-01	1.00E+00	9.88E-01	1.00E+00	9.45E-01	1.00E+00	1.67E-02	4.71E-01	6.33E-01	1.00E+00	regulation of cell size	P
GO:0008366	38	3.52E-01	1.00E+00	5.42E-01	1.00E+00	4.42E-01	1.00E+00	6.72E-01	1.00E+00	3.81E-01	1.00E+00	7.02E-01	1.00E+00	4.09E-01	1.00E+00	1.70E-01	1.00E+00	axon ensheathment	P
GO:0008373	21	3.64E-01	1.00E+00	8.18E-01	1.00E+00	5.70E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	6.95E-01	1.00E+00	1.14E-02	4.39E-01	1.29E-01	1.00E+00	sialyltransferase activity	F
GO:0008374	36	3.30E-02	1.00E+00	3.92E-02	1.00E+00	3.42E-02	1.00E+00	4.18E-02	1.00E+00	2.35E-01	1.00E+00	1.02E-01	1.00E+00	2.89E-01	1.00E+00	4.05E-01	1.00E+00	O-acyltransferase activity	F
GO:0008375	31	7.91E-01	1.00E+00	4.06E-01	1.00E+00	4.58E-01	1.00E+00	4.02E-01	1.00E+00	7.89E-01	1.00E+00	5.70E-01	1.00E+00	8.23E-01	1.00E+00	3.21E-01	1.00E+00	acetylglucosaminyltransferase activity	F
GO:0008376	27	7.96E-01	1.00E+00	7.88E-01	1.00E+00	9.99E-01	1.00E+00	9.15E-01	1.00E+00	8.02E-01	1.00E+00	6.52E-01	1.00E+00	1.94E-01	1.00E+00	2.34E-01	1.00E+00	acetylgalactosaminyltransferase activity	F
GO:0008378	32	9.72E-01	1.00E+00	7.97E-01	1.00E+00	9.79E-01	1.00E+00	7.72E-01	1.00E+00	9.84E-01	1.00E+00	3.91E-01	1.00E+00	8.19E-01	1.00E+00	5.63E-01	1.00E+00	galactosyltransferase activity	F
GO:0008380	189	5.17E-07	2.00E-03	2.46E-15	0.00E+00	2.69E-05	3.00E-03	2.05E-12	0.00E+00	9.35E-04	4.40E-02	1.36E-10	7.71E-04	3.67E-01	1.00E+00	5.56E-02	1.00E+00	RNA splicing	P
GO:0008406	66	8.14E-01	1.00E+00	3.21E-01	1.00E+00	5.57E-01	1.00E+00	4.48E-01	1.00E+00	7.88E-01	1.00E+00	4.67E-01	1.00E+00	9.32E-01	1.00E+00	3.77E-01	1.00E+00	gonad development	P
GO:0008408	21	5.67E-03	3.48E-01	3.54E-02	1.00E+00	1.69E-02	8.10E-01	1.03E-01	1.00E+00	2.21E-02	1.00E+00	3.05E-02	1.00E+00	1.75E-02	4.71E-01	2.36E-01	1.00E+00	3'-5' exonuclease activity	F
GO:0008415	186	8.32E-03	6.18E-01	5.46E-04	7.30E-02	5.71E-03	1.88E-01	1.42E-03	4.40E-02	1.05E-01	1.00E+00	1.69E-02	1.00E+00	2.76E-01	1.00E+00	3.45E-02	1.00E+00	acyltransferase activity	F
GO:0008417	11	3.60E-01	1.00E+00	9.24E-01	1.00E+00	4.20E-01	1.00E+00	6.38E-01	1.00E+00	2.78E-01	1.00E+00	1.00E+00	1.00E+00	7.30E-01	1.00E+00	8.62E-01	1.00E+00	fucosyltransferase activity	F
GO:0008430	30	2.33E-02	1.00E+00	3.43E-02	1.00E+00	3.87E-01	1.00E+00	6.75E-03	3.78E-01	4.55E-02	1.00E+00	1.70E-01	1.00E+00	8.64E-02	1.00E+00	4.29E-01	1.00E+00	selenium binding	F
GO:0008443	11	7.86E-01	1.00E+00	4.99E-01	1.00E+00	2.63E-01	1.00E+00	6.78E-01	1.00E+00	9.94E-01	1.00E+00	4.66E-01	1.00E+00	5.78E-01	1.00E+00	4.50E-01	1.00E+00	phosphofructokinase activity	F
GO:0008483	26	5.23E-02	1.00E+00	2.63E-02	1.00E+00	1.66E-01	1.00E+00	2.29E-01	1.00E+00	6.76E-02	1.00E+00	1.33E-02	1.00E+00	3.11E-02	7.53E-01	7.12E-02	1.00E+00	transaminase activity	F
GO:0008484	14	8.37E-01	1.00E+00	7.85E-01	1.00E+00	9.93E-01	1.00E+00	8.03E-01	1.00E+00	8.41E-01	1.00E+00	7.85E-01	1.00E+00	4.34E-01	1.00E+00	7.01E-01	1.00E+00	sulfuric ester hydrolase activity	F
GO:0008493	22	1.99E-01	1.00E+00	2.20E-01	1.00E+00	8.99E-01	1.00E+00	5.43E-01	1.00E+00	3.16E-01	1.00E+00	2.38E-01	1.00E+00	6.77E-02	1.00E+00	1.77E-01	1.00E+00	tetracycline transporter activity	F
GO:0008509	166	4.35E-01	1.00E+00	9.99E-01	1.00E+00	8.40E-01	1.00E+00	9.99E-01	1.00E+00	7.19E-01	1.00E+00	9.90E-01	1.00E+00	1.49E-01	1.00E+00	9.70E-01	1.00E+00	anion transporter activity	F
GO:0008514	11	2.82E-01	1.00E+00	9.48E-01	1.00E+00	5.31E-01	1.00E+00	6.81E-01	1.00E+00	4.56E-01	1.00E+00	9.35E-01	1.00E+00	5.52E-02	1.00E+00	9.40E-01	1.00E+00	organic anion transporter activity	F
GO:0008528	301	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	6.79E-01	1.00E+00	7.12E-01	1.00E+00	peptide receptor activity, G-protein coupled	F
GO:0008533	15	9.09E-01	1.00E+00	9.62E-01	1.00E+00	8.75E-01	1.00E+00	7.35E-01	1.00E+00	8.20E-01	1.00E+00	6.16E-01	1.00E+00	5.25E-01	1.00E+00	9.96E-01	1.00E+00	astacin activity	F
GO:0008542	26	5.41E-01	1.00E+00	9.83E-01	1.00E+00	8.80E-01	1.00E+00	8.69E-01	1.00E+00	3.02E-01	1.00E+00	1.00E+00	1.00E+00	4.23E-01	1.00E+00	9.60E-01	1.00E+00	visual learning	P
GO:0008543	15	9.90E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.60E-01	1.00E+00	3.54E-01	1.00E+00	9.40E-01	1.00E+00	9.84E-01	1.00E+00	fibroblast growth factor receptor signaling pa	P
GO:0008544	124	9.94E-01	1.00E+00	9.69E-01	1.00E+00	9.49E-01	1.00E+00	5.73E-01	1.00E+00	9.06E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	9.02E-01	1.00E+00	epidermis development	P
GO:0008553	23	3.00E-01	1.00E+00	3.93E-01	1.00E+00	8.92E-01	1.00E+00	6.41E-01	1.00E+00	2.38E-01	1.00E+00	2.08E-01	1.00E+00	2.14E-01	1.00E+00	6.71E-01	1.00E+00	hydrogen-exporting ATPase activity, phosph	F
GO:0008565	124	8.81E-06	5.00E-03	1.90E-13	0.00E+00	1.01E-04	1.61E-02	4.30E-09	0.00E+00	1.02E-03	4.40E-02	2.19E-07	1.75E-03	2.18E-02	5.60E-01	1.23E-05	3.91E-03	protein transporter activity	F
GO:0008584	26	9.28E-01	1.00E+00	5.03E-01	1.00E+00	9.88E-01	1.00E+00	3.86E-01	1.00E+00	7.84E-01	1.00E+00	6.92E-01	1.00E+00	9.95E-01	1.00E+00	9.85E-01	1.00E+00	male gonad development	P
GO:0008585	43	4.96E-01	1.00E+00	2.90E-01	1.00E+00	1.90E-01	1.00E+00	6.61E-01	1.00E+00	8.28E-01	1.00E+00	3.66E-01	1.00E+00	5.62E-01	1.00E+00	9.39E-02	1.00E+00	female gonad development	P
GO:0008589	14	6.46E-01	1.00E+00	8.55E-01	1.00E+00	9.78E-01	1.00E+00	8.70E-01	1.00E+00	8.43E-01	1.00E+00	8.36E-01	1.00E+00	8.01E-02	1.00E+00	8.27E-01	1.00E+00	regulation of smoothened signaling pathway	P
GO:0008601	21	1.56E-01	1.00E+00	6.88E-01	1.00E+00	1.20E-01	1.00E+00	4.91E-01	1.00E+00	1.86E-01	1.00E+00	7.74E-01	1.00E+00	8.98E-01	1.00E+00	8.09E-01	1.00E+00	protein phosphatase type 2A regulator activ	F
GO:0008603	26	5.40E-01	1.00E+00	3.65E-01	1.00E+00	9.72E-01	1.00E+00	5.90E-01	1.00E+00	2.75E-01	1.00E+00	6.84E-01	1.00E+00	4.18E-01	1.00E+00	3.68E-02	1.00E+00	cAMP-dependent protein kinase regulator a	F
GO:0008610	299	5.87E-02	1.00E+00	1.91E-01	1.00E+00	6.11E-02	1.00E+00	2.63E-01	1.00E+00	2.59E-01	1.00E+00	1.62E-01	1.00E+00	1.84E-01	1.00E+00	5.12E-01	1.00E+00	lipid biosynthesis	P
GO:0008624	22	7.76E-01	1.00E+00	6.47E-02	1.00E+00	7.81E-01	1.00E+00	4.87E-02	1.00E+00	7.99E-01	1.00E+00	1.49E-01	1.00E+00	4.00E-01	1.00E+00	2.50E-01	1.00E+00	induction of apoptosis by extracellular signa	P
GO:0008629	33	5.91E-03	3.64E-01	2.03E-02	1.00E+00	4.87E-02	1.00E+00	9.09E-03	3.78E-01	1.99E-02	7.19E-01	2.56E-02	1.00E+00	3.04E-02	7.53E-01	2.33E-01	1.00E+00	induction of apoptosis by intracellular signal	P
GO:0008630	20	3.84E-02	1.00E+00	9.07E-03	5.59E-01	1.35E-01	1.00E+00	1.22E-02	3.78E-01	1.18E-01	1.00E+00	1.42E-02	1.00E+00	5.21E-02	1.00E+00	6.33E-02	1.00E+00	DNA damage response, signal transduction	P
GO:0008632	74	1.64E-03	9.30E-02	1.80E-03	1.62E-01	1.43E-02	8.10E-01	1.52E-03	4.40E-02	6.69E-03	1.65E-01	3.15E-02	1.00E+00	3.73E-02	7.83E-01	3.34E-02	1.00E+00	apoptotic program	P
GO:0008637	24	3.79E-02	1.00E+00	1.00E-01	1.00E+00	2.67E-01	1.00E+00	3.01E-02	1.00E+00	1.09E-01	1.00E+00	2.00E-01	1.00E+00	1.47E-01	1.00E+00	6.29E-01	1.00E+00	apoptotic mitochondrial changes	P
GO:0008641	10	3.02E-01	1.00E+00	1.07E-01	1.00E+00	2.34E-01	1.00E+00	2.15E-01	1.00E+00	4.46E-01	1.00E+00	2.14E-02	1.00E+00	6.10E-01	1.00E+00	6.34E-01	1.00E+00	small protein activating enzyme activity	F
GO:0008643	76	5.68E-01	1.00E+00	8.87E-01	1.00E+00	9.96E-01	1.00E+00	9.78E-01	1.00E+00	5.99E-01	1.00E+00	9.74E-01	1.00E+00	6.62E-02	1.00E+00	2.97E-01	1.00E+00	carbohydrate transport	P
GO:0008645	41	7.97E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	8.32E-01	1.00E+00	9.99E-01	1.00E+00	1.98E-01	1.00E+00	5.18E-01	1.00E+00	hexose transport	P
GO:0008652	88	1.31E-01	1.00E+00	2.05E-01	1.00E+00	3.22E-01	1.00E+00	3.45E-01	1.00E+00	1.85E-01	1.00E+00	1.36E-01	1.00E+00	2.47E-01	1.00E+00	4.52E-01	1.00E+00	amino acid biosynthesis	P
GO:0008654	75	4.76E-02	1.00E+00	8.78E-02	1.00E+00	6.83E-03	2.83E-01	1.96E-02	7.69E-01	1.90E-01	1.00E+00	1.91E-01	1.00E+00	7.45E-01	1.00E+00	9.30E-01	1.00E+00	phospholipid biosynthesis	P
GO:0008667	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	2,3-dihydro-2,3-dihydroxybenzoate dehydro	F
GO:0008757	80	5.89E-06	5.00E-03	2.91E-08	2.66E-03	1.34E-04	1.61E-02	1.24E-05	1.77E-03	1.87E-04	8.00E-03	7.35E-06	2.00E-03	1.95E-01	1.00E+00	1.44E-04	4.00E-03	S-adenosylmethionine-dependent methyltra	F
GO:0008943	22	1.00E+00	1.00E+00	7.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.63E-01	1.00E+00	2.93E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	glyceraldehyde-3-phosphate dehydrogenas	F
GO:0009055	343	2.23E-02	1.00E+00	6.03E-02	1.00E+00	2.18E-01	1.00E+00	1.13E-01	1.00E+00	7.20E-02	1.00E+00	2.95E-01	1.00E+00	4.57E-03	7.75E-02	2.73E-02	1.00E+00	electron carrier activity	F
GO:0009056	654	1.59E-10	9.73E-04	5.42E-11	2.66E-03	1.19E-07	9.88E-04	6.00E-08	0.00E+00	5.25E-05	1.56E-03	7.29E-07	2.00E-03	1.09E-05	2.00E-03	1.06E-06	3.91E-03	catabolism	P
GO:0009057	362	2.11E-09	9.73E-04	7.06E-11	2.66E-03	2.76E-07	9.88E-04	1.12E-08	0.00E+00	1.36E-06	7.65E-04	8.14E-07	2.00E-03	4.76E-03	7.75E-02	7.59E-05	3.91E-03	macromolecule catabolism	P
GO:0009058	1446	9.87E-04	9.30E-02	8.89E-08	2.66E-03	1.37E-02	8.10E-01	7.39E-06	1.77E-03	7.87E-03	3.18E-01	6.73E-05	5.36E-03	4.15E-01	1.00E+00	3.19E-03	2.16E-01	biosynthesis	P
GO:0009059	800	1.21E-02	9.83E-01	3.60E-07	2.66E-03	5.97E-03	1.88E-01	2.06E-05	1.92E-03	4.31E-02	1.00E+00	5.69E-05	5.36E-03	8.14E-01	1.00E+00	2.22E-02	1.00E+00	macromolecule biosynthesis	P
GO:0009060	27	3.73E-03	1.86E-01	6.62E-02	1.00E+00	3.02E-02	1.00E+00	2.12E-02	7.69E-01	7.81E-02	1.00E+00	2.62E-01	1.00E+00	1.58E-02	4.39E-01	1.30E-01	1.00E+00	aerobic respiration	P
GO:0009063	56	2.77E-01	1.00E+00	5.05E-02	1.00E+00	2.79E-01	1.00E+00	3.30E-01	1.00E+00	4.41E-01	1.00E+00	3.43E-02	1.00E+00	8.68E-02	1.00E+00	7.24E-02	1.00E+00	amino acid catabolism	P
GO:0009064	40	2.16E-01	1.00E+00	6.76E-02	1.00E+00	3.70E-01	1.00E+00	2.44E-02	7.69E-01	1.07E-01	1.00E+00	1.15E-01	1.00E+00	5.74E-01	1.00E+00	2.33E-01	1.00E+00	glutamine family amino acid metabolism	P
GO:0009065	10	2.97E-01	1.00E+00	5.39E-01	1.00E+00	5.56E-01	1.00E+00	3.09E-01	1.00E+00	1.70E-01	1.00E+00	6.77E-01	1.00E+00	2.84E-01	1.00E+00	7.55E-01	1.00E+00	glutamine family amino acid catabolism	P
GO:0009066	23	2.35E-01	1.00E+00	7.99E-01	1.00E+00	2.79E-01	1.00E+00	6.52E-01	1.00E+00	8.22E-02	1.00E+00	9.05E-01	1.00E+00	7.15E-01	1.00E+00	4.60E-01	1.00E+00	aspartate family amino acid metabolism	P
GO:0009067	13	9.04E-02	1.00E+00	2.51E-01	1.00E+00	2.98E-01	1.00E+00	2.20E-01	1.00E+00	4.87E-02	1.00E+00	6.38E-01	1.00E+00	3.82E-01	1.00E+00	1.30E-01	1.00E+00	aspartate family amino acid biosynthesis	P
GO:0009069	23	8.42E-02	1.00E+00	5.77E-04	7.30E-02	4.09E-02	1.00E+00	1.03E-02	3.78E-01	1.48E-01	1.00E+00	7.65E-05	5.36E-03	2.73E-01	1.00E+00	9.27E-03	4.48E-01	serine family amino acid metabolism	P
GO:0009071	10	4.70E-02	1.00E+00	1.84E-02	1.00E+00	2.45E-02	1.00E+00	6.38E-02	1.00E+00	2.18E-01	1.00E+00	5.91E-03	2.02E-01	1.45E-01	1.00E+00	4.68E-02	1.00E+00	serine family amino acid catabolism	P
GO:0009072	74	2.38E-01	1.00E+00	6.54E-01	1.00E+00	4.18E-01	1.00E+00	9.02E-01	1.00E+00	3.78E-01	1.00E+00	4.11E-01	1.00E+00	1.16E-01	1.00E+00	4.97E-01	1.00E+00	aromatic amino acid family metabolism	P
GO:0009073	48	2.64E-01	1.00E+00	5.36E-01	1.00E+00	2.57E-01	1.00E+00	6.06E-01	1.00E+00	5.08E-01	1.00E+00	4.22E-01	1.00E+00	2.18E-01	1.00E+00	6.46E-01	1.00E+00	aromatic amino acid family biosynthesis	P
GO:0009074	12	5.03E-01	1.00E+00	5.97E-01	1.00E+00	8.23E-01	1.00E+00	9.86E-01	1.00E+00	4.54E-01	1.00E+00	3.69E-01	1.00E+00	2.11E-01	1.00E+00	3.66E-01	1.00E+00	aromatic amino acid family catabolism	P
GO:0009075	11	8.98E-01	1.00E+00	6.00E-01	1.00E+00	8.25E-01	1.00E+00	4.47E-01	1.00E+00	9.82E-01	1.00E+00	7.67E-01	1.00E+00	3.76E-01	1.00E+00	3.74E-01	1.00E+00	histidine family amino acid metabolism	P
GO:0009077	11	8.98E-01	1.00E+00	6.00E-01	1.00E+00	8.25E-01	1.00E+00	4.47E-01	1.00E+00	9.82E-01	1.00E+00	7.67E-01	1.00E+00	3.76E-01	1.00E+00	3.74E-01	1.00E+00	histidine family amino acid catabolism	P
GO:0009081	12	1.46E-01	1.00E+00	7.48E-02	1.00E+00	1.39E-01	1.00E+00	3.49E-01	1.00E+00	2.06E-01	1.00E+00	1.82E-01	1.00E+00	2.38E-01	1.00E+00	1.30E-01	1.00E+00	branched chain family amino acid metabolis	P
GO:0009084	16	1.85E-01	1.00E+00	2.87E-01	1.00E+00	4.40E-01	1.00E+00	2.16E-01	1.00E+00	1.79E-01	1.00E+00	2.14E-01	1.00E+00	2.99E-01	1.00E+00	6.76E-01	1.00E+00	glutamine family amino acid biosynthesis	P

GO:0009100	110	4.51E-01	1.00E+00	1.60E-02	1.00E+00	5.06E-01	1.00E+00	1.22E-01	1.00E+00	8.74E-01	1.00E+00	1.06E-01	1.00E+00	1.28E-01	1.00E+00	6.78E-04	3.30E-02	glycoprotein metabolism	P
GO:0009101	93	4.65E-01	1.00E+00	3.04E-02	1.00E+00	6.24E-01	1.00E+00	1.38E-01	1.00E+00	8.64E-01	1.00E+00	1.47E-01	1.00E+00	1.24E-01	1.00E+00	2.33E-03	6.30E-02	glycoprotein biosynthesis	P
GO:0009108	87	1.04E-01	1.00E+00	4.00E-02	1.00E+00	4.77E-01	1.00E+00	8.59E-02	1.00E+00	9.43E-02	1.00E+00	2.82E-01	1.00E+00	1.63E-01	1.00E+00	3.37E-02	1.00E+00	coenzyme biosynthesis	P
GO:0009109	29	3.22E-02	1.00E+00	4.51E-02	1.00E+00	3.06E-02	1.00E+00	5.31E-02	1.00E+00	2.14E-01	1.00E+00	1.85E-01	1.00E+00	6.42E-02	1.00E+00	1.63E-02	9.40E-01	coenzyme catabolism	P
GO:0009110	25	5.63E-01	1.00E+00	1.28E-01	1.00E+00	2.57E-01	1.00E+00	1.63E-01	1.00E+00	7.23E-01	1.00E+00	4.08E-01	1.00E+00	8.05E-01	1.00E+00	2.02E-01	1.00E+00	vitamin biosynthesis	P
GO:0009112	18	1.45E-01	1.00E+00	1.27E-01	1.00E+00	4.39E-02	1.00E+00	1.12E-01	1.00E+00	1.28E-01	1.00E+00	9.55E-02	1.00E+00	9.00E-01	1.00E+00	3.35E-01	1.00E+00	nucleobase metabolism	P
GO:0009116	27	3.78E-01	1.00E+00	9.05E-03	5.59E-01	2.05E-01	1.00E+00	1.25E-02	3.78E-01	7.83E-01	1.00E+00	5.19E-03	2.02E-01	1.37E-01	1.00E+00	8.47E-02	1.00E+00	nucleoside metabolism	P
GO:0009117	199	5.31E-02	1.00E+00	2.17E-02	1.00E+00	5.73E-01	1.00E+00	6.82E-02	1.00E+00	3.58E-02	1.00E+00	5.94E-02	1.00E+00	7.73E-02	1.00E+00	1.27E-01	1.00E+00	nucleotide metabolism	P
GO:0009119	10	4.27E-01	1.00E+00	2.57E-02	1.00E+00	7.45E-01	1.00E+00	3.65E-02	1.00E+00	6.45E-01	1.00E+00	1.94E-02	1.00E+00	8.06E-02	1.00E+00	7.86E-02	1.00E+00	ribonucleoside metabolism	P
GO:0009123	21	2.95E-01	1.00E+00	1.40E-03	7.50E-02	5.20E-01	1.00E+00	4.00E-03	1.42E-01	2.57E-01	1.00E+00	6.09E-02	1.00E+00	3.67E-01	1.00E+00	8.55E-02	1.00E+00	nucleoside monophosphate metabolism	P
GO:0009124	20	2.50E-01	1.00E+00	2.40E-03	1.87E-01	4.42E-01	1.00E+00	7.29E-03	3.78E-01	2.07E-01	1.00E+00	7.82E-02	1.00E+00	3.06E-01	1.00E+00	1.01E-01	1.00E+00	nucleoside monophosphate biosynthesis	P
GO:0009126	15	2.51E-01	1.00E+00	2.24E-03	1.62E-01	5.69E-01	1.00E+00	7.09E-03	3.78E-01	1.58E-01	1.00E+00	1.21E-01	1.00E+00	4.98E-01	1.00E+00	6.45E-02	1.00E+00	purine nucleoside monophosphate metaboli	P
GO:0009127	14	2.01E-01	1.00E+00	4.85E-03	3.82E-01	4.81E-01	1.00E+00	1.49E-02	7.69E-01	1.13E-01	1.00E+00	1.63E-01	1.00E+00	4.07E-01	1.00E+00	8.33E-02	1.00E+00	purine nucleoside monophosphate biosynth	P
GO:0009132	14	7.09E-01	1.00E+00	1.39E-01	1.00E+00	7.09E-01	1.00E+00	2.25E-01	1.00E+00	2.59E-01	1.00E+00	1.90E-01	1.00E+00	7.72E-01	1.00E+00	2.88E-01	1.00E+00	nucleoside diphosphate metabolism	P
GO:0009141	68	1.05E-01	1.00E+00	5.48E-02	1.00E+00	4.48E-01	1.00E+00	9.19E-02	1.00E+00	6.57E-02	1.00E+00	6.62E-02	1.00E+00	3.60E-01	1.00E+00	2.31E-01	1.00E+00	nucleoside triphosphate metabolism	P
GO:0009142	50	2.88E-01	1.00E+00	2.24E-01	1.00E+00	6.88E-01	1.00E+00	2.37E-01	1.00E+00	1.18E-01	1.00E+00	2.86E-01	1.00E+00	6.46E-01	1.00E+00	4.29E-01	1.00E+00	nucleoside triphosphate biosynthesis	P
GO:0009144	59	1.35E-01	1.00E+00	1.26E-01	1.00E+00	5.33E-01	1.00E+00	2.12E-01	1.00E+00	7.00E-02	1.00E+00	1.40E-01	1.00E+00	4.89E-01	1.00E+00	2.82E-01	1.00E+00	purine nucleoside triphosphate metabolism	P
GO:0009145	46	3.06E-01	1.00E+00	3.30E-01	1.00E+00	7.35E-01	1.00E+00	4.09E-01	1.00E+00	1.08E-01	1.00E+00	4.04E-01	1.00E+00	6.90E-01	1.00E+00	4.46E-01	1.00E+00	purine nucleoside triphosphate biosynthesis	P
GO:0009147	16	9.15E-02	1.00E+00	5.92E-02	1.00E+00	5.22E-02	1.00E+00	7.84E-02	1.00E+00	7.07E-02	1.00E+00	3.62E-02	1.00E+00	6.01E-01	1.00E+00	3.23E-01	1.00E+00	pyrimidine nucleoside triphosphate metabol	P
GO:0009150	74	1.66E-01	1.00E+00	4.00E-02	1.00E+00	7.07E-01	1.00E+00	4.32E-02	1.00E+00	7.04E-02	1.00E+00	8.74E-02	1.00E+00	4.95E-01	1.00E+00	1.50E-01	1.00E+00	purine ribonucleotide metabolism	P
GO:0009152	62	1.90E-01	1.00E+00	8.10E-02	1.00E+00	6.93E-01	1.00E+00	9.03E-02	1.00E+00	6.19E-02	1.00E+00	1.62E-01	1.00E+00	6.28E-01	1.00E+00	2.37E-01	1.00E+00	purine ribonucleotide biosynthesis	P
GO:0009156	18	2.96E-01	1.00E+00	1.42E-03	7.50E-02	4.47E-01	1.00E+00	5.86E-03	3.78E-01	2.50E-01	1.00E+00	4.53E-02	1.00E+00	4.55E-01	1.00E+00	6.76E-02	1.00E+00	ribonucleoside monophosphate biosynthesis	P
GO:0009161	19	3.49E-01	1.00E+00	7.87E-04	7.30E-02	5.28E-01	1.00E+00	3.05E-03	1.42E-01	3.07E-01	1.00E+00	3.38E-02	1.00E+00	5.33E-01	1.00E+00	5.54E-02	1.00E+00	ribonucleoside monophosphate metabolism	P
GO:0009165	132	2.82E-01	1.00E+00	3.38E-02	1.00E+00	7.86E-01	1.00E+00	4.65E-02	1.00E+00	1.18E-01	1.00E+00	1.81E-01	1.00E+00	5.19E-01	1.00E+00	1.45E-01	1.00E+00	nucleotide biosynthesis	P
GO:0009166	27	4.71E-01	1.00E+00	9.41E-01	1.00E+00	5.17E-01	1.00E+00	7.54E-01	1.00E+00	4.64E-01	1.00E+00	7.34E-01	1.00E+00	6.77E-01	1.00E+00	9.90E-01	1.00E+00	nucleotide catabolism	P
GO:0009167	15	2.51E-01	1.00E+00	2.24E-03	1.62E-01	5.69E-01	1.00E+00	7.09E-03	3.78E-01	1.58E-01	1.00E+00	1.21E-01	1.00E+00	4.98E-01	1.00E+00	6.45E-02	1.00E+00	purine ribonucleoside monophosphate meta	P
GO:0009168	14	2.01E-01	1.00E+00	4.85E-03	3.82E-01	4.81E-01	1.00E+00	1.49E-02	7.69E-01	1.13E-01	1.00E+00	1.63E-01	1.00E+00	4.07E-01	1.00E+00	8.33E-02	1.00E+00	purine ribonucleoside monophosphate biosy	P
GO:0009187	46	9.80E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.94E-01	1.00E+00	9.59E-01	1.00E+00	cyclic nucleotide metabolism	P
GO:0009190	34	9.46E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	6.43E-01	1.00E+00	9.97E-01	1.00E+00	cyclic nucleotide biosynthesis	P
GO:0009199	57	2.07E-01	1.00E+00	1.26E-01	1.00E+00	5.91E-01	1.00E+00	1.90E-01	1.00E+00	1.11E-01	1.00E+00	1.58E-01	1.00E+00	5.12E-01	1.00E+00	2.82E-01	1.00E+00	ribonucleoside triphosphate metabolism	P
GO:0009200	10	1.70E-01	1.00E+00	6.06E-02	1.00E+00	3.43E-01	1.00E+00	7.08E-02	1.00E+00	2.10E-01	1.00E+00	6.01E-02	1.00E+00	6.30E-02	1.00E+00	3.01E-01	1.00E+00	deoxyribonucleoside triphosphate metabolis	P
GO:0009201	47	2.99E-01	1.00E+00	2.93E-01	1.00E+00	7.08E-01	1.00E+00	3.46E-01	1.00E+00	1.13E-01	1.00E+00	3.63E-01	1.00E+00	6.92E-01	1.00E+00	4.48E-01	1.00E+00	ribonucleoside triphosphate biosynthesis	P
GO:0009205	55	2.23E-01	1.00E+00	1.67E-01	1.00E+00	6.52E-01	1.00E+00	2.53E-01	1.00E+00	1.09E-01	1.00E+00	2.10E-01	1.00E+00	5.21E-01	1.00E+00	2.90E-01	1.00E+00	purine ribonucleoside triphosphate metaboli	P
GO:0009206	46	3.06E-01	1.00E+00	3.30E-01	1.00E+00	7.35E-01	1.00E+00	4.09E-01	1.00E+00	1.08E-01	1.00E+00	4.04E-01	1.00E+00	6.90E-01	1.00E+00	4.46E-01	1.00E+00	purine ribonucleoside triphosphate biosynth	P
GO:0009208	12	9.92E-02	1.00E+00	7.31E-02	1.00E+00	4.69E-02	1.00E+00	1.04E-01	1.00E+00	6.29E-02	1.00E+00	6.78E-02	1.00E+00	7.71E-01	1.00E+00	2.86E-01	1.00E+00	pyrimidine ribonucleoside triphosphate meta	P
GO:0009209	12	9.92E-02	1.00E+00	7.31E-02	1.00E+00	4.69E-02	1.00E+00	1.04E-01	1.00E+00	6.29E-02	1.00E+00	6.78E-02	1.00E+00	7.71E-01	1.00E+00	2.86E-01	1.00E+00	pyrimidine ribonucleoside triphosphate biosy	P
GO:0009218	14	1.35E-01	1.00E+00	4.02E-02	1.00E+00	6.65E-02	1.00E+00	9.12E-02	1.00E+00	6.55E-02	1.00E+00	3.86E-02	1.00E+00	8.70E-01	1.00E+00	1.94E-01	1.00E+00	pyrimidine ribonucleotide metabolism	P
GO:0009220	14	1.35E-01	1.00E+00	4.02E-02	1.00E+00	6.65E-02	1.00E+00	9.12E-02	1.00E+00	6.55E-02	1.00E+00	3.86E-02	1.00E+00	8.70E-01	1.00E+00	1.94E-01	1.00E+00	pyrimidine ribonucleotide biosynthesis	P
GO:0009225	15	4.49E-03	2.28E-01	4.11E-01	1.00E+00	6.61E-02	1.00E+00	4.46E-01	1.00E+00	1.13E-01	1.00E+00	4.49E-01	1.00E+00	3.30E-02	7.53E-01	4.45E-01	1.00E+00	nucleotide-sugar metabolism	P
GO:0009237	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	siderophore metabolism	P
GO:0009238	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	enterobactin metabolism	P
GO:0009239	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	enterobactin biosynthesis	P
GO:0009250	26	1.06E-01	1.00E+00	9.63E-01	1.00E+00	2.81E-01	1.00E+00	9.97E-01	1.00E+00	6.33E-02	1.00E+00	7.33E-01	1.00E+00	1.51E-01	1.00E+00	6.33E-01	1.00E+00	glucan biosynthesis	P
GO:0009259	82	1.97E-01	1.00E+00	1.06E-02	7.51E-01	6.61E-01	1.00E+00	1.42E-02	7.69E-01	9.01E-02	1.00E+00	2.76E-02	1.00E+00	5.53E-01	1.00E+00	1.00E-01	1.00E+00	ribonucleotide metabolism	P
GO:0009260	68	2.12E-01	1.00E+00	2.01E-02	1.00E+00	6.38E-01	1.00E+00	2.87E-02	1.00E+00	7.61E-02	1.00E+00	5.33E-02	1.00E+00	6.58E-01	1.00E+00	1.47E-01	1.00E+00	ribonucleotide biosynthesis	P
GO:0009262	15	1.00E-01	1.00E+00	4.63E-02	1.00E+00	2.19E-01	1.00E+00	5.24E-02	1.00E+00	9.37E-02	1.00E+00	4.98E-02	1.00E+00	9.60E-02	1.00E+00	2.88E-01	1.00E+00	deoxyribonucleotide metabolism	P
GO:0009266	202	9.99E-01	1.00E+00	9.33E-01	1.00E+00	9.88E-01	1.00E+00	3.31E-01	1.00E+00	9.59E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to temperature stimulus	P
GO:0009267	12	2.40E-01	1.00E+00	9.86E-01	1.00E+00	5.28E-01	1.00E+00	4.27E-01	1.00E+00	5.17E-01	1.00E+00	1.00E+00	1.00E+00	1.87E-01	1.00E+00	8.28E-01	1.00E+00	cellular response to starvation	P
GO:0009288	37	1.75E-01	1.00E+00	9.67E-01	1.00E+00	8.20E-01	1.00E+00	8.54E-01	1.00E+00	9.13E-02	1.00E+00	1.00E+00	1.00E+00	1.96E-01	1.00E+00	6.10E-01	1.00E+00	flagellum (sensu Bacteria)	C
GO:0009296	14	3.53E-02	1.00E+00	1.80E-02	1.00E+00	8.16E-02	1.00E+00	4.32E-03	1.42E-01	3.74E-01	1.00E+00	3.18E-02	1.00E+00	1.66E-01	1.00E+00	5.68E-01	1.00E+00	flagellum biogenesis	P
GO:0009306	56	1.18E-01	1.00E+00	3.07E-01	1.00E+00	6.25E-01	1.00E+00	4.17E-01	1.00E+00	4.02E-01	1.00E+00	5.58E-01	1.00E+00	4.09E-02	8.34E-01	1.65E-01	1.00E+00	protein secretion	P
GO:0009308	521	1.12E-01	1.00E+00	1.63E-01	1.00E+00	3.42E-01	1.00E+00	2.40E-01	1.00E+00	4.25E-01	1.00E+00	2.12E-01	1.00E+00	8.34E-02	1.00E+00	1.78E-01	1.00E+00	amine metabolism	P
GO:0009309	118	1.66E-01	1.00E+00	4.09E-01	1.00E+00	5.53E-01	1.00E+00	6.24E-01	1.00E+00	3.82E-01	1.00E+00	3.99E-01	1.00E+00	2.50E-01	1.00E+00	3.27E-01	1.00E+00	amine biosynthesis	P
GO:0009310	65	3.64E-01	1.00E+00	6.41E-02	1.00E+00	4.04E-01	1.00E+00	1.69E-01	1.00E+00	4.73E-01	1.00E+00	1.18E-01	1.00E+00	1.42E-01	1.00E+00	1.02E-01	1.00E+00	amine catabolism	P
GO:0009311	10	4.60E-01	1.00E+00	1.55E-01	1.00E+00	4.93E-01	1.00E+00	1.98E-01	1.00E+00	8.24E-01	1.00E+00	2.87E-01	1.00E+00	3.41E-01	1.00E+00	1.86E-01	1.00E+00	oligosaccharide metabolism	P
GO:0009314	120	1.77E-04	1.90E-02	1.16E-02	7.51E-01	8.06E-03	3.43E-01	2.41E-02	7.69E-01	2.54E-03	1.35E-01	8.99E-02	1.00E+00	3.02E-03	5.54E-02	3.65E-02	1.00E+00	response to radiation	P
GO:0009331	12	1.62E-01	1.00E+00	2.71E-01	1.00E+00	1.95E-01	1.00E+00	2.69E-01	1.00E+00	8.28E-01	1.00E+00	4.94E-01	1.00E+00	1.34E-01	1.00E+00	4.24E-01	1.00E+00	glycerol-3-phosphate dehydrogenase comp	C
GO:0009395	14	1.48E-01	1.00E+00	4.76E-01	1.00E+00	3.92E-02	1.00E+00	5.32E-01	1.00E+00	5.80E-01	1.00E+00	4.41E-01	1.00E+00	4.79E-01	1.00E+00	4.31E-01	1.00E+00	phospholipid catabolism	P
GO:0009396	10	4.41E-01	1.00E+00	1.72E-02	1.00E+00	9.28E-01	1.00E+00	1.16E-01	1.00E+00	2.35E-01	1.00E+00	7.94E-02	1.00E+00	2.42E-01	1.00E+00	1.27E-03	4.40E-02	folic acid and derivative biosynthesis	P
GO:0009405	30	1.51E-01	1.00E+00	4.72E-01	1.00E+00	1.67E-01	1.00E+00	6.27E-01	1.00E+00	2.40E-01	1.00E+00	5.16E-01	1.00E+00	3.64E-01	1.00E+00	3.02E-01	1.00E+00	pathogenesis	P
GO:0009408	15	1.78E-01	1.00E+00	5.20E-01	1.00E+00	9.39E-02	1.00E+00	3.74E-01	1.00E+00	1.70E-01	1.00E+00	3.85E-01	1.00E+00	4.96E-01	1.00E+00	7.84E-01	1.00E+00	response to heat	P
GO:0009409	180	1.00E+00	1.00E+00	9.33E-01	1.00E+00	9.98E-01	1.00E+00	3.08E-01	1.00E+00	9.92E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to cold	P
GO:0009410	16	3.33E-01	1.00E+00	7.86E-01	1.00E+00	5.52E-01	1.00E+00	9.96E-01	1.00E+00	3.00E-01	1.00E+00	5.68E-01	1.00E+00	2.20E-01	1.00E+00	4.45E-01	1.00E+00	response to xenobiotic stimulus	P
GO:0009411	40	1.63E-03	9.30E-02	8.65E-03	5.59E-01	4.05E-02	1.00E+00	4.56E-03	1.42E-01	2.01E-02	7.19E-01	7.17E-02	1.00E+00	1.27E-02	4.39E-01	3.52E-02	1.00E+00	response to UV	P
GO:0009416	94	4.12E-03	1.86E-01	1.15E-01	1.00E+00	6.50E-02	1.00E+00	4.78E-02	1.00E+00	1.51E-02	4.81E-01	4.58E-01	1.00E+00	3.16E-02	7.53E-01	2.19E-01	1.00E+00	response to light stimulus	P
GO:0009434	23	1.80E-01	1.00E+00	4.17E-01	1.00E+00	7.63E-01	1.00E+00	2.90E-01	1.00E+00	1.30E-01	1.00E+00	4.09E-01	1.00E+00	6.48E-01	1.00E+00	6.77E-01	1.00E+00	flagellum (sensu Eukaryota)	C
GO:0009451	31	1.64E-01	1.00E+00	1.11E-03	7.30E-02	8.00E-02	1.00E+00	6.04E-02	1.00E+00	1.05E-01	1.00E+00	1.09E-02	4.01E-01	9.08E-01	1.00E+00	2.03E-02	1.00E+00	RNA modification	P
GO:0009566	58	3.08E-01	1.00E+00	5.72E-02	1.00E+00	1.07E-01	1.00E+00	3.21E-02	1.00E+00	9.96E-01	1.00E+00	1.14E-01	1.00E+00	2.27E-01	1.00E+00	4.89E-01	1.00E+00	fertilization	P
GO:0009581	54	3.96E-01	1.00E+00	8.02E-01	1.00E+00	3.31E-01	1.00E+00	7.86E-01	1.00E+00	7.94E-01	1.00E+00	7.28E-01	1.00E+00	1.71E-01	1.00E+00	6.77E-01	1.00E+00	detection of external stimulus	P
GO:0009582	44	4.44E-01	1.00E+00	8.07E-01	1.00E+00	2.74E-01	1.00E+00	9.04E-01	1.00E+00	5.72E-01	1.00E+00	6.39E-01	1.00E+00	3.98E-01	1.00E+00	6.95E-01	1.00E+00	detection of abiotic stimulus	P
GO:0009583	25	1.17E-01	1.00E+00	1.69E-01	1.00E+00	1.05E-01	1.00E+00	2.65E-01	1.00E+00	1.32E-01	1.00E+00	2.96E-01	1.00E+00	1.81E-01	1.00E+00	3.84E-01	1.00E+00	detection of light stimulus	P
GO:0009593	14	8.56E-01	1.00E+00	9.91E-01	1.00E+00	8.87E-01	1.00E+00	9.68E-01	1.00E+00	8.19E-01	1.00E+00	9.93E-01	1.00E+00	2.77E-01	1.00E+00	8.40E-01	1.00E+00	detection of chemical stimulus	P
GO:0009595	11	2.53E-01	1.00E+00	4.24E-01	1.00E+00	6.04E-01	1.00E+00	3.91E-01	1.00E+00	9.96E-01	1.00E+00	6.91E-01	1.00E+00	5.12E-02	1.00E+00	2.21E-01	1.00E+00	detection of biotic stimulus	P
GO:0009605	696	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.87E-01	1.00E+00	5.55E-01	1.00E+00	response to external stimulus	P
GO:0009607	228	7.29E-02	1.00E+00	9.91E-01	1.00E+00	2.37E-01	1.00E+00	6.90E-01	1.00E+00	4.46E-01	1.00E+00	9.67E-01	1.00E+00	1.29E-02	4.39E-01	1.00E+00	1.00E+00	response to biotic stimulus	P

GO:0009611	449	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	8.81E-01	1.00E+00	response to wounding	P
GO:0009612	30	9.80E-01	1.00E+00	9.43E-01	1.00E+00	9.24E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	5.67E-01	1.00E+00	8.41E-01	1.00E+00	7.47E-01	1.00E+00	response to mechanical stimulus	P
GO:0009615	58	9.14E-01	1.00E+00	1.00E+00	1.00E+00	7.11E-01	1.00E+00	9.77E-01	1.00E+00	9.48E-01	1.00E+00	9.94E-01	1.00E+00	8.19E-01	1.00E+00	1.00E+00	1.00E+00	response to virus	P
GO:0009617	99	4.00E-01	1.00E+00	9.49E-01	1.00E+00	8.32E-01	1.00E+00	5.81E-01	1.00E+00	8.15E-01	1.00E+00	9.52E-01	1.00E+00	2.85E-02	6.06E-01	9.99E-01	1.00E+00	response to bacterium	P
GO:0009620	14	7.64E-03	6.18E-01	9.37E-01	1.00E+00	5.23E-02	1.00E+00	8.89E-01	1.00E+00	3.74E-02	1.00E+00	8.03E-01	1.00E+00	3.20E-02	7.53E-01	5.03E-01	1.00E+00	response to fungus	P
GO:0009628	375	5.43E-01	1.00E+00	4.41E-01	1.00E+00	6.31E-01	1.00E+00	1.35E-01	1.00E+00	2.37E-01	1.00E+00	6.26E-01	1.00E+00	8.68E-01	1.00E+00	9.03E-01	1.00E+00	response to abiotic stimulus	P
GO:0009636	31	4.12E-01	1.00E+00	5.35E-01	1.00E+00	8.06E-01	1.00E+00	9.06E-01	1.00E+00	4.90E-01	1.00E+00	3.62E-01	1.00E+00	2.50E-01	1.00E+00	4.27E-01	1.00E+00	response to toxin	P
GO:0009653	1308	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.50E-01	1.00E+00	9.99E-01	1.00E+00	morphogenesis	P
GO:0009698	48	2.64E-01	1.00E+00	5.36E-01	1.00E+00	2.57E-01	1.00E+00	6.06E-01	1.00E+00	5.08E-01	1.00E+00	4.22E-01	1.00E+00	2.18E-01	1.00E+00	6.46E-01	1.00E+00	phenylpropanoid metabolism	P
GO:0009712	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	catechol metabolism	P
GO:0009719	414	2.85E-06	2.00E-03	1.48E-09	2.66E-03	1.92E-05	3.00E-03	7.22E-07	1.00E-03	6.74E-05	1.56E-03	1.46E-07	1.75E-03	1.16E-01	1.00E+00	7.35E-04	3.30E-02	response to endogenous stimulus	P
GO:0009725	97	9.35E-01	1.00E+00	9.68E-01	1.00E+00	6.24E-01	1.00E+00	9.98E-01	1.00E+00	9.45E-01	1.00E+00	8.62E-01	1.00E+00	9.98E-01	1.00E+00	6.07E-01	1.00E+00	response to hormone stimulus	P
GO:0009743	24	4.39E-01	1.00E+00	2.83E-01	1.00E+00	5.19E-01	1.00E+00	5.24E-01	1.00E+00	4.67E-01	1.00E+00	4.52E-01	1.00E+00	2.62E-01	1.00E+00	4.75E-02	1.00E+00	response to carbohydrate stimulus	P
GO:0009746	20	3.85E-01	1.00E+00	2.45E-01	1.00E+00	4.18E-01	1.00E+00	4.04E-01	1.00E+00	3.01E-01	1.00E+00	3.62E-01	1.00E+00	4.59E-01	1.00E+00	8.26E-02	1.00E+00	response to hexose stimulus	P
GO:0009749	20	3.85E-01	1.00E+00	2.45E-01	1.00E+00	4.18E-01	1.00E+00	4.04E-01	1.00E+00	3.01E-01	1.00E+00	3.62E-01	1.00E+00	4.59E-01	1.00E+00	8.26E-02	1.00E+00	response to glucose stimulus	P
GO:0009755	11	4.70E-01	1.00E+00	2.60E-01	1.00E+00	5.39E-01	1.00E+00	1.40E-01	1.00E+00	3.53E-01	1.00E+00	4.28E-01	1.00E+00	8.92E-01	1.00E+00	1.83E-01	1.00E+00	hormone-mediated signaling	P
GO:0009790	518	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	embryonic development	P
GO:0009791	88	5.71E-01	1.00E+00	5.09E-01	1.00E+00	6.75E-01	1.00E+00	9.14E-01	1.00E+00	5.56E-01	1.00E+00	6.28E-01	1.00E+00	2.61E-01	1.00E+00	7.45E-02	1.00E+00	post-embryonic development	P
GO:0009792	304	1.00E+00	1.00E+00	6.76E-01	1.00E+00	1.00E+00	1.00E+00	3.36E-01	1.00E+00	1.00E+00	1.00E+00	8.24E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	embryonic development (sensu Metazoa)	P
GO:0009798	18	7.91E-01	1.00E+00	2.27E-01	1.00E+00	9.91E-01	1.00E+00	4.78E-01	1.00E+00	2.69E-01	1.00E+00	1.46E-01	1.00E+00	8.62E-01	1.00E+00	1.93E-01	1.00E+00	axis specification	P
GO:0009799	36	9.61E-01	1.00E+00	7.55E-01	1.00E+00	9.75E-01	1.00E+00	7.61E-01	1.00E+00	8.67E-01	1.00E+00	7.45E-01	1.00E+00	9.88E-01	1.00E+00	6.38E-01	1.00E+00	determination of symmetry	P
GO:0009855	36	9.61E-01	1.00E+00	7.55E-01	1.00E+00	9.75E-01	1.00E+00	7.61E-01	1.00E+00	8.67E-01	1.00E+00	7.45E-01	1.00E+00	9.88E-01	1.00E+00	6.38E-01	1.00E+00	determination of bilateral symmetry	P
GO:0009880	46	9.90E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	6.49E-01	1.00E+00	6.16E-01	1.00E+00	8.73E-01	1.00E+00	embryonic pattern specification	P
GO:0009881	11	5.36E-01	1.00E+00	9.74E-01	1.00E+00	6.94E-01	1.00E+00	6.34E-01	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	1.27E-01	1.00E+00	2.00E-01	1.00E+00	photoreceptor activity	F
GO:0009887	734	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organ morphogenesis	P
GO:0009888	384	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.55E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.50E-01	1.00E+00	tissue development	P
GO:0009889	203	1.55E-01	1.00E+00	3.38E-01	1.00E+00	9.76E-02	1.00E+00	3.91E-01	1.00E+00	5.11E-01	1.00E+00	3.93E-01	1.00E+00	4.05E-01	1.00E+00	4.37E-01	1.00E+00	regulation of biosynthesis	P
GO:0009890	47	3.72E-02	1.00E+00	1.43E-02	1.00E+00	1.18E-02	4.74E-01	3.95E-02	1.00E+00	1.58E-01	1.00E+00	1.23E-01	1.00E+00	2.48E-01	1.00E+00	6.42E-03	2.58E-01	negative regulation of biosynthesis	P
GO:0009891	88	7.11E-01	1.00E+00	9.99E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.97E-01	1.00E+00	1.00E-01	1.00E+00	7.57E-01	1.00E+00	positive regulation of biosynthesis	P
GO:0009892	454	4.13E-02	1.00E+00	2.20E-03	1.62E-01	1.17E-01	1.00E+00	6.40E-04	2.70E-02	9.15E-02	1.00E+00	7.58E-02	1.00E+00	6.25E-02	1.00E+00	5.49E-02	1.00E+00	negative regulation of metabolism	P
GO:0009893	573	6.33E-01	1.00E+00	9.91E-01	1.00E+00	6.76E-01	1.00E+00	8.93E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	3.12E-01	1.00E+00	5.69E-01	1.00E+00	positive regulation of metabolism	P
GO:0009894	32	1.60E-02	9.83E-01	1.13E-01	1.00E+00	6.20E-02	1.00E+00	4.70E-02	1.00E+00	5.49E-02	1.00E+00	1.01E-01	1.00E+00	8.56E-02	1.00E+00	4.48E-01	1.00E+00	regulation of catabolism	P
GO:0009896	10	7.35E-01	1.00E+00	7.57E-01	1.00E+00	6.01E-01	1.00E+00	4.13E-01	1.00E+00	8.49E-01	1.00E+00	7.82E-01	1.00E+00	8.71E-01	1.00E+00	9.36E-01	1.00E+00	positive regulation of catabolism	P
GO:0009897	148	9.99E-01	1.00E+00	9.83E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.27E-01	1.00E+00	1.75E-01	1.00E+00	external side of plasma membrane	C
GO:0009913	57	9.88E-01	1.00E+00	1.00E+00	1.00E+00	7.03E-01	1.00E+00	1.00E+00	1.00E+00	9.11E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.47E-01	1.00E+00	epidermal cell differentiation	P
GO:0009925	30	8.29E-01	1.00E+00	9.17E-01	1.00E+00	6.15E-01	1.00E+00	9.96E-01	1.00E+00	9.80E-01	1.00E+00	5.16E-01	1.00E+00	6.33E-01	1.00E+00	9.94E-01	1.00E+00	basal plasma membrane	C
GO:0009948	12	8.54E-01	1.00E+00	3.49E-01	1.00E+00	9.78E-01	1.00E+00	4.18E-01	1.00E+00	3.63E-01	1.00E+00	3.71E-01	1.00E+00	9.34E-01	1.00E+00	2.58E-01	1.00E+00	anterior/posterior axis specification	P
GO:0009952	138	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	anterior/posterior pattern formation	P
GO:0009953	50	9.89E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.07E-01	1.00E+00	9.76E-01	1.00E+00	9.13E-01	1.00E+00	6.85E-01	1.00E+00	dorsal/ventral pattern formation	P
GO:0009954	24	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	8.85E-01	1.00E+00	proximal/distal pattern formation	P
GO:0009966	510	9.88E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.76E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	6.64E-01	1.00E+00	8.66E-01	1.00E+00	regulation of signal transduction	P
GO:0009967	159	8.56E-01	1.00E+00	5.15E-01	1.00E+00	8.48E-01	1.00E+00	1.80E-01	1.00E+00	9.94E-01	1.00E+00	8.36E-01	1.00E+00	4.04E-01	1.00E+00	4.35E-01	1.00E+00	positive regulation of signal transduction	P
GO:0009968	125	8.37E-01	1.00E+00	9.61E-01	1.00E+00	8.23E-01	1.00E+00	9.57E-01	1.00E+00	8.23E-01	1.00E+00	9.50E-01	1.00E+00	4.13E-01	1.00E+00	7.19E-01	1.00E+00	negative regulation of signal transduction	P
GO:0009975	24	8.26E-01	1.00E+00	8.21E-01	1.00E+00	8.95E-01	1.00E+00	5.53E-01	1.00E+00	8.84E-01	1.00E+00	8.88E-01	1.00E+00	4.00E-01	1.00E+00	6.84E-01	1.00E+00	cyclase activity	F
GO:0009982	35	2.02E-01	1.00E+00	1.25E-01	1.00E+00	1.90E-01	1.00E+00	2.85E-01	1.00E+00	5.82E-01	1.00E+00	1.18E-01	1.00E+00	2.32E-01	1.00E+00	3.08E-01	1.00E+00	pseudouridine synthase activity	F
GO:0009986	276	9.99E-01	1.00E+00	9.75E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.94E-01	1.00E+00	6.82E-01	1.00E+00	2.10E-01	1.00E+00	cell surface	C
GO:0009987	12239	2.02E-20	0.00E+00	5.46E-42	0.00E+00	6.60E-09	0.00E+00	1.53E-25	0.00E+00	1.55E-12	0.00E+00	5.80E-19	0.00E+00	2.22E-06	2.00E-03	4.71E-15	0.00E+00	cellular process	P
GO:0009991	77	1.92E-02	9.83E-01	4.76E-01	1.00E+00	2.29E-02	1.00E+00	3.29E-01	1.00E+00	2.62E-01	1.00E+00	5.14E-01	1.00E+00	6.50E-02	1.00E+00	4.20E-01	1.00E+00	response to extracellular stimulus	P
GO:0009994	13	2.84E-01	1.00E+00	7.03E-02	1.00E+00	1.00E-01	1.00E+00	1.21E-01	1.00E+00	6.73E-01	1.00E+00	2.08E-01	1.00E+00	4.19E-01	1.00E+00	5.85E-02	1.00E+00	oocyte differentiation	P
GO:0010001	42	9.93E-01	1.00E+00	9.97E-01	1.00E+00	9.32E-01	1.00E+00	9.99E-01	1.00E+00	9.69E-01	1.00E+00	9.60E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	glial cell differentiation	P
GO:0010008	90	5.03E-02	1.00E+00	1.32E-03	7.50E-02	2.70E-01	1.00E+00	2.12E-03	4.50E-02	3.59E-01	1.00E+00	1.28E-01	1.00E+00	8.32E-02	1.00E+00	7.97E-03	4.48E-01	endosome membrane	C
GO:0010033	79	2.70E-01	1.00E+00	9.77E-01	1.00E+00	4.61E-01	1.00E+00	9.91E-01	1.00E+00	3.55E-01	1.00E+00	9.98E-01	1.00E+00	2.39E-01	1.00E+00	5.09E-01	1.00E+00	response to organic substance	P
GO:0010035	54	7.28E-01	1.00E+00	6.99E-01	1.00E+00	8.63E-01	1.00E+00	9.79E-01	1.00E+00	8.02E-01	1.00E+00	5.25E-01	1.00E+00	4.05E-01	1.00E+00	1.37E-01	1.00E+00	response to inorganic substance	P
GO:0010038	48	7.44E-01	1.00E+00	7.52E-01	1.00E+00	8.95E-01	1.00E+00	9.74E-01	1.00E+00	7.46E-01	1.00E+00	6.21E-01	1.00E+00	3.41E-01	1.00E+00	1.67E-01	1.00E+00	response to metal ion	P
GO:0010092	14	9.94E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	8.76E-01	1.00E+00	8.84E-01	1.00E+00	8.02E-01	1.00E+00	9.26E-01	1.00E+00	9.78E-01	1.00E+00	specification of organ identity	P
GO:0010165	14	5.45E-03	3.48E-01	6.12E-02	1.00E+00	4.29E-02	1.00E+00	8.99E-02	1.00E+00	3.48E-02	1.00E+00	9.75E-02	1.00E+00	1.90E-01	1.00E+00	1.15E-01	1.00E+00	response to X-ray	P
GO:0010181	12	1.24E-01	1.00E+00	3.28E-01	1.00E+00	3.26E-01	1.00E+00	6.87E-01	1.00E+00	7.57E-01	1.00E+00	4.24E-01	1.00E+00	4.92E-02	1.00E+00	1.88E-01	1.00E+00	FMN binding	F
GO:0010212	13	1.12E-02	9.83E-01	2.27E-02	1.00E+00	3.53E-02	1.00E+00	6.01E-02	1.00E+00	1.45E-01	1.00E+00	2.29E-02	1.00E+00	4.01E-02	8.34E-01	3.99E-02	1.00E+00	response to ionizing radiation	P
GO:0012501	767	6.28E-03	3.64E-01	4.59E-02	1.00E+00	4.80E-02	1.00E+00	4.61E-02	1.00E+00	1.60E-02	7.19E-01	2.31E-01	1.00E+00	7.50E-02	1.00E+00	1.20E-01	1.00E+00	programmed cell death	P
GO:0012502	185	8.29E-03	6.18E-01	2.43E-02	1.00E+00	9.49E-02	1.00E+00	2.84E-02	1.00E+00	8.13E-02	1.00E+00	1.22E-01	1.00E+00	2.65E-03	5.54E-02	9.16E-02	1.00E+00	induction of programmed cell death	P
GO:0012505	995	1.36E-08	9.73E-04	4.55E-12	0.00E+00	2.53E-04	1.61E-02	1.53E-09	0.00E+00	1.42E-05	1.56E-03	2.45E-05	2.00E-03	3.25E-05	2.00E-03	3.27E-07	1.94E-03	endomembrane system	C
GO:0012506	116	6.50E-03	3.64E-01	2.37E-02	1.00E+00	4.46E-02	1.00E+00	4.96E-02	1.00E+00	5.03E-02	1.00E+00	7.48E-02	1.00E+00	2.61E-02	6.06E-01	1.04E-01	1.00E+00	vesicle membrane	C
GO:0012510	11	4.89E-02	1.00E+00	1.84E-01	1.00E+00	3.42E-01	1.00E+00	3.84E-02	1.00E+00	7.85E-02	1.00E+00	3.18E-01	1.00E+00	1.02E-02	2.17E-01	3.41E-01	1.00E+00	trans-Golgi network transport vesicle memb	C
GO:0014003	11	4.42E-01	1.00E+00	4.37E-01	1.00E+00	1.79E-01	1.00E+00	4.85E-01	1.00E+00	4.95E-01	1.00E+00	3.83E-01	1.00E+00	8.68E-01	1.00E+00	4.57E-01	1.00E+00	oligodendrocyte development	P
GO:0014013	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of gliogenesis	P
GO:0014020	35	8.16E-01	1.00E+00	3.37E-01	1.00E+00	6.31E-01	1.00E+00	2.68E-01	1.00E+00	5.21E-01	1.00E+00	4.47E-01	1.00E+00	9.99E-01	1.00E+00	5.08E-01	1.00E+00	primary neural tube formation	P
GO:0014031	40	9.94E-01	1.00E+00	6.73E-01	1.00E+00	9.90E-01	1.00E+00	2.19E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	mesenchymal cell development	P
GO:0014032	29	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	neural crest cell development	P
GO:0014033	29	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	neural crest cell differentiation	P
GO:0014069	22	9.38E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.19E-01	1.00E+00	1.00E+00	1.00E+00	3.37E-01	1.00E+00	7.61E-01	1.00E+00	postsynaptic density	C
GO:0015002	25	1.54E-01	1.00E+00	7.74E-02	1.00E+00	5.86E-02	1.00E+00	3.32E-01	1.00E+00	1.31E-01	1.00E+00	8.33E-02	1.00E+00	7.86E-01	1.00E+00	1.77E-01	1.00E+00	heme-copper terminal oxidase activity	F
GO:0015020	16	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.29E-01	1.00E+00	9.00E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.24E-01	1.00E+00	9.99E-01	1.00E+00	glucuronosyltransferase activity	F
GO:0015031	796	9.81E-16	0.00E+00	1.13E-26	0.00E+00	6.45E-11	0.00E+00	1.09E-18	0.00E+00	4.56E-11	0.00E+00	5.43E-15	0.00E+00	6.41E-05	2.00E-03	2.94E-10	0.00E+00	protein transport	P
GO:0015035	11	6.68E-01	1.00E+00	6.81E-01	1.00E+00	5.58E-01	1.00E+00	8.16E-01	1.00E+00	4.53E-01	1.00E+00	9.84E-01	1.00E+00	9.27E-01	1.00E+00	1.68E-01	1.00E+00	protein disulfide oxidoreductase activity	F
GO:0015036	17	1.68E-01	1.00E+00	2.08E-01	1.00E+00	1.74E-01	1.00E+00	4.65E-01	1.00E+00	9.67E-02	1.00E+00	4.23E-01	1.00E+00	5.85E-01	1.00E+00	1.40E-01	1.00E+00	disulfide oxidoreductase activity	F

GO:0015057	33	5.37E-01	1.00E+00	8.49E-01	1.00E+00	1.38E-01	1.00E+00	9.61E-01	1.00E+00	5.71E-01	1.00E+00	9.80E-01	1.00E+00	9.94E-01	1.00E+00	2.41E-01	1.00E+00	thrombin receptor activity	F
GO:0015075	839	1.33E-01	1.00E+00	9.77E-01	1.00E+00	9.74E-01	1.00E+00	9.97E-01	1.00E+00	4.46E-01	1.00E+00	9.97E-01	1.00E+00	9.63E-04	2.40E-02	3.43E-01	1.00E+00	ion transporter activity	F
GO:0015077	124	7.34E-02	1.00E+00	4.08E-02	1.00E+00	4.57E-01	1.00E+00	3.40E-01	1.00E+00	5.37E-02	1.00E+00	4.02E-02	1.00E+00	3.14E-01	1.00E+00	1.45E-01	1.00E+00	monovalent inorganic cation transporter acti	F
GO:0015078	119	9.28E-02	1.00E+00	4.26E-02	1.00E+00	4.70E-01	1.00E+00	3.74E-01	1.00E+00	5.78E-02	1.00E+00	4.05E-02	1.00E+00	3.84E-01	1.00E+00	1.46E-01	1.00E+00	hydrogen ion transporter activity	F
GO:0015082	38	3.65E-01	1.00E+00	1.25E-01	1.00E+00	5.32E-01	1.00E+00	5.07E-02	1.00E+00	1.03E-01	1.00E+00	6.74E-01	1.00E+00	8.73E-01	1.00E+00	2.80E-01	1.00E+00	di-, tri-valent inorganic cation transporter ac	F
GO:0015103	39	4.65E-01	1.00E+00	7.66E-01	1.00E+00	7.26E-01	1.00E+00	8.10E-01	1.00E+00	8.21E-01	1.00E+00	6.36E-01	1.00E+00	5.08E-01	1.00E+00	7.80E-01	1.00E+00	inorganic anion transporter activity	F
GO:0015106	22	3.99E-01	1.00E+00	5.50E-01	1.00E+00	4.30E-01	1.00E+00	6.23E-01	1.00E+00	8.54E-01	1.00E+00	4.20E-01	1.00E+00	2.29E-01	1.00E+00	5.36E-01	1.00E+00	bicarbonate transporter activity	F
GO:0015108	23	3.92E-01	1.00E+00	6.44E-01	1.00E+00	4.64E-01	1.00E+00	6.90E-01	1.00E+00	8.31E-01	1.00E+00	4.60E-01	1.00E+00	2.07E-01	1.00E+00	6.91E-01	1.00E+00	chloride transporter activity	F
GO:0015116	11	2.01E-01	1.00E+00	9.79E-01	1.00E+00	2.81E-01	1.00E+00	9.70E-01	1.00E+00	1.05E-01	1.00E+00	8.79E-01	1.00E+00	3.36E-01	1.00E+00	9.94E-01	1.00E+00	sulfate transporter activity	F
GO:0015144	47	1.00E-01	1.00E+00	6.32E-01	1.00E+00	4.66E-01	1.00E+00	8.92E-01	1.00E+00	1.97E-01	1.00E+00	6.68E-01	1.00E+00	3.04E-02	7.53E-01	5.17E-01	1.00E+00	carbohydrate transporter activity	F
GO:0015145	14	1.88E-01	1.00E+00	9.46E-01	1.00E+00	6.37E-01	1.00E+00	9.95E-01	1.00E+00	2.70E-01	1.00E+00	9.11E-01	1.00E+00	1.38E-01	1.00E+00	9.56E-01	1.00E+00	monosaccharide transporter activity	F
GO:0015149	13	1.11E-01	1.00E+00	9.00E-01	1.00E+00	4.85E-01	1.00E+00	9.87E-01	1.00E+00	1.97E-01	1.00E+00	8.56E-01	1.00E+00	9.60E-02	1.00E+00	9.23E-01	1.00E+00	hexose transporter activity	F
GO:0015171	54	9.37E-01	1.00E+00	8.20E-01	1.00E+00	9.97E-01	1.00E+00	9.05E-01	1.00E+00	9.92E-01	1.00E+00	7.31E-01	1.00E+00	5.19E-01	1.00E+00	5.36E-01	1.00E+00	amino acid transporter activity	F
GO:0015172	10	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	9.91E-01	1.00E+00	9.91E-01	1.00E+00	9.87E-01	1.00E+00	9.01E-01	1.00E+00	9.09E-01	1.00E+00	acidic amino acid transporter activity	F
GO:0015175	12	3.57E-01	1.00E+00	3.72E-01	1.00E+00	7.49E-01	1.00E+00	5.51E-01	1.00E+00	5.42E-01	1.00E+00	6.73E-01	1.00E+00	1.43E-01	1.00E+00	1.67E-01	1.00E+00	neutral amino acid transporter activity	F
GO:0015179	30	9.95E-01	1.00E+00	9.41E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.94E-01	1.00E+00	9.03E-01	1.00E+00	6.70E-01	1.00E+00	2.95E-01	1.00E+00	L-amino acid transporter activity	F
GO:0015197	13	8.24E-02	1.00E+00	3.66E-01	1.00E+00	3.88E-01	1.00E+00	6.52E-01	1.00E+00	2.43E-01	1.00E+00	1.46E-01	1.00E+00	2.49E-02	5.60E-01	5.84E-01	1.00E+00	peptide transporter activity	F
GO:0015198	10	1.15E-01	1.00E+00	4.35E-01	1.00E+00	8.16E-01	1.00E+00	8.21E-01	1.00E+00	2.84E-01	1.00E+00	1.96E-01	1.00E+00	1.71E-02	4.71E-01	3.65E-01	1.00E+00	oligopeptide transporter activity	F
GO:0015203	19	9.86E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	9.06E-01	1.00E+00	2.65E-01	1.00E+00	4.67E-01	1.00E+00	polyamine transporter activity	F
GO:0015232	15	9.08E-01	1.00E+00	5.74E-01	1.00E+00	9.68E-01	1.00E+00	5.42E-01	1.00E+00	5.48E-01	1.00E+00	8.12E-01	1.00E+00	8.53E-01	1.00E+00	3.61E-01	1.00E+00	heme transporter activity	F
GO:0015238	30	4.80E-01	1.00E+00	5.83E-01	1.00E+00	9.91E-01	1.00E+00	9.13E-01	1.00E+00	5.30E-01	1.00E+00	5.29E-01	1.00E+00	1.01E-01	1.00E+00	2.72E-01	1.00E+00	drug transporter activity	F
GO:0015247	16	8.31E-01	1.00E+00	8.67E-01	1.00E+00	9.74E-01	1.00E+00	9.63E-01	1.00E+00	8.86E-01	1.00E+00	8.98E-01	1.00E+00	2.23E-01	1.00E+00	7.63E-01	1.00E+00	aminophospholipid transporter activity	F
GO:0015250	10	6.77E-01	1.00E+00	5.68E-01	1.00E+00	7.03E-01	1.00E+00	2.66E-01	1.00E+00	7.95E-01	1.00E+00	7.59E-01	1.00E+00	4.25E-01	1.00E+00	5.91E-01	1.00E+00	water channel activity	F
GO:0015267	441	3.41E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	6.95E-01	1.00E+00	1.00E+00	1.00E+00	2.27E-03	5.54E-02	7.43E-01	1.00E+00	channel or pore class transporter activity	F
GO:0015268	441	3.41E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	6.95E-01	1.00E+00	1.00E+00	1.00E+00	2.27E-03	5.54E-02	7.43E-01	1.00E+00	alpha-type channel activity	F
GO:0015269	12	8.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	2.55E-01	1.00E+00	8.29E-01	1.00E+00	calcium-activated potassium channel activit	F
GO:0015276	99	4.99E-01	1.00E+00	1.00E+00	1.00E+00	9.44E-01	1.00E+00	1.00E+00	1.00E+00	8.49E-01	1.00E+00	1.00E+00	1.00E+00	6.35E-03	2.01E-01	9.83E-01	1.00E+00	ligand-gated ion channel activity	F
GO:0015290	278	4.37E-01	1.00E+00	9.75E-01	1.00E+00	8.30E-01	1.00E+00	9.99E-01	1.00E+00	8.50E-01	1.00E+00	9.81E-01	1.00E+00	4.04E-02	8.34E-01	3.19E-01	1.00E+00	electrochemical potential-driven transporter	F
GO:0015291	278	4.37E-01	1.00E+00	9.75E-01	1.00E+00	8.30E-01	1.00E+00	9.99E-01	1.00E+00	8.50E-01	1.00E+00	9.81E-01	1.00E+00	4.04E-02	8.34E-01	3.19E-01	1.00E+00	porter activity	F
GO:0015293	167	6.51E-01	1.00E+00	9.99E-01	1.00E+00	7.01E-01	1.00E+00	9.98E-01	1.00E+00	9.05E-01	1.00E+00	1.00E+00	1.00E+00	2.80E-01	1.00E+00	6.84E-01	1.00E+00	symporter activity	F
GO:0015294	106	7.10E-01	1.00E+00	9.96E-01	1.00E+00	5.26E-01	1.00E+00	9.95E-01	1.00E+00	8.60E-01	1.00E+00	9.97E-01	1.00E+00	7.45E-01	1.00E+00	7.77E-01	1.00E+00	solute:cation symporter activity	F
GO:0015296	61	5.76E-01	1.00E+00	9.86E-01	1.00E+00	5.30E-01	1.00E+00	9.75E-01	1.00E+00	8.53E-01	1.00E+00	9.99E-01	1.00E+00	4.91E-01	1.00E+00	7.44E-01	1.00E+00	anion:cation symporter activity	F
GO:0015297	78	3.76E-01	1.00E+00	6.50E-01	1.00E+00	7.88E-01	1.00E+00	8.10E-01	1.00E+00	5.17E-01	1.00E+00	6.36E-01	1.00E+00	1.19E-01	1.00E+00	2.80E-01	1.00E+00	antiporter activity	F
GO:0015298	35	3.71E-01	1.00E+00	3.44E-01	1.00E+00	9.67E-01	1.00E+00	5.88E-01	1.00E+00	2.62E-01	1.00E+00	4.03E-01	1.00E+00	1.39E-01	1.00E+00	2.09E-01	1.00E+00	solute:cation antiporter activity	F
GO:0015299	35	3.71E-01	1.00E+00	3.44E-01	1.00E+00	9.67E-01	1.00E+00	5.88E-01	1.00E+00	2.62E-01	1.00E+00	4.03E-01	1.00E+00	1.39E-01	1.00E+00	2.09E-01	1.00E+00	solute:hydrogen antiporter activity	F
GO:0015300	36	3.81E-01	1.00E+00	4.39E-01	1.00E+00	9.80E-01	1.00E+00	6.67E-01	1.00E+00	3.22E-01	1.00E+00	4.71E-01	1.00E+00	1.73E-01	1.00E+00	2.83E-01	1.00E+00	solute:solute antiporter activity	F
GO:0015301	22	3.99E-01	1.00E+00	5.50E-01	1.00E+00	4.30E-01	1.00E+00	6.23E-01	1.00E+00	8.54E-01	1.00E+00	4.20E-01	1.00E+00	2.29E-01	1.00E+00	5.36E-01	1.00E+00	anion:anion antiporter activity	F
GO:0015307	22	1.99E-01	1.00E+00	2.20E-01	1.00E+00	8.99E-01	1.00E+00	5.43E-01	1.00E+00	3.16E-01	1.00E+00	2.38E-01	1.00E+00	6.77E-02	1.00E+00	1.77E-01	1.00E+00	drug:hydrogen antiporter activity	F
GO:0015370	103	7.30E-01	1.00E+00	9.97E-01	1.00E+00	4.48E-01	1.00E+00	9.92E-01	1.00E+00	8.42E-01	1.00E+00	9.96E-01	1.00E+00	8.80E-01	1.00E+00	8.79E-01	1.00E+00	solute:sodium symporter activity	F
GO:0015380	21	3.31E-01	1.00E+00	4.99E-01	1.00E+00	3.67E-01	1.00E+00	5.69E-01	1.00E+00	8.43E-01	1.00E+00	3.77E-01	1.00E+00	1.77E-01	1.00E+00	5.56E-01	1.00E+00	anion exchanger activity	F
GO:0015385	16	8.48E-01	1.00E+00	9.05E-01	1.00E+00	9.74E-01	1.00E+00	7.75E-01	1.00E+00	4.25E-01	1.00E+00	9.70E-01	1.00E+00	7.86E-01	1.00E+00	8.78E-01	1.00E+00	sodium:hydrogen antiporter activity	F
GO:0015399	111	3.18E-01	1.00E+00	6.93E-02	1.00E+00	9.20E-01	1.00E+00	2.25E-01	1.00E+00	2.06E-01	1.00E+00	1.44E-01	1.00E+00	3.34E-01	1.00E+00	2.08E-01	1.00E+00	primary active transporter activity	F
GO:0015405	111	3.18E-01	1.00E+00	6.93E-02	1.00E+00	9.20E-01	1.00E+00	2.25E-01	1.00E+00	2.06E-01	1.00E+00	1.44E-01	1.00E+00	3.34E-01	1.00E+00	2.08E-01	1.00E+00	P-P-bond-hydrolysis-driven transporter activ	F
GO:0015450	19	1.48E-01	1.00E+00	2.30E-02	1.00E+00	1.59E-01	1.00E+00	3.19E-02	1.00E+00	1.36E-01	1.00E+00	2.94E-01	1.00E+00	4.54E-01	1.00E+00	2.30E-01	1.00E+00	protein translocase activity	F
GO:0015457	26	6.97E-01	1.00E+00	9.92E-01	1.00E+00	9.58E-01	1.00E+00	9.99E-01	1.00E+00	1.80E-01	1.00E+00	9.90E-01	1.00E+00	7.92E-01	1.00E+00	6.90E-01	1.00E+00	auxiliary transport protein activity	F
GO:0015464	18	7.42E-01	1.00E+00	8.43E-01	1.00E+00	9.13E-01	1.00E+00	8.91E-01	1.00E+00	9.10E-01	1.00E+00	8.19E-01	1.00E+00	1.63E-01	1.00E+00	2.45E-01	1.00E+00	acetylcholine receptor activity	F
GO:0015485	11	4.33E-02	1.00E+00	5.43E-01	1.00E+00	2.44E-02	1.00E+00	3.30E-01	1.00E+00	9.69E-02	1.00E+00	8.39E-01	1.00E+00	1.65E-01	1.00E+00	1.97E-01	1.00E+00	cholesterol binding	F
GO:0015491	23	9.59E-01	1.00E+00	9.61E-01	1.00E+00	9.93E-01	1.00E+00	9.42E-01	1.00E+00	6.94E-01	1.00E+00	9.97E-01	1.00E+00	8.51E-01	1.00E+00	6.92E-01	1.00E+00	cation:cation antiporter activity	F
GO:0015520	22	1.99E-01	1.00E+00	2.20E-01	1.00E+00	8.99E-01	1.00E+00	5.43E-01	1.00E+00	3.16E-01	1.00E+00	2.38E-01	1.00E+00	6.77E-02	1.00E+00	1.77E-01	1.00E+00	tetracycline:hydrogen antiporter activity	F
GO:0015629	280	5.40E-04	5.20E-02	3.25E-02	1.00E+00	4.34E-02	1.00E+00	1.38E-01	1.00E+00	3.20E-03	1.35E-01	1.79E-01	1.00E+00	8.11E-04	2.40E-02	4.29E-02	1.00E+00	actin cytoskeleton	C
GO:0015630	408	2.75E-12	6.62E-04	1.78E-13	0.00E+00	1.82E-11	0.00E+00	2.05E-09	0.00E+00	6.52E-08	0.00E+00	8.27E-09	7.71E-04	1.76E-04	6.45E-03	2.02E-05	3.91E-03	microtubule cytoskeleton	C
GO:0015631	74	1.39E-06	2.00E-03	1.91E-07	2.66E-03	3.41E-04	1.61E-02	1.29E-03	4.40E-02	2.36E-06	7.65E-04	1.50E-05	2.00E-03	4.26E-03	7.75E-02	5.45E-04	2.10E-02	tubulin binding	F
GO:0015645	15	4.64E-01	1.00E+00	1.19E-01	1.00E+00	2.62E-01	1.00E+00	1.50E-01	1.00E+00	8.90E-01	1.00E+00	1.78E-01	1.00E+00	5.49E-01	1.00E+00	2.03E-01	1.00E+00	fatty-acid ligase activity	F
GO:0015662	68	4.98E-01	1.00E+00	5.29E-01	1.00E+00	9.84E-01	1.00E+00	7.81E-01	1.00E+00	5.93E-01	1.00E+00	3.74E-01	1.00E+00	1.49E-01	1.00E+00	7.10E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0015669	16	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gas transport	P
GO:0015671	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen transport	P
GO:0015672	438	5.56E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	7.11E-01	1.00E+00	1.00E+00	1.00E+00	4.98E-02	1.00E+00	9.55E-01	1.00E+00	monovalent inorganic cation transport	P
GO:0015674	224	2.43E-01	1.00E+00	6.44E-01	1.00E+00	8.82E-01	1.00E+00	4.22E-01	1.00E+00	5.12E-01	1.00E+00	9.94E-01	1.00E+00	1.75E-03	5.54E-02	8.80E-02	1.00E+00	di-, tri-valent inorganic cation transport	P
GO:0015698	178	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.80E-01	1.00E+00	1.00E+00	1.00E+00	5.09E-01	1.00E+00	9.92E-01	1.00E+00	inorganic anion transport	P
GO:0015711	15	1.99E-01	1.00E+00	8.26E-01	1.00E+00	2.17E-01	1.00E+00	4.98E-01	1.00E+00	6.04E-01	1.00E+00	9.71E-01	1.00E+00	1.34E-01	1.00E+00	4.50E-01	1.00E+00	organic anion transport	P
GO:0015749	41	7.97E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	8.32E-01	1.00E+00	9.99E-01	1.00E+00	1.98E-01	1.00E+00	5.18E-01	1.00E+00	monosaccharide transport	P
GO:0015758	40	7.94E-01	1.00E+00	9.69E-01	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	8.67E-01	1.00E+00	9.98E-01	1.00E+00	1.73E-01	1.00E+00	4.73E-01	1.00E+00	glucose transport	P
GO:0015800	16	9.29E-01	1.00E+00	8.23E-01	1.00E+00	9.27E-01	1.00E+00	8.54E-01	1.00E+00	9.21E-01	1.00E+00	7.01E-01	1.00E+00	9.43E-01	1.00E+00	8.28E-01	1.00E+00	acidic amino acid transport	P
GO:0015804	11	8.85E-01	1.00E+00	6.22E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	9.40E-01	1.00E+00	8.88E-01	1.00E+00	3.22E-01	1.00E+00	1.26E-01	1.00E+00	neutral amino acid transport	P
GO:0015807	15	6.00E-01	1.00E+00	7.82E-01	1.00E+00	9.95E-01	1.00E+00	6.29E-01	1.00E+00	8.30E-01	1.00E+00	9.82E-01	1.00E+00	3.82E-01	1.00E+00	2.94E-01	1.00E+00	L-amino acid transport	P
GO:0015813	16	9.29E-01	1.00E+00	8.23E-01	1.00E+00	9.27E-01	1.00E+00	8.54E-01	1.00E+00	9.21E-01	1.00E+00	7.01E-01	1.00E+00	9.43E-01	1.00E+00	8.28E-01	1.00E+00	glutamate transport	P
GO:0015833	58	4.43E-01	1.00E+00	6.13E-01	1.00E+00	8.22E-01	1.00E+00	8.93E-01	1.00E+00	1.61E-01	1.00E+00	3.90E-01	1.00E+00	4.63E-01	1.00E+00	3.43E-01	1.00E+00	peptide transport	P
GO:0015837	88	8.08E-01	1.00E+00	5.54E-01	1.00E+00	9.54E-01	1.00E+00	8.54E-01	1.00E+00	9.67E-01	1.00E+00	5.30E-01	1.00E+00	3.32E-01	1.00E+00	9.76E-02	1.00E+00	amine transport	P
GO:0015849	133	7.08E-01	1.00E+00	9.12E-01	1.00E+00	8.23E-01	1.00E+00	9.52E-01	1.00E+00	9.24E-01	1.00E+00	9.52E-01	1.00E+00	4.87E-01	1.00E+00	3.55E-01	1.00E+00	organic acid transport	P
GO:0015886	15	9.08E-01	1.00E+00	5.74E-01	1.00E+00	9.68E-01	1.00E+00	5.42E-01	1.00E+00	5.48E-01	1.00E+00	8.12E-01	1.00E+00	8.53E-01	1.00E+00	3.61E-01	1.00E+00	heme transport	P
GO:0015893	29	3.07E-01	1.00E+00	4.86E-01	1.00E+00	9.88E-01	1.00E+00	9.20E-01	1.00E+00	2.80E-01	1.00E+00	5.41E-01	1.00E+00	5.98E-02	1.00E+00	1.04E-01	1.00E+00	drug transport	P
GO:0015904	22	1.99E-01	1.00E+00	2.20E-01	1.00E+00	8.99E-01	1.00E+00	5.43E-01	1.00E+00	3.16E-01	1.00E+00	2.38E-01	1.00E+00	6.77E-02	1.00E+00	1.77E-01	1.00E+00	tetracycline transport	P
GO:0015914	20	4.88E-01	1.00E+00	9.09E-01	1.00E+00	8.61E-01	1.00E+00	9.49E-01	1.00E+00	9.48E-01	1.00E+00	9.89E-01	1.00E+00	1.24E-01	1.00E+00	4.79E-01	1.00E+00	phospholipid transport	P
GO:0015918	16	2.45E-01	1.00E+00	6.28E-01	1.00E+00	2.94E-01	1.00E+00	7.04E-01	1.00E+00	2.41E-01	1.00E+00	5.00E-01	1.00E+00	2.87E-01	1.00E+00	5.42E-01	1.00E+00	sterol transport	P
GO:0015923	16	1.31E-01	1.00E+00	1.48E-02	1.00E+00	2.90E-01	1.00E+00	2.36E-02	7.69E-01	1.16E-01	1.00E+00	7.24E-01	1.00E+00	3.16E-01	1.00E+00	3.25E-03	2.16E-01	mannosidase activity	F

GO:0015924	10	1.84E-01	1.00E+00	6.90E-02	1.00E+00	3.33E-01	1.00E+00	8.73E-02	1.00E+00	2.43E-01	1.00E+00	6.45E-01	1.00E+00	2.83E-01	1.00E+00	9.29E-04	3.30E-02	mannosyl-oligosaccharide mannosidase act	F
GO:0015929	15	1.73E-01	1.00E+00	4.49E-01	1.00E+00	2.94E-02	1.00E+00	3.96E-01	1.00E+00	9.16E-01	1.00E+00	7.23E-01	1.00E+00	3.73E-01	1.00E+00	1.58E-01	1.00E+00	hexosaminidase activity	F
GO:0015931	68	1.62E-04	1.90E-02	2.76E-07	2.66E-03	1.09E-04	1.61E-02	1.67E-07	9.57E-04	4.39E-03	1.35E-01	3.27E-05	2.00E-03	3.71E-01	1.00E+00	3.18E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	P
GO:0015932	12	4.78E-01	1.00E+00	1.11E-01	1.00E+00	6.37E-01	1.00E+00	2.59E-01	1.00E+00	2.10E-01	1.00E+00	1.25E-01	1.00E+00	4.06E-01	1.00E+00	2.15E-01	1.00E+00	nucleobase, nucleoside, nucleotide and nuc	F
GO:0015934	30	5.46E-01	1.00E+00	6.06E-02	1.00E+00	4.70E-01	1.00E+00	4.77E-01	1.00E+00	3.84E-01	1.00E+00	4.65E-02	1.00E+00	9.71E-01	1.00E+00	2.42E-01	1.00E+00	large ribosomal subunit	C
GO:0015935	30	1.37E-01	1.00E+00	1.53E-02	1.00E+00	4.29E-02	1.00E+00	4.03E-02	1.00E+00	7.74E-01	1.00E+00	1.30E-01	1.00E+00	5.79E-01	1.00E+00	3.84E-02	1.00E+00	small ribosomal subunit	C
GO:0015936	11	1.75E-01	1.00E+00	4.06E-02	1.00E+00	2.73E-01	1.00E+00	2.09E-01	1.00E+00	3.04E-01	1.00E+00	2.64E-01	1.00E+00	2.56E-01	1.00E+00	6.29E-02	1.00E+00	coenzyme A metabolism	P
GO:0015980	175	4.55E-05	6.00E-03	1.07E-01	1.00E+00	1.12E-02	4.74E-01	2.96E-01	1.00E+00	1.13E-03	4.40E-02	5.40E-02	1.00E+00	5.14E-04	1.89E-02	2.37E-01	1.00E+00	energy derivation by oxidation of organic co	P
GO:0015985	27	8.87E-01	1.00E+00	8.20E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	3.66E-01	1.00E+00	8.43E-01	1.00E+00	9.48E-01	1.00E+00	5.44E-01	1.00E+00	energy coupled proton transport, down elec	P
GO:0015986	27	8.87E-01	1.00E+00	8.20E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	3.66E-01	1.00E+00	8.43E-01	1.00E+00	9.48E-01	1.00E+00	5.44E-01	1.00E+00	ATP synthesis coupled proton transport	P
GO:0015988	10	3.72E-01	1.00E+00	1.98E-01	1.00E+00	9.22E-01	1.00E+00	3.21E-01	1.00E+00	1.67E-01	1.00E+00	6.74E-02	1.00E+00	6.98E-01	1.00E+00	3.70E-01	1.00E+00	energy coupled proton transport, against ele	P
GO:0015992	70	3.07E-01	1.00E+00	1.37E-01	1.00E+00	9.81E-01	1.00E+00	2.98E-01	1.00E+00	2.31E-01	1.00E+00	1.45E-01	1.00E+00	1.64E-01	1.00E+00	2.96E-01	1.00E+00	proton transport	P
GO:0016010	13	7.53E-01	1.00E+00	7.75E-01	1.00E+00	9.88E-01	1.00E+00	7.63E-01	1.00E+00	4.24E-01	1.00E+00	7.47E-01	1.00E+00	3.73E-01	1.00E+00	7.06E-01	1.00E+00	dystrophin-associated glycoprotein complex	C
GO:0016020	6607	2.08E-02	1.00E+00	1.48E-01	1.00E+00	9.73E-01	1.00E+00	7.93E-01	1.00E+00	3.43E-01	1.00E+00	9.71E-01	1.00E+00	2.24E-08	6.33E-04	1.39E-09	0.00E+00	membrane	C
GO:0016021	4783	6.94E-01	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	1.00E+00	1.00E+00	8.56E-05	2.00E-03	1.26E-03	4.40E-02	integral to membrane	C
GO:0016023	349	8.54E-04	9.30E-02	7.86E-03	5.59E-01	2.41E-02	1.00E+00	4.32E-02	1.00E+00	1.97E-02	7.19E-01	2.98E-02	1.00E+00	1.29E-02	4.39E-01	2.66E-02	1.00E+00	cytoplasmic membrane-bound vesicle	C
GO:0016032	30	3.64E-01	1.00E+00	8.20E-01	1.00E+00	8.99E-01	1.00E+00	7.78E-01	1.00E+00	1.94E-01	1.00E+00	9.16E-01	1.00E+00	2.31E-01	1.00E+00	3.46E-01	1.00E+00	viral life cycle	P
GO:0016042	114	7.10E-03	3.64E-01	9.99E-02	1.00E+00	6.75E-03	2.83E-01	3.85E-01	1.00E+00	3.88E-01	1.00E+00	4.26E-01	1.00E+00	6.51E-03	2.01E-01	4.43E-03	2.58E-01	lipid catabolism	P
GO:0016043	2082	2.93E-21	0.00E+00	1.69E-27	0.00E+00	4.15E-14	0.00E+00	4.31E-23	0.00E+00	1.73E-13	0.00E+00	4.12E-13	0.00E+00	3.18E-07	6.33E-04	1.80E-08	0.00E+00	cell organization and biogenesis	P
GO:0016044	87	2.65E-03	1.39E-01	1.43E-01	1.00E+00	1.68E-02	8.10E-01	5.03E-02	1.00E+00	3.23E-02	1.00E+00	3.48E-01	1.00E+00	6.69E-02	1.00E+00	4.41E-01	1.00E+00	membrane organization and biogenesis	P
GO:0016049	147	3.13E-01	1.00E+00	8.32E-01	1.00E+00	5.03E-01	1.00E+00	4.95E-01	1.00E+00	9.55E-01	1.00E+00	9.95E-01	1.00E+00	2.22E-02	5.60E-01	5.35E-01	1.00E+00	cell growth	P
GO:0016051	118	2.12E-02	1.00E+00	3.01E-01	1.00E+00	4.36E-01	1.00E+00	5.84E-01	1.00E+00	7.43E-02	1.00E+00	2.72E-01	1.00E+00	5.19E-03	9.40E-02	1.34E-01	1.00E+00	carbohydrate biosynthesis	P
GO:0016052	92	3.23E-02	1.00E+00	2.47E-01	1.00E+00	1.32E-01	1.00E+00	4.04E-01	1.00E+00	2.81E-01	1.00E+00	1.70E-01	1.00E+00	4.00E-02	8.34E-01	4.15E-01	1.00E+00	carbohydrate catabolism	P
GO:0016053	93	4.17E-01	1.00E+00	5.72E-01	1.00E+00	9.28E-01	1.00E+00	9.01E-01	1.00E+00	2.84E-01	1.00E+00	5.43E-01	1.00E+00	1.39E-01	1.00E+00	8.64E-02	1.00E+00	organic acid biosynthesis	P
GO:0016055	122	9.09E-01	1.00E+00	8.22E-01	1.00E+00	9.11E-01	1.00E+00	6.83E-01	1.00E+00	9.34E-01	1.00E+00	8.83E-01	1.00E+00	7.30E-01	1.00E+00	7.27E-01	1.00E+00	Wnt receptor signaling pathway	P
GO:0016064	118	7.81E-01	1.00E+00	8.87E-01	1.00E+00	8.50E-01	1.00E+00	8.54E-01	1.00E+00	9.67E-01	1.00E+00	7.37E-01	1.00E+00	4.15E-01	1.00E+00	9.33E-01	1.00E+00	immunoglobulin mediated immune response	P
GO:0016068	49	9.98E-01	1.00E+00	9.70E-01	1.00E+00	9.88E-01	1.00E+00	8.86E-01	1.00E+00	9.93E-01	1.00E+00	8.16E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	type I hypersensitivity	P
GO:0016070	516	3.03E-12	6.62E-04	3.52E-28	0.00E+00	5.11E-10	0.00E+00	5.56E-23	0.00E+00	3.61E-08	0.00E+00	3.92E-17	0.00E+00	6.23E-02	1.00E+00	2.57E-04	1.70E-02	RNA metabolism	P
GO:0016071	271	7.75E-08	9.73E-04	2.45E-16	0.00E+00	9.92E-07	9.88E-04	6.36E-15	0.00E+00	2.85E-04	8.00E-03	7.51E-11	0.00E+00	2.18E-01	1.00E+00	4.62E-02	1.00E+00	mRNA metabolism	P
GO:0016072	68	2.74E-03	1.39E-01	2.49E-03	1.87E-01	6.98E-02	1.00E+00	1.89E-04	1.10E-02	6.60E-03	1.65E-01	8.11E-02	1.00E+00	1.24E-01	1.00E+00	7.39E-01	1.00E+00	rRNA metabolism	P
GO:0016073	12	3.28E-01	1.00E+00	2.00E-03	1.62E-01	3.89E-01	1.00E+00	3.39E-03	1.42E-01	3.86E-01	1.00E+00	2.34E-01	1.00E+00	3.92E-01	1.00E+00	1.69E-01	1.00E+00	snRNA metabolism	P
GO:0016079	15	8.40E-02	1.00E+00	6.51E-01	1.00E+00	1.73E-01	1.00E+00	4.43E-01	1.00E+00	2.19E-01	1.00E+00	9.81E-01	1.00E+00	1.92E-01	1.00E+00	3.07E-01	1.00E+00	synaptic vesicle exocytosis	P
GO:0016089	48	2.64E-01	1.00E+00	5.36E-01	1.00E+00	2.57E-01	1.00E+00	6.06E-01	1.00E+00	5.08E-01	1.00E+00	4.22E-01	1.00E+00	2.18E-01	1.00E+00	6.46E-01	1.00E+00	aromatic amino acid family biosynthesis, sh	P
GO:0016125	82	3.50E-01	1.00E+00	5.09E-01	1.00E+00	5.01E-01	1.00E+00	8.59E-01	1.00E+00	4.77E-01	1.00E+00	3.27E-01	1.00E+00	2.58E-01	1.00E+00	4.84E-01	1.00E+00	sterol metabolism	P
GO:0016126	35	3.38E-01	1.00E+00	2.12E-01	1.00E+00	4.39E-01	1.00E+00	3.83E-01	1.00E+00	4.26E-01	1.00E+00	1.10E-01	1.00E+00	3.40E-01	1.00E+00	7.37E-01	1.00E+00	sterol biosynthesis	P
GO:0016180	12	3.28E-01	1.00E+00	2.00E-03	1.62E-01	3.89E-01	1.00E+00	3.39E-03	1.42E-01	3.86E-01	1.00E+00	2.34E-01	1.00E+00	3.92E-01	1.00E+00	1.69E-01	1.00E+00	snRNA processing	P
GO:0016192	499	5.47E-09	9.73E-04	3.43E-07	2.66E-03	6.35E-04	3.00E-02	4.03E-05	5.41E-03	1.02E-04	6.00E-03	2.37E-03	1.43E-01	6.11E-07	8.79E-04	1.31E-05	3.91E-03	vesicle-mediated transport	P
GO:0016197	33	1.80E-01	1.00E+00	3.55E-02	1.00E+00	3.66E-01	1.00E+00	1.73E-01	1.00E+00	8.01E-02	1.00E+00	7.24E-02	1.00E+00	2.68E-01	1.00E+00	4.00E-02	1.00E+00	endosome transport	P
GO:0016202	15	3.57E-01	1.00E+00	6.15E-01	1.00E+00	3.22E-01	1.00E+00	6.67E-01	1.00E+00	4.52E-01	1.00E+00	6.71E-01	1.00E+00	4.63E-01	1.00E+00	5.38E-01	1.00E+00	regulation of striated muscle development	P
GO:0016208	24	9.88E-01	1.00E+00	5.02E-01	1.00E+00	1.00E+00	1.00E+00	8.44E-01	1.00E+00	6.94E-01	1.00E+00	4.52E-01	1.00E+00	8.52E-01	1.00E+00	1.68E-01	1.00E+00	AMP binding	F
GO:0016209	59	1.41E-01	1.00E+00	6.71E-02	1.00E+00	9.58E-01	1.00E+00	2.41E-01	1.00E+00	2.91E-01	1.00E+00	1.57E-01	1.00E+00	2.49E-02	5.60E-01	1.80E-01	1.00E+00	antioxidant activity	F
GO:0016229	36	6.93E-01	1.00E+00	8.54E-01	1.00E+00	7.29E-01	1.00E+00	9.89E-01	1.00E+00	5.13E-01	1.00E+00	6.33E-01	1.00E+00	6.43E-01	1.00E+00	5.67E-01	1.00E+00	steroid dehydrogenase activity	F
GO:0016234	10	1.71E-01	1.00E+00	2.05E-01	1.00E+00	1.57E-01	1.00E+00	1.83E-01	1.00E+00	1.03E-01	1.00E+00	3.88E-01	1.00E+00	7.28E-01	1.00E+00	7.53E-02	1.00E+00	inclusion body	C
GO:0016236	18	5.46E-02	1.00E+00	4.74E-03	3.82E-01	9.12E-02	1.00E+00	6.40E-02	1.00E+00	2.46E-01	1.00E+00	2.78E-01	1.00E+00	4.87E-02	1.00E+00	2.38E-02	1.00E+00	macroautophagy	P
GO:0016247	25	6.63E-01	1.00E+00	9.91E-01	1.00E+00	9.45E-01	1.00E+00	9.98E-01	1.00E+00	1.60E-01	1.00E+00	9.88E-01	1.00E+00	7.97E-01	1.00E+00	7.80E-01	1.00E+00	channel regulator activity	F
GO:0016251	19	3.54E-02	1.00E+00	5.58E-04	7.30E-02	5.08E-03	1.88E-01	4.80E-05	5.41E-03	1.31E-01	1.00E+00	6.58E-02	1.00E+00	2.35E-01	1.00E+00	1.23E-01	1.00E+00	general RNA polymerase II transcription fac	F
GO:0016265	799	4.90E-03	3.48E-01	5.02E-02	1.00E+00	4.67E-02	1.00E+00	5.26E-02	1.00E+00	3.06E-02	1.00E+00	2.21E-01	1.00E+00	4.13E-02	8.34E-01	1.16E-01	1.00E+00	death	P
GO:0016272	10	1.51E-01	1.00E+00	1.15E-05	7.00E-03	9.40E-01	1.00E+00	6.87E-03	3.78E-01	2.40E-02	1.00E+00	3.28E-01	1.00E+00	2.27E-01	1.00E+00	1.18E-03	4.40E-02	prefoldin complex	C
GO:0016278	24	8.80E-04	9.30E-02	8.22E-06	3.00E-03	4.18E-04	1.61E-02	4.50E-04	1.30E-02	1.20E-02	4.21E-01	1.73E-05	2.00E-03	3.55E-01	1.00E+00	9.15E-03	4.48E-01	lysine N-methyltransferase activity	F
GO:0016279	24	8.80E-04	9.30E-02	8.22E-06	3.00E-03	4.18E-04	1.61E-02	4.50E-04	1.30E-02	1.20E-02	4.21E-01	1.73E-05	2.00E-03	3.55E-01	1.00E+00	9.15E-03	4.48E-01	protein-lysine N-methyltransferase activity	F
GO:0016284	12	5.82E-01	1.00E+00	5.50E-01	1.00E+00	3.65E-01	1.00E+00	4.12E-01	1.00E+00	6.80E-01	1.00E+00	4.43E-01	1.00E+00	7.66E-01	1.00E+00	9.34E-01	1.00E+00	alanine aminopeptidase activity	F
GO:0016289	21	8.48E-01	1.00E+00	2.28E-01	1.00E+00	5.09E-01	1.00E+00	7.49E-01	1.00E+00	7.93E-01	1.00E+00	2.27E-01	1.00E+00	6.31E-01	1.00E+00	4.34E-02	1.00E+00	CoA hydrolase activity	F
GO:0016290	15	5.05E-01	1.00E+00	1.74E-01	1.00E+00	2.91E-01	1.00E+00	3.83E-01	1.00E+00	6.74E-01	1.00E+00	1.70E-01	1.00E+00	3.49E-01	1.00E+00	9.75E-02	1.00E+00	palmitoyl-CoA hydrolase activity	F
GO:0016298	79	1.28E-01	1.00E+00	4.46E-01	1.00E+00	4.08E-02	1.00E+00	6.38E-01	1.00E+00	9.83E-01	1.00E+00	6.02E-01	1.00E+00	3.70E-02	7.83E-01	9.09E-02	1.00E+00	lipase activity	F
GO:0016301	963	1.21E-05	5.00E-03	5.18E-07	2.66E-03	1.89E-04	1.61E-02	5.82E-04	2.70E-02	1.91E-03	5.40E-02	7.78E-06	2.00E-03	6.77E-03	2.01E-01	1.25E-03	4.40E-02	kinase activity	F
GO:0016303	11	1.40E-01	1.00E+00	1.72E-01	1.00E+00	3.09E-01	1.00E+00	3.87E-01	1.00E+00	2.46E-01	1.00E+00	1.15E-01	1.00E+00	1.74E-01	1.00E+00	1.30E-01	1.00E+00	phosphatidylinositol 3-kinase activity	F
GO:0016310	828	3.05E-02	1.00E+00	5.41E-04	7.30E-02	3.77E-01	1.00E+00	6.52E-02	1.00E+00	1.04E-01	1.00E+00	3.64E-03	1.43E-01	1.24E-02	4.39E-01	1.30E-03	4.40E-02	phosphorylation	P
GO:0016311	148	4.21E-02	1.00E+00	6.30E-03	5.59E-01	1.98E-01	1.00E+00	3.84E-02	1.00E+00	7.18E-02	1.00E+00	1.49E-01	1.00E+00	2.84E-02	6.06E-01	2.11E-03	6.30E-02	dephosphorylation	P
GO:0016323	139	5.08E-01	1.00E+00	9.68E-01	1.00E+00	5.03E-01	1.00E+00	9.17E-01	1.00E+00	8.16E-01	1.00E+00	9.05E-01	1.00E+00	1.45E-01	1.00E+00	9.57E-01	1.00E+00	basolateral plasma membrane	C
GO:0016324	104	6.36E-01	1.00E+00	1.00E+00	1.00E+00	8.43E-01	1.00E+00	9.96E-01	1.00E+00	6.89E-01	1.00E+00	9.98E-01	1.00E+00	4.15E-01	1.00E+00	9.80E-01	1.00E+00	apical plasma membrane	C
GO:0016327	110	6.79E-01	1.00E+00	2.92E-01	1.00E+00	6.98E-01	1.00E+00	2.28E-01	1.00E+00	9.84E-01	1.00E+00	9.17E-01	1.00E+00	4.72E-02	1.00E+00	8.35E-02	1.00E+00	apicolateral plasma membrane	C
GO:0016331	68	9.96E-01	1.00E+00	6.29E-01	1.00E+00	9.91E-01	1.00E+00	6.22E-01	1.00E+00	9.87E-01	1.00E+00	6.57E-01	1.00E+00	9.90E-01	1.00E+00	6.80E-01	1.00E+00	morphogenesis of embryonic epithelium	P
GO:0016337	192	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.06E-01	1.00E+00	9.94E-01	1.00E+00	cell-cell adhesion	P
GO:0016338	15	6.10E-01	1.00E+00	1.00E+00	1.00E+00	6.34E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	1.52E-01	1.00E+00	7.03E-01	1.00E+00	calcium-independent cell-cell adhesion	P
GO:0016339	11	9.15E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	9.49E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	3.57E-01	1.00E+00	7.05E-01	1.00E+00	calcium-dependent cell-cell adhesion	P
GO:0016358	41	1.78E-01	1.00E+00	7.61E-01	1.00E+00	2.08E-01	1.00E+00	4.90E-01	1.00E+00	1.75E-01	1.00E+00	9.10E-01	1.00E+00	2.65E-01	1.00E+00	7.26E-01	1.00E+00	dendrite development	P
GO:0016363	39	5.07E-03	3.48E-01	9.37E-04	7.30E-02	4.39E-03	1.88E-01	7.89E-04	2.70E-02	1.64E-01	1.00E+00	1.54E-02	1.00E+00	1.63E-01	1.00E+00	4.49E-02	1.00E+00	nuclear matrix	C
GO:0016407	64	1.45E-01	1.00E+00	3.28E-02	1.00E+00	6.59E-02	1.00E+00	2.37E-02	7.69E-01	2.52E-01	1.00E+00	1.94E-01	1.00E+00	6.54E-01	1.00E+00	1.72E-01	1.00E+00	acetyltransferase activity	F
GO:0016408	13	1.88E-01	1.00E+00	3.92E-02	1.00E+00	1.72E-01	1.00E+00	9.06E-02	1.00E+00	1.82E-01	1.00E+00	2.32E-02	1.00E+00	4.29E-01	1.00E+00	1.18E-01	1.00E+00	C-acyltransferase activity	F
GO:0016409	16	3.36E-01	1.00E+00	3.97E-01	1.00E+00	1.71E-01	1.00E+00	1.87E-01	1.00E+00	7.88E-01	1.00E+00	6.57E-01	1.00E+00	6.24E-01	1.00E+00	3.72E-01	1.00E+00	palmitoyltransferase activity	F
GO:0016410	65	1.99E-01	1.00E+00	1.54E-02	1.00E+00	1.59E-01	1.00E+00	1.78E-02	7.69E-01	4.66E-01	1.00E+00	2.29E-01	1.00E+00	5.62E-01	1.00E+00	6.33E-02	1.00E+00	N-acyltransferase activity	F
GO:0016411	14	2.00E-01	1.00E+00	6.90E-01	1.00E+00	6.05E-01	1.00E+00	1.41E-01	1.00E+00	3.71E-01	1.00E+00	9.42E-01	1.00E+00	1.47E-01	1.00E+00	8.37E-01	1.00E+00	acylglycerol O-acyltransferase activity	F
GO:0016439	29	3.18E-01	1.00E+00	5.38E-01	1.00E+00	3.14E-01	1.00E+00	5.81E-01	1.00E+00	5.77E-01	1.00E+00	3.96E-01	1.00E+00	2.69E-01	1.00E+00	5.61E-01	1.00E+00	tRNA-pseudouridine synthase activity	F
GO:0016444	28	9.04E-03	9.83E-01	2.12E-02	1.00E+00	4.45E-02	1.00E+00	5.88E-02	1.00E+00	1.55E-01	1.00E+00	2.56E-01	1.00E+00	1.54E-02	4.39E-01	2.95E-03	2.16E-01	somatic cell DNA recombination	P
GO:0016445	30	1.77E-02	9.83E-01	2.33E-02	1.00E+00	3.96E-02	1.00E+00	6.16E-02	1.00E+00	2.24E-01	1.00E+00	2.44E-01	1.00E+00	3.38E-02	7.53E-01	5.70E-03	2.58E-01	somatic diversification of immunoglobulins	P

GO:0016447	28	9.04E-03	9.83E-01	2.12E-02	1.00E+00	4.45E-02	1.00E+00	5.88E-02	1.00E+00	1.55E-01	1.00E+00	2.56E-01	1.00E+00	1.54E-02	4.39E-01	2.95E-03	2.16E-01	somatic recombination of immunoglobulin g		P
GO:0016458	33	9.29E-02	1.00E+00	8.57E-04	7.30E-02	1.57E-01	1.00E+00	4.36E-02	1.00E+00	7.77E-02	1.00E+00	9.03E-03	3.55E-01	2.88E-01	1.00E+00	3.74E-03	2.16E-01	gene silencing		P
GO:0016459	57	1.06E-01	1.00E+00	9.23E-01	1.00E+00	3.53E-01	1.00E+00	9.90E-01	1.00E+00	4.81E-01	1.00E+00	9.60E-01	1.00E+00	8.62E-03	2.17E-01	2.68E-01	1.00E+00	myosin complex		C
GO:0016462	730	1.51E-07	9.73E-04	5.99E-10	2.66E-03	2.99E-04	1.61E-02	3.88E-06	1.00E-03	9.87E-08	0.00E+00	2.17E-08	7.71E-04	4.01E-03	7.75E-02	8.99E-05	3.91E-03	pyrophosphatase activity		F
GO:0016469	58	4.95E-01	1.00E+00	2.79E-01	1.00E+00	9.75E-01	1.00E+00	6.66E-01	1.00E+00	1.40E-01	1.00E+00	1.63E-01	1.00E+00	7.56E-01	1.00E+00	4.33E-01	1.00E+00	proton-transporting two-sector ATPase com		C
GO:0016477	350	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.08E-01	1.00E+00	9.26E-01	1.00E+00	cell migration		P
GO:0016481	315	3.77E-01	1.00E+00	3.80E-02	1.00E+00	4.86E-01	1.00E+00	2.18E-02	7.69E-01	5.76E-01	1.00E+00	1.68E-01	1.00E+00	3.19E-01	1.00E+00	2.13E-01	1.00E+00	negative regulation of transcription		P
GO:0016485	108	4.61E-01	1.00E+00	2.10E-01	1.00E+00	5.26E-01	1.00E+00	3.16E-01	1.00E+00	4.57E-01	1.00E+00	3.85E-01	1.00E+00	4.61E-01	1.00E+00	8.80E-02	1.00E+00	protein processing		P
GO:0016491	919	3.27E-03	1.86E-01	2.75E-03	1.87E-01	2.57E-01	1.00E+00	1.21E-01	1.00E+00	5.29E-03	1.65E-01	5.36E-03	2.02E-01	2.14E-03	5.54E-02	1.45E-02	9.40E-01	oxidoreductase activity		F
GO:0016493	34	2.10E-01	1.00E+00	4.11E-01	1.00E+00	6.37E-01	1.00E+00	6.88E-01	1.00E+00	2.08E-01	1.00E+00	8.68E-01	1.00E+00	1.94E-01	1.00E+00	4.31E-02	1.00E+00	C-C chemokine receptor activity		F
GO:0016494	28	2.58E-01	1.00E+00	3.12E-01	1.00E+00	7.52E-01	1.00E+00	7.17E-01	1.00E+00	6.92E-02	1.00E+00	7.22E-01	1.00E+00	3.79E-01	1.00E+00	2.58E-02	1.00E+00	C-X-C chemokine receptor activity		F
GO:0016500	25	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.02E-01	1.00E+00	9.76E-01	1.00E+00	8.81E-01	1.00E+00	protein-hormone receptor activity		F
GO:0016502	109	9.91E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.94E-01	1.00E+00	1.00E+00	1.00E+00	8.66E-01	1.00E+00	2.67E-01	1.00E+00	nucleotide receptor activity		F
GO:0016503	27	1.00E+00	1.00E+00	5.32E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	9.59E-02	1.00E+00	1.00E+00	1.00E+00	5.51E-01	1.00E+00	pheromone receptor activity		F
GO:0016504	15	2.54E-01	1.00E+00	1.03E-01	1.00E+00	2.67E-01	1.00E+00	1.74E-01	1.00E+00	1.26E-01	1.00E+00	4.35E-02	1.00E+00	6.38E-01	1.00E+00	3.86E-01	1.00E+00	protease activator activity		F
GO:0016525	20	8.95E-01	1.00E+00	1.00E+00	1.00E+00	5.71E-01	1.00E+00	9.70E-01	1.00E+00	9.54E-01	1.00E+00	9.94E-01	1.00E+00	6.54E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of angiogenesis		P
GO:0016528	30	2.82E-01	1.00E+00	1.32E-01	1.00E+00	4.21E-01	1.00E+00	2.09E-01	1.00E+00	8.59E-01	1.00E+00	1.67E-01	1.00E+00	8.04E-02	1.00E+00	1.19E-01	1.00E+00	sarcoplasm		C
GO:0016529	27	2.15E-01	1.00E+00	8.76E-02	1.00E+00	5.41E-01	1.00E+00	1.26E-01	1.00E+00	7.46E-01	1.00E+00	1.33E-01	1.00E+00	4.11E-02	8.34E-01	9.57E-02	1.00E+00	sarcoplasmic reticulum		C
GO:0016538	10	2.71E-01	1.00E+00	4.32E-01	1.00E+00	2.44E-01	1.00E+00	4.14E-01	1.00E+00	8.55E-01	1.00E+00	3.73E-01	1.00E+00	9.52E-01	1.00E+00	9.74E-01	1.00E+00	cyclin-dependent protein kinase regulator ac		F
GO:0016540	65	2.20E-01	1.00E+00	1.32E-01	1.00E+00	1.96E-01	1.00E+00	2.56E-01	1.00E+00	3.16E-01	1.00E+00	1.93E-01	1.00E+00	3.99E-01	1.00E+00	1.02E-01	1.00E+00	protein autoprocessing		P
GO:0016563	240	1.01E-02	9.83E-01	3.84E-02	1.00E+00	2.66E-03	1.18E-01	1.36E-02	3.78E-01	8.00E-02	1.00E+00	5.75E-01	1.00E+00	2.21E-01	1.00E+00	6.34E-02	1.00E+00	transcriptional activator activity		F
GO:0016564	181	4.29E-01	1.00E+00	1.72E-01	1.00E+00	4.50E-01	1.00E+00	5.84E-02	1.00E+00	5.04E-01	1.00E+00	5.44E-01	1.00E+00	5.34E-01	1.00E+00	4.78E-01	1.00E+00	transcriptional repressor activity		F
GO:0016566	16	8.84E-01	1.00E+00	9.54E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	5.30E-01	1.00E+00	9.21E-01	1.00E+00	7.16E-01	1.00E+00	7.23E-01	1.00E+00	specific transcriptional repressor activity		F
GO:0016567	97	1.09E-03	9.30E-02	2.09E-03	1.62E-01	1.71E-03	1.18E-01	1.57E-03	4.40E-02	4.30E-04	1.90E-02	1.61E-02	1.00E+00	1.61E-01	1.00E+00	9.25E-02	1.00E+00	protein ubiquitination		P
GO:0016568	185	3.02E-08	9.73E-04	1.04E-16	0.00E+00	4.35E-08	0.00E+00	2.29E-09	0.00E+00	6.91E-07	7.65E-04	2.45E-13	0.00E+00	1.19E-01	1.00E+00	1.27E-07	0.00E+00	chromatin modification		P
GO:0016569	54	6.90E-03	3.64E-01	5.83E-04	7.30E-02	4.11E-03	1.88E-01	1.62E-03	4.40E-02	1.28E-02	4.81E-01	7.39E-04	2.06E-02	4.05E-01	1.00E+00	8.10E-02	1.00E+00	covalent chromatin modification		P
GO:0016570	50	1.77E-02	9.83E-01	3.97E-03	3.82E-01	8.75E-03	4.69E-01	6.25E-03	3.78E-01	3.14E-02	1.00E+00	5.83E-03	2.02E-01	4.53E-01	1.00E+00	1.95E-01	1.00E+00	histone modification		P
GO:0016571	18	3.87E-02	1.00E+00	2.91E-03	1.87E-01	1.92E-02	8.10E-01	1.10E-02	3.78E-01	1.12E-01	1.00E+00	1.39E-03	5.10E-02	3.60E-01	1.00E+00	2.55E-01	1.00E+00	histone methylation		P
GO:0016573	12	2.19E-01	1.00E+00	1.13E-01	1.00E+00	2.08E-01	1.00E+00	1.40E-01	1.00E+00	2.59E-01	1.00E+00	1.05E-01	1.00E+00	5.48E-01	1.00E+00	1.04E-01	1.00E+00	histone acetylation		P
GO:0016575	11	5.69E-02	1.00E+00	9.04E-02	1.00E+00	1.66E-01	1.00E+00	6.93E-02	1.00E+00	1.31E-02	4.81E-01	1.83E-01	1.00E+00	7.10E-01	1.00E+00	4.99E-01	1.00E+00	histone deacetylation		P
GO:0016579	11	9.15E-01	1.00E+00	6.24E-01	1.00E+00	8.83E-01	1.00E+00	2.45E-01	1.00E+00	7.06E-01	1.00E+00	8.51E-01	1.00E+00	1.00E+00	1.00E+00	8.02E-01	1.00E+00	protein deubiquitination		P
GO:0016581	11	3.66E-02	1.00E+00	9.06E-04	7.30E-02	7.89E-02	1.00E+00	2.45E-04	1.15E-02	9.48E-02	1.00E+00	1.39E-02	1.00E+00	4.98E-01	1.00E+00	6.73E-02	1.00E+00	NuRD complex		C
GO:0016585	24	6.57E-03	3.64E-01	3.15E-04	4.20E-02	6.58E-03	2.83E-01	4.18E-04	1.30E-02	1.03E-01	1.00E+00	1.49E-02	1.00E+00	1.51E-01	1.00E+00	3.27E-02	1.00E+00	chromatin remodeling complex		C
GO:0016591	74	8.11E-05	7.00E-03	2.49E-06	2.86E-03	2.34E-04	1.61E-02	5.23E-07	1.00E-03	1.20E-03	4.40E-02	3.02E-03	1.43E-01	3.07E-01	1.00E+00	2.72E-01	1.00E+00	DNA-directed RNA polymerase II, holoenzyı		C
GO:0016597	16	8.33E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	4.94E-01	1.00E+00	1.00E+00	1.00E+00	3.82E-01	1.00E+00	2.36E-01	1.00E+00	amino acid binding		F
GO:0016599	17	4.82E-02	1.00E+00	7.73E-02	1.00E+00	4.10E-02	1.00E+00	4.83E-02	1.00E+00	9.00E-02	1.00E+00	1.37E-01	1.00E+00	1.26E-01	1.00E+00	6.47E-01	1.00E+00	caveolar membrane		C
GO:0016601	19	4.35E-02	1.00E+00	3.29E-01	1.00E+00	4.94E-02	1.00E+00	1.36E-01	1.00E+00	3.60E-02	1.00E+00	2.09E-01	1.00E+00	5.06E-01	1.00E+00	9.80E-01	1.00E+00	Rac protein signal transduction		P
GO:0016604	124	1.15E-08	9.73E-04	1.89E-12	0.00E+00	5.25E-06	1.69E-03	5.53E-09	0.00E+00	1.34E-05	1.56E-03	5.50E-08	7.71E-04	9.65E-03	2.17E-01	4.90E-05	3.91E-03	nuclear body		C
GO:0016605	24	4.30E-04	5.20E-02	1.44E-09	2.66E-03	1.65E-02	8.10E-01	4.52E-08	0.00E+00	3.83E-03	1.35E-01	2.14E-04	1.36E-02	4.56E-02	8.34E-01	2.04E-03	6.30E-02	PML body		C
GO:0016607	83	1.93E-05	5.00E-03	3.57E-07	2.66E-03	1.18E-05	1.69E-03	1.65E-06	1.00E-03	1.57E-03	4.80E-02	3.55E-05	2.00E-03	5.08E-02	1.00E+00	3.61E-03	2.16E-01	nuclear speck		C
GO:0016614	147	2.23E-01	1.00E+00	2.08E-01	1.00E+00	4.06E-01	1.00E+00	4.51E-01	1.00E+00	1.59E-01	1.00E+00	1.99E-01	1.00E+00	2.45E-01	1.00E+00	3.90E-01	1.00E+00	oxidoreductase activity, acting on CH-OH gr		F
GO:0016616	130	1.10E-01	1.00E+00	3.69E-01	1.00E+00	2.29E-01	1.00E+00	7.02E-01	1.00E+00	8.46E-02	1.00E+00	2.54E-01	1.00E+00	1.60E-01	1.00E+00	5.88E-01	1.00E+00	oxidoreductase activity, acting on the CH-OI		F
GO:0016620	47	9.93E-01	1.00E+00	6.02E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.11E-01	1.00E+00	1.60E-01	1.00E+00	8.61E-01	1.00E+00	8.72E-01	1.00E+00	oxidoreductase activity, acting on the aldehy		F
GO:0016627	92	2.61E-03	1.39E-01	3.02E-02	1.00E+00	1.13E-02	4.74E-01	9.12E-02	1.00E+00	3.02E-03	1.35E-01	2.97E-02	1.00E+00	2.73E-02	6.06E-01	2.92E-01	1.00E+00	oxidoreductase activity, acting on the CH-CI		F
GO:0016628	59	6.37E-02	1.00E+00	2.25E-01	1.00E+00	6.79E-02	1.00E+00	5.92E-01	1.00E+00	1.08E-01	1.00E+00	7.69E-02	1.00E+00	1.17E-01	1.00E+00	4.62E-01	1.00E+00	oxidoreductase activity, acting on the CH-CI		F
GO:0016634	10	1.88E-01	1.00E+00	7.54E-01	1.00E+00	9.01E-01	1.00E+00	6.85E-01	1.00E+00	1.71E-02	7.19E-01	9.24E-01	1.00E+00	3.00E-01	1.00E+00	4.42E-01	1.00E+00	oxidoreductase activity, acting on the CH-CI		F
GO:0016638	21	8.16E-01	1.00E+00	9.89E-01	1.00E+00	5.33E-01	1.00E+00	9.94E-01	1.00E+00	7.19E-01	1.00E+00	9.68E-01	1.00E+00	9.91E-01	1.00E+00	6.83E-01	1.00E+00	oxidoreductase activity, acting on the CH-NI		F
GO:0016641	19	9.35E-01	1.00E+00	1.00E+00	1.00E+00	7.14E-01	1.00E+00	9.98E-01	1.00E+00	8.20E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	8.06E-01	1.00E+00	oxidoreductase activity, acting on the CH-NI		F
GO:0016645	26	9.23E-02	1.00E+00	2.97E-02	1.00E+00	3.26E-01	1.00E+00	2.66E-01	1.00E+00	3.08E-02	1.00E+00	1.55E-02	1.00E+00	2.13E-01	1.00E+00	1.27E-02	9.40E-01	oxidoreductase activity, acting on the CH-NI		F
GO:0016646	16	2.44E-01	1.00E+00	2.07E-01	1.00E+00	3.92E-01	1.00E+00	4.97E-01	1.00E+00	6.11E-02	1.00E+00	9.68E-02	1.00E+00	4.34E-01	1.00E+00	1.06E-01	1.00E+00	oxidoreductase activity, acting on the CH-NI		F
GO:0016651	58	2.71E-02	1.00E+00	7.40E-04	7.30E-02	1.06E-01	1.00E+00	1.23E-03	4.40E-02	3.11E-01	1.00E+00	1.48E-02	1.00E+00	2.79E-02	6.06E-01	3.58E-02	1.00E+00	oxidoreductase activity, acting on NADH or I		F
GO:0016655	33	2.78E-02	1.00E+00	1.58E-03	7.50E-02	5.14E-02	1.00E+00	2.19E-03	4.50E-02	3.99E-01	1.00E+00	1.72E-02	1.00E+00	6.08E-02	1.00E+00	5.87E-02	1.00E+00	oxidoreductase activity, acting on NADH or I		F
GO:0016667	20	1.27E-01	1.00E+00	1.69E-01	1.00E+00	1.79E-01	1.00E+00	4.14E-01	1.00E+00	1.14E-01	1.00E+00	1.13E-01	1.00E+00	5.34E-01	1.00E+00	1.70E-01	1.00E+00	oxidoreductase activity, acting on sulfur grou		F
GO:0016675	25	1.54E-01	1.00E+00	7.74E-02	1.00E+00	5.86E-02	1.00E+00	3.32E-01	1.00E+00	1.31E-01	1.00E+00	8.33E-02	1.00E+00	7.86E-01	1.00E+00	1.77E-01	1.00E+00	oxidoreductase activity, acting on heme grou		F
GO:0016676	25	1.54E-01	1.00E+00	7.74E-02	1.00E+00	5.86E-02	1.00E+00	3.32E-01	1.00E+00	1.31E-01	1.00E+00	8.33E-02	1.00E+00	7.86E-01	1.00E+00	1.77E-01	1.00E+00	oxidoreductase activity, acting on heme grou		F
GO:0016679	12	9.75E-02	1.00E+00	2.66E-02	1.00E+00	5.09E-01	1.00E+00	2.51E-01	1.00E+00	2.15E-01	1.00E+00	1.12E-01	1.00E+00	2.28E-01	1.00E+00	8.44E-02	1.00E+00	oxidoreductase activity, acting on diphenols		F
GO:0016681	12	9.75E-02	1.00E+00	2.66E-02	1.00E+00	5.09E-01	1.00E+00	2.51E-01	1.00E+00	2.15E-01	1.00E+00	1.12E-01	1.00E+00	2.28E-01	1.00E+00	8.44E-02	1.00E+00	oxidoreductase activity, acting on diphenols		F
GO:0016684	49	1.32E-01	1.00E+00	1.50E-01	1.00E+00	8.61E-01	1.00E+00	2.39E-01	1.00E+00	2.15E-01	1.00E+00	2.27E-01	1.00E+00	5.02E-02	1.00E+00	2.09E-01	1.00E+00	oxidoreductase activity, acting on peroxide a		F
GO:0016701	61	1.36E-01	1.00E+00	5.78E-02	1.00E+00	3.96E-01	1.00E+00	5.57E-02	1.00E+00	8.45E-02	1.00E+00	6.63E-02	1.00E+00	1.68E-01	1.00E+00	4.37E-01	1.00E+00	oxidoreductase activity, acting on single dor		F
GO:0016702	60	1.06E-01	1.00E+00	4.16E-02	1.00E+00	3.51E-01	1.00E+00	4.33E-02	1.00E+00	6.89E-02	1.00E+00	5.25E-02	1.00E+00	1.44E-01	1.00E+00	3.82E-01	1.00E+00	oxidoreductase activity, acting on single dor		F
GO:0016705	168	8.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.62E-01	1.00E+00	1.00E+00	1.00E+00	4.34E-02	8.34E-01	8.33E-01	1.00E+00	oxidoreductase activity, acting on paired dor		F
GO:0016706	25	5.42E-02	1.00E+00	9.12E-02	1.00E+00	1.95E-01	1.00E+00	1.37E-01	1.00E+00	2.94E-01	1.00E+00	5.92E-02	1.00E+00	4.55E-02	8.34E-01	5.63E-01	1.00E+00	oxidoreductase activity, acting on paired dor		F
GO:0016709	35	1.27E-01	1.00E+00	8.09E-01	1.00E+00	8.83E-01	1.00E+00	9.27E-01	1.00E+00	1.24E-01	1.00E+00	9.93E-01	1.00E+00	1.01E-02	2.17E-01	1.64E-01	1.00E+00	oxidoreductase activity, acting on paired dor		F
GO:0016712	71	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	6.04E-01	1.00E+00	9.67E-01	1.00E+00	oxidoreductase activity, acting on paired dor		F
GO:0016740	1918	1.69E-13	6.62E-04	3.85E-18	0.00E+00	1.88E-09	0.00E+00	1.33E-10	0.00E+00	3.91E-08	0.00E+00	8.05E-13	0.00E+00	3.50E-04	1.89E-02	2.20E-09	0.00E+00	transferase activity		F
GO:0016741	187	9.71E-07	2.00E-03	1.72E-08	2.66E-03	1.44E-05	1.69E-03	1.41E-04	5.80E-03	5.34E-06	9.62E-04	1.46E-07	1.75E-03	5.03E-01	1.00E+00	4.45E-04	2.10E-02	transferase activity, transferring one-carbon		F
GO:0016746	205	1.34E-02	9.83E-01	9.05E-04	7.30E-02	1.15E-02	4.74E-01	1.79E-03	4.40E-02	1.13E-01	1.00E+00	1.40E-02	1.00E+00	3.25E-01	1.00E+00	4.83E-02	1.00E+00	transferase activity, transferring acyl groups		F
GO:0016747	189	1.01E-02	9.83E-01	6.51E-04	7.30E-02	7.33E-03	2.83E-01	1.73E-03	4.40E-02	1.24E-01	1.00E+00	1.83E-02	1.00E+00	2.60E-01	1.00E+00	3.73E-02	1.00E+00	transferase activity, transferring groups othe		F
GO:0016755	22	8.17E-01	1.00E+00	5.39E-01	1.00E+00	8.12E-01	1.00E+00	3.27E-01	1.00E+00	6.12E-01	1.00E+00	2.80E-01	1.00E+00	9.27E-01	1.00E+00	9.98E-01	1.00E+00	transferase activity, transferring amino-acyl		F
GO:0016757	241	3.40E-02	1.00E+00	6.42E-03	5.59E-01	1.89E-01	1.00E+00	6.78E-02	1.00E+00	6.81E-02	1.00E+00	2.12E-02	1.00E+00	4.27E-02	8.34E-01	3.79E-03	2.16E-01	transferase activity, transferring glycosyl gro		F
GO:0016758	157	1.91E-01	1.00E+00	3.03E-01	1.00E+00	3.17E-01	1.00E+00	5.36E-01	1.00E+00	1.84E-01	1.00E+00	1.84E-01	1.00E+00	3.50E-01	1.00E+00	1.74E-01	1.00E+00	transferase activity, transferring hexosyl gro		F
GO:0016763	47	7.55E-03	6.18E-01	3.24E-04	4.20E-02	5.63E-02	1.00E+00	7.64E-04	2.70E-02	3.05E-02	1.00E+00	8.35E-03	3.55E-01	2.80E-02	6.06E-01	1.08E-02	6.43E-01	transferase activity, transferring pentosyl gro		F
GO:0016765	57	5.01E-01	1.00E+00	9.40E-01	1.00E+00	9.17E-01	1.00E+00	8.17E-01	1.00E+00	5.70E-01	1.00E+00	8.11E-01	1.00E+00	4.54E-01	1.00E+00	9.73E-01	1.00E+00	transferase activity, transferring alkyl or aryl		F
GO:0016769	34	8.35E-02	1.00E+00	2.52E-02	1.00E+00	2.41E-01	1.00E+00	1.80E-01	1.00E+00	9.68E-02	1.00E+00	9.04E-03	3.55E-01	6.34E-02	1.00E+00	1.03E-01	1.00E+00	transferase activity, transferring nitrogenous		F
GO:0016772	1105	2.05E-08	9.73E-04	1.88E-11	2.66E-03	3.78E-07	9.88E-04	1.92E-07	9.57E-04	8.72E-05	3.00E-03	2.34E-08	7.71E-04	3.36E-03	6.72E-02	1.77E-05	3.91E-03	transferase activity, transferring phosphorus		F

GO:0016773	815	1.20E-04	1.90E-02	2.95E-05	2.80E-02	3.17E-03	1.88E-01	1.27E-02	3.78E-01	6.47E-03	1.65E-01	1.56E-04	1.36E-02	2.20E-03	5.54E-02	1.97E-03	6.30E-02	phosphotransferase activity, alcohol group a	F
GO:0016775	34	8.30E-01	1.00E+00	8.72E-01	1.00E+00	9.85E-01	1.00E+00	9.78E-01	1.00E+00	7.99E-01	1.00E+00	7.73E-01	1.00E+00	7.94E-01	1.00E+00	5.54E-01	1.00E+00	phosphotransferase activity, nitrogenous gro	F
GO:0016776	33	1.01E-02	9.83E-01	2.49E-03	1.87E-01	2.17E-02	1.00E+00	1.05E-02	3.78E-01	7.69E-03	3.18E-01	2.95E-03	1.43E-01	1.40E-01	1.00E+00	3.09E-02	1.00E+00	phosphotransferase activity, phosphate grou	F
GO:0016779	117	9.66E-05	1.90E-02	1.44E-05	7.00E-03	1.01E-04	1.61E-02	6.02E-05	5.80E-03	5.48E-03	1.65E-01	2.21E-04	1.36E-02	2.06E-01	1.00E+00	5.39E-03	2.58E-01	nucleotidyltransferase activity	F
GO:0016780	18	1.93E-01	1.00E+00	5.39E-02	1.00E+00	2.77E-01	1.00E+00	3.36E-02	1.00E+00	1.82E-01	1.00E+00	2.92E-01	1.00E+00	7.41E-01	1.00E+00	1.24E-01	1.00E+00	phosphotransferase activity, for other substi	F
GO:0016782	62	9.95E-01	1.00E+00	9.09E-01	1.00E+00	9.94E-01	1.00E+00	9.68E-01	1.00E+00	7.38E-01	1.00E+00	9.48E-01	1.00E+00	9.42E-01	1.00E+00	4.34E-01	1.00E+00	transferase activity, transferring sulfur-conta	F
GO:0016787	2450	6.48E-12	6.62E-04	2.18E-12	0.00E+00	1.45E-06	9.88E-04	9.64E-06	1.77E-03	3.39E-06	7.65E-04	6.67E-08	7.71E-04	4.98E-09	0.00E+00	6.36E-11	0.00E+00	hydrolase activity	F
GO:0016788	672	3.85E-05	6.00E-03	1.78E-05	7.00E-03	4.32E-03	1.88E-01	4.85E-03	1.42E-01	7.85E-03	3.18E-01	2.19E-04	1.36E-02	1.86E-04	6.45E-03	3.93E-04	2.10E-02	hydrolase activity, acting on ester bonds	F
GO:0016789	129	1.09E-01	1.00E+00	7.66E-01	1.00E+00	2.16E-01	1.00E+00	8.98E-01	1.00E+00	9.71E-01	1.00E+00	7.23E-01	1.00E+00	5.58E-03	1.54E-01	1.99E-01	1.00E+00	carboxylic ester hydrolase activity	F
GO:0016790	95	6.86E-02	1.00E+00	1.78E-04	2.80E-02	5.07E-02	1.00E+00	3.29E-03	1.42E-01	1.42E-02	4.81E-01	4.39E-03	1.52E-01	8.16E-01	1.00E+00	4.22E-04	2.10E-02	thiolester hydrolase activity	F
GO:0016791	251	2.59E-03	1.39E-01	1.81E-04	2.80E-02	1.08E-01	1.00E+00	1.57E-02	7.69E-01	1.92E-02	7.19E-01	8.87E-03	3.55E-01	2.49E-03	5.54E-02	1.34E-04	4.00E-03	phosphoric monoester hydrolase activity	F
GO:0016796	20	1.13E-01	1.00E+00	2.89E-01	1.00E+00	1.35E-01	1.00E+00	5.05E-01	1.00E+00	3.56E-01	1.00E+00	2.72E-01	1.00E+00	1.95E-01	1.00E+00	2.51E-01	1.00E+00	exonuclease activity, active with either ribo-	F
GO:0016798	139	3.66E-02	1.00E+00	2.74E-01	1.00E+00	8.16E-03	3.43E-01	2.92E-01	1.00E+00	4.41E-01	1.00E+00	6.78E-01	1.00E+00	1.67E-01	1.00E+00	3.01E-02	1.00E+00	hydrolase activity, acting on glycosyl bonds	F
GO:0016799	19	4.10E-01	1.00E+00	7.36E-01	1.00E+00	2.16E-01	1.00E+00	6.53E-01	1.00E+00	3.84E-01	1.00E+00	8.97E-01	1.00E+00	7.23E-01	1.00E+00	5.53E-01	1.00E+00	hydrolase activity, hydrolyzing N-glycosyl cc	F
GO:0016805	15	8.75E-02	1.00E+00	7.61E-02	1.00E+00	7.27E-02	1.00E+00	9.45E-02	1.00E+00	1.23E-01	1.00E+00	1.24E-01	1.00E+00	3.52E-01	1.00E+00	9.71E-01	1.00E+00	dipeptidase activity	F
GO:0016806	12	5.17E-02	1.00E+00	1.93E-01	1.00E+00	5.28E-02	1.00E+00	5.31E-01	1.00E+00	3.41E-01	1.00E+00	1.63E-01	1.00E+00	5.54E-02	1.00E+00	3.29E-01	1.00E+00	dipeptidyl-peptidase and tripeptidyl-peptidas	F
GO:0016810	110	2.81E-03	1.39E-01	4.27E-03	3.82E-01	2.24E-02	1.00E+00	3.58E-02	1.00E+00	3.39E-02	1.00E+00	7.79E-02	1.00E+00	1.22E-02	4.39E-01	1.41E-03	4.40E-02	hydrolase activity, acting on carbon-nitroger	F
GO:0016811	53	9.13E-03	9.83E-01	7.16E-03	5.59E-01	3.57E-02	1.00E+00	1.97E-02	7.69E-01	3.04E-02	1.00E+00	1.55E-01	1.00E+00	9.86E-02	1.00E+00	2.57E-02	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016813	14	1.90E-01	1.00E+00	4.42E-01	1.00E+00	2.09E-01	1.00E+00	9.10E-01	1.00E+00	2.45E-01	1.00E+00	2.32E-01	1.00E+00	2.27E-01	1.00E+00	2.67E-01	1.00E+00	hydrolase activity, acting on carbon-nitroger	F
GO:0016814	25	8.41E-02	1.00E+00	4.36E-02	1.00E+00	1.70E-01	1.00E+00	1.23E-01	1.00E+00	1.82E-01	1.00E+00	2.19E-01	1.00E+00	6.22E-02	1.00E+00	9.04E-03	4.48E-01	hydrolase activity, acting on carbon-nitroger	F
GO:0016817	736	1.81E-07	9.73E-04	4.61E-10	2.66E-03	2.85E-04	1.61E-02	5.67E-06	1.77E-03	1.28E-07	0.00E+00	1.48E-08	7.71E-04	4.56E-03	7.75E-02	6.77E-05	3.91E-03	hydrolase activity, acting on acid anhydrides	F
GO:0016818	735	1.81E-07	9.73E-04	5.26E-10	2.66E-03	3.15E-04	1.61E-02	6.70E-06	1.77E-03	1.20E-07	0.00E+00	1.52E-08	7.71E-04	4.32E-03	7.75E-02	7.12E-05	3.91E-03	hydrolase activity, acting on acid anhydrides	F
GO:0016820	130	3.69E-01	1.00E+00	3.30E-01	1.00E+00	9.59E-01	1.00E+00	8.94E-01	1.00E+00	2.51E-01	1.00E+00	1.32E-01	1.00E+00	2.72E-01	1.00E+00	3.13E-01	1.00E+00	hydrolase activity, acting on acid anhydrides	F
GO:0016829	161	5.57E-02	1.00E+00	1.98E-01	1.00E+00	9.42E-02	1.00E+00	4.81E-01	1.00E+00	3.95E-02	1.00E+00	1.64E-01	1.00E+00	1.93E-01	1.00E+00	1.42E-01	1.00E+00	lyase activity	F
GO:0016830	43	6.28E-02	1.00E+00	3.48E-02	1.00E+00	1.32E-01	1.00E+00	3.66E-02	1.00E+00	3.82E-02	1.00E+00	7.35E-02	1.00E+00	2.24E-01	1.00E+00	7.74E-02	1.00E+00	carbon-carbon lyase activity	F
GO:0016831	31	4.85E-02	1.00E+00	3.91E-02	1.00E+00	8.79E-02	1.00E+00	4.47E-02	1.00E+00	5.71E-02	1.00E+00	6.49E-02	1.00E+00	1.95E-01	1.00E+00	1.16E-01	1.00E+00	carboxy-lyase activity	F
GO:0016835	58	2.38E-01	1.00E+00	5.02E-01	1.00E+00	1.49E-01	1.00E+00	8.83E-01	1.00E+00	1.68E-01	1.00E+00	2.42E-01	1.00E+00	7.28E-01	1.00E+00	5.92E-01	1.00E+00	carbon-oxygen lyase activity	F
GO:0016836	48	1.13E-01	1.00E+00	4.07E-01	1.00E+00	1.08E-01	1.00E+00	7.19E-01	1.00E+00	1.27E-01	1.00E+00	2.30E-01	1.00E+00	4.99E-01	1.00E+00	4.80E-01	1.00E+00	hydro-lyase activity	F
GO:0016846	15	2.49E-01	1.00E+00	7.55E-01	1.00E+00	4.34E-01	1.00E+00	8.81E-01	1.00E+00	3.05E-01	1.00E+00	6.40E-01	1.00E+00	9.30E-02	1.00E+00	5.10E-01	1.00E+00	carbon-sulfur lyase activity	F
GO:0016849	23	9.21E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	7.87E-01	1.00E+00	9.56E-01	1.00E+00	1.00E+00	1.00E+00	4.30E-01	1.00E+00	8.54E-01	1.00E+00	phosphorus-oxygen lyase activity	F
GO:0016853	179	4.22E-03	1.86E-01	3.80E-04	4.30E-02	1.97E-03	1.18E-01	9.43E-03	3.78E-01	5.08E-02	1.00E+00	1.04E-03	4.80E-02	2.11E-01	1.00E+00	3.52E-02	1.00E+00	isomerase activity	F
GO:0016854	15	1.35E-01	1.00E+00	2.69E-01	1.00E+00	1.09E-01	1.00E+00	3.29E-01	1.00E+00	1.53E-01	1.00E+00	2.63E-01	1.00E+00	2.76E-01	1.00E+00	1.49E-01	1.00E+00	racemase and epimerase activity	F
GO:0016859	34	6.36E-04	5.20E-02	1.18E-04	2.80E-02	1.79E-03	1.18E-01	8.83E-03	3.78E-01	1.39E-02	4.81E-01	1.55E-04	1.36E-02	9.72E-03	2.17E-01	2.83E-02	1.00E+00	cis-trans isomerase activity	F
GO:0016860	41	6.13E-01	1.00E+00	5.24E-02	1.00E+00	2.82E-01	1.00E+00	5.27E-02	1.00E+00	4.47E-01	1.00E+00	8.69E-02	1.00E+00	9.98E-01	1.00E+00	3.12E-01	1.00E+00	intramolecular oxidoreductase activity	F
GO:0016863	14	6.22E-01	1.00E+00	2.06E-01	1.00E+00	1.16E-01	1.00E+00	3.24E-01	1.00E+00	7.38E-01	1.00E+00	9.00E-02	1.00E+00	1.00E+00	1.00E+00	8.78E-01	1.00E+00	intramolecular oxidoreductase activity, trans	F
GO:0016866	47	2.85E-01	1.00E+00	1.88E-01	1.00E+00	2.27E-01	1.00E+00	3.53E-01	1.00E+00	7.81E-01	1.00E+00	1.24E-01	1.00E+00	2.97E-01	1.00E+00	4.82E-01	1.00E+00	intramolecular transferase activity	F
GO:0016868	10	5.41E-01	1.00E+00	4.30E-01	1.00E+00	4.96E-01	1.00E+00	4.92E-01	1.00E+00	7.83E-01	1.00E+00	3.17E-01	1.00E+00	6.32E-01	1.00E+00	8.11E-01	1.00E+00	intramolecular transferase activity, phosphol	F
GO:0016874	407	2.05E-08	9.73E-04	1.79E-14	0.00E+00	1.20E-07	9.88E-04	1.77E-12	0.00E+00	3.18E-08	0.00E+00	1.08E-11	0.00E+00	3.55E-02	7.53E-01	5.23E-06	3.91E-03	ligase activity	F
GO:0016875	69	1.74E-03	1.02E-01	2.06E-04	2.80E-02	4.63E-03	1.88E-01	1.90E-04	1.10E-02	5.78E-03	1.65E-01	4.96E-03	2.02E-01	8.55E-02	1.00E+00	1.12E-01	1.00E+00	ligase activity, forming carbon-oxygen bonds	F
GO:0016876	69	1.74E-03	1.02E-01	2.06E-04	2.80E-02	4.63E-03	1.88E-01	1.90E-04	1.10E-02	5.78E-03	1.65E-01	4.96E-03	2.02E-01	8.55E-02	1.00E+00	1.12E-01	1.00E+00	ligase activity, forming aminoacyl-tRNA and	F
GO:0016877	27	2.91E-01	1.00E+00	1.55E-01	1.00E+00	3.77E-01	1.00E+00	1.60E-01	1.00E+00	5.87E-01	1.00E+00	3.15E-01	1.00E+00	1.48E-01	1.00E+00	2.05E-01	1.00E+00	ligase activity, forming carbon-sulfur bonds	F
GO:0016878	15	2.48E-01	1.00E+00	3.07E-01	1.00E+00	4.68E-01	1.00E+00	2.24E-01	1.00E+00	3.25E-01	1.00E+00	5.04E-01	1.00E+00	8.53E-02	1.00E+00	6.46E-01	1.00E+00	acid-thiol ligase activity	F
GO:0016879	228	4.85E-06	2.00E-03	6.12E-09	2.66E-03	1.44E-05	1.69E-03	7.81E-08	0.00E+00	1.93E-06	7.65E-04	4.30E-08	7.71E-04	1.17E-01	1.00E+00	9.36E-05	4.00E-03	ligase activity, forming carbon-nitrogen bonc	F
GO:0016881	189	2.28E-06	2.00E-03	4.11E-08	2.66E-03	6.33E-06	1.69E-03	2.90E-07	1.00E-03	6.52E-07	7.65E-04	1.07E-07	1.75E-03	1.10E-01	1.00E+00	4.47E-04	2.10E-02	acid-amino acid ligase activity	F
GO:0016884	11	6.50E-01	1.00E+00	4.68E-01	1.00E+00	7.76E-01	1.00E+00	3.74E-01	1.00E+00	4.49E-01	1.00E+00	3.83E-01	1.00E+00	6.89E-01	1.00E+00	5.30E-01	1.00E+00	carbon-nitrogen ligase activity, with glutamir	F
GO:0016887	349	5.21E-06	2.00E-03	1.46E-07	2.66E-03	4.48E-04	1.61E-02	7.92E-05	5.80E-03	1.70E-04	8.00E-03	2.74E-06	2.00E-03	1.20E-02	4.39E-01	1.70E-04	6.00E-03	ATPase activity	F
GO:0016891	20	5.87E-02	1.00E+00	1.51E-01	1.00E+00	3.01E-02	1.00E+00	1.79E-02	7.69E-01	1.92E-01	1.00E+00	1.08E-01	1.00E+00	9.52E-02	1.00E+00	9.97E-01	1.00E+00	endoribonuclease activity, producing 5'-phos	F
GO:0016892	18	9.36E-01	1.00E+00	9.70E-01	1.00E+00	5.03E-01	1.00E+00	9.93E-01	1.00E+00	9.96E-01	1.00E+00	9.28E-01	1.00E+00	1.00E+00	1.00E+00	9.41E-01	1.00E+00	endoribonuclease activity, producing 3'-phos	F
GO:0016893	26	6.78E-02	1.00E+00	1.83E-01	1.00E+00	8.47E-02	1.00E+00	2.91E-02	1.00E+00	1.88E-01	1.00E+00	1.29E-01	1.00E+00	7.43E-02	1.00E+00	9.83E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016894	20	9.40E-01	1.00E+00	9.31E-01	1.00E+00	5.60E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.72E-01	1.00E+00	9.99E-01	1.00E+00	9.76E-01	1.00E+00	endonuclease activity, active with either ribo	F
GO:0016896	12	9.13E-02	1.00E+00	8.21E-02	1.00E+00	2.06E-01	1.00E+00	4.73E-01	1.00E+00	1.87E-01	1.00E+00	1.82E-01	1.00E+00	1.37E-01	1.00E+00	7.14E-02	1.00E+00	exoribonuclease activity, producing 5'-phosp	F
GO:0016903	56	9.81E-01	1.00E+00	5.29E-01	1.00E+00	9.94E-01	1.00E+00	9.99E-01	1.00E+00	7.26E-01	1.00E+00	1.22E-01	1.00E+00	8.57E-01	1.00E+00	8.98E-01	1.00E+00	oxidoreductase activity, acting on the aldehy	F
GO:0016917	66	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	9.17E-01	1.00E+00	GABA receptor activity	F
GO:0016918	11	6.06E-01	1.00E+00	6.93E-01	1.00E+00	5.54E-01	1.00E+00	2.91E-01	1.00E+00	5.81E-01	1.00E+00	7.24E-01	1.00E+00	5.91E-01	1.00E+00	6.18E-01	1.00E+00	retinal binding	F
GO:0016998	17	3.18E-01	1.00E+00	6.13E-01	1.00E+00	5.58E-01	1.00E+00	7.36E-01	1.00E+00	9.78E-01	1.00E+00	3.49E-01	1.00E+00	1.78E-01	1.00E+00	4.63E-01	1.00E+00	cell wall catabolism	P
GO:0017004	15	9.73E-01	1.00E+00	5.76E-01	1.00E+00	9.59E-01	1.00E+00	5.07E-01	1.00E+00	7.72E-01	1.00E+00	7.88E-01	1.00E+00	9.63E-01	1.00E+00	3.23E-01	1.00E+00	cytochrome complex assembly	P
GO:0017015	25	4.77E-01	1.00E+00	4.51E-01	1.00E+00	5.47E-01	1.00E+00	4.21E-01	1.00E+00	3.24E-01	1.00E+00	4.99E-01	1.00E+00	6.20E-01	1.00E+00	4.01E-01	1.00E+00	regulation of transforming growth factor beta	P
GO:0017016	57	2.16E-02	1.00E+00	1.31E-01	1.00E+00	2.90E-01	1.00E+00	2.71E-01	1.00E+00	4.94E-02	1.00E+00	3.31E-01	1.00E+00	1.36E-02	4.39E-01	7.93E-02	1.00E+00	Ras GTPase binding	F
GO:0017017	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	MAP kinase phosphatase activity	F
GO:0017022	17	2.22E-01	1.00E+00	3.69E-01	1.00E+00	8.10E-01	1.00E+00	3.68E-01	1.00E+00	1.44E-01	1.00E+00	4.83E-01	1.00E+00	1.63E-01	1.00E+00	3.14E-01	1.00E+00	myosin binding	F
GO:0017038	99	6.37E-03	3.64E-01	2.42E-06	2.86E-03	4.39E-02	1.00E+00	3.46E-05	5.41E-03	3.72E-02	1.00E+00	4.64E-04	2.00E-02	1.15E-01	1.00E+00	4.13E-03	2.16E-01	protein import	P
GO:0017046	12	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.82E-01	1.00E+00	3.74E-01	1.00E+00	peptide hormone binding	F
GO:0017048	24	2.07E-01	1.00E+00	2.89E-01	1.00E+00	5.51E-01	1.00E+00	4.12E-01	1.00E+00	2.07E-01	1.00E+00	7.17E-01	1.00E+00	9.08E-02	1.00E+00	9.52E-02	1.00E+00	Rho GTPase binding	F
GO:0017053	10	4.60E-01	1.00E+00	2.65E-01	1.00E+00	8.36E-01	1.00E+00	1.66E-01	1.00E+00	2.58E-01	1.00E+00	3.14E-01	1.00E+00	7.85E-01	1.00E+00	7.62E-01	1.00E+00	transcriptional repressor complex	C
GO:0017076	1933	4.42E-19	0.00E+00	3.89E-26	0.00E+00	6.20E-12	0.00E+00	2.53E-15	0.00E+00	8.86E-15	0.00E+00	1.89E-18	0.00E+00	6.49E-08	6.33E-04	5.39E-11	0.00E+00	purine nucleotide binding	F
GO:0017110	10	4.18E-01	1.00E+00	5.78E-01	1.00E+00	6.91E-01	1.00E+00	6.43E-01	1.00E+00	1.89E-01	1.00E+00	6.07E-01	1.00E+00	3.54E-01	1.00E+00	6.15E-01	1.00E+00	nucleoside-diphosphatase activity	F
GO:0017111	701	1.74E-07	9.73E-04	8.23E-10	2.66E-03	2.22E-04	1.61E-02	3.41E-06	1.00E-03	2.91E-07	0.00E+00	6.52E-08	7.71E-04	3.35E-03	6.72E-02	9.85E-05	4.00E-03	nucleoside-triphosphatase activity	F
GO:0017124	26	1.82E-01	1.00E+00	6.73E-01	1.00E+00	3.19E-01	1.00E+00	2.36E-01	1.00E+00	6.37E-01	1.00E+00	9.08E-01	1.00E+00	9.81E-02	1.00E+00	9.26E-01	1.00E+00	SH3 domain binding	F
GO:0017137	22	1.02E-01	1.00E+00	1.52E-01	1.00E+00	7.63E-01	1.00E+00	2.10E-01	1.00E+00	7.30E-02	1.00E+00	1.48E-01	1.00E+00	9.94E-02	1.00E+00	1.63E-01	1.00E+00	Rab GTPase binding	F
GO:0017144	11	1.20E-03	9.30E-02	6.37E-01	1.00E+00	1.12E-01	1.00E+00	9.96E-01	1.00E+00	3.69E-01	1.00E+00	2.83E-01	1.00E+00	3.81E-02	7.83E-01	5.90E-01	1.00E+00	drug metabolism	P
GO:0017145	10	9.83E-01	1.00E+00	4.69E-01	1.00E+00	7.98E-01	1.00E+00	4.91E-01	1.00E+00	9.78E-01	1.00E+00	3.14E-01	1.00E+00	9.89E-01	1.00E+00	9.36E-01	1.00E+00	stem cell division	P
GO:0017148	38	7.38E-02	1.00E+00	1.55E-02	1.00E+00	3.70E-02	1.00E+00	5.45E-02	1.00E+00	2.14E-01	1.00E+00	1.44E-01	1.00E+00	2.89E-01	1.00E+00	3.73E-03	2.16E-01	negative regulation of protein biosynthesis	P
GO:0017153	53	6.13E-01	1.00E+00	9.94E-01	1.00E+00	5.99E-01	1.00E+00	9.87E-01	1.00E+00	8.38E-01	1.00E+00	9.97E-01	1.00E+00	5.19E-01	1.00E+00	8.82E-01	1.00E+00	sodium:dicarboxylate symporter activity	F
GO:0017156	24	5.16E-01	1.00E+00	6.96E-01	1.00E+00	8.41E-01	1.00E+00	9.16E-01	1.00E+00	4.47E-01	1.00E+00	6.68E-01	1.00E+00	2.61E-01	1.00E+00	3.48E-01	1.00E+00	calcium ion-dependent exocytosis	P
GO:0017157	23	3.02E-01	1.00E+00	8.98E-01	1.00E+00	6.30E-01	1.00E+00	9.57E-01	1.00E+00	3.80E-01	1.00E+00	9.99E-01	1.00E+00	9.64E-02	1.00E+00	2.96E-01	1.00E+00	regulation of exocytosis	P

GO:0018024	24	8.80E-04	9.30E-02	8.22E-06	3.00E-03	4.18E-04	1.61E-02	4.50E-04	1.30E-02	1.20E-02	4.21E-01	1.73E-05	2.00E-03	3.55E-01	1.00E+00	9.15E-03	4.48E-01	histone-lysine N-methyltransferase activity	F
GO:0018105	17	2.76E-02	1.00E+00	1.25E-02	7.51E-01	1.78E-02	8.10E-01	2.06E-02	7.69E-01	1.64E-01	1.00E+00	5.11E-02	1.00E+00	1.21E-01	1.00E+00	4.73E-02	1.00E+00	peptidyl-serine phosphorylation	P
GO:0018107	10	1.62E-01	1.00E+00	1.09E-01	1.00E+00	2.81E-01	1.00E+00	1.39E-01	1.00E+00	1.34E-01	1.00E+00	1.01E-01	1.00E+00	3.95E-01	1.00E+00	3.80E-01	1.00E+00	peptidyl-threonine phosphorylation	P
GO:0018108	74	7.90E-01	1.00E+00	4.98E-01	1.00E+00	7.59E-01	1.00E+00	2.78E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	1.62E-01	1.00E+00	1.29E-01	1.00E+00	peptidyl-tyrosine phosphorylation	P
GO:0018149	14	9.14E-01	1.00E+00	9.90E-01	1.00E+00	6.88E-01	1.00E+00	9.78E-01	1.00E+00	9.92E-01	1.00E+00	8.75E-01	1.00E+00	9.80E-01	1.00E+00	9.96E-01	1.00E+00	peptide cross-linking	P
GO:0018193	144	2.53E-02	1.00E+00	1.28E-03	7.50E-02	4.40E-02	1.00E+00	5.74E-03	3.78E-01	3.71E-01	1.00E+00	1.29E-01	1.00E+00	3.25E-02	7.53E-01	7.24E-04	3.30E-02	peptidyl-amino acid modification	P
GO:0018195	10	3.15E-02	1.00E+00	3.28E-01	1.00E+00	4.36E-02	1.00E+00	3.71E-01	1.00E+00	7.59E-02	1.00E+00	4.17E-01	1.00E+00	2.76E-02	6.06E-01	2.74E-01	1.00E+00	peptidyl-arginine modification	P
GO:0018209	20	7.10E-02	1.00E+00	2.97E-02	1.00E+00	4.55E-02	1.00E+00	5.31E-02	1.00E+00	1.80E-01	1.00E+00	6.32E-02	1.00E+00	2.40E-01	1.00E+00	7.09E-02	1.00E+00	peptidyl-serine modification	P
GO:0018210	13	3.12E-01	1.00E+00	1.96E-01	1.00E+00	4.13E-01	1.00E+00	2.47E-01	1.00E+00	1.54E-01	1.00E+00	1.25E-01	1.00E+00	6.30E-01	1.00E+00	4.86E-01	1.00E+00	peptidyl-threonine modification	P
GO:0018212	74	7.90E-01	1.00E+00	4.98E-01	1.00E+00	7.59E-01	1.00E+00	2.78E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	1.62E-01	1.00E+00	1.29E-01	1.00E+00	peptidyl-tyrosine modification	P
GO:0018298	15	9.75E-01	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	7.89E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	4.80E-02	1.00E+00	2.11E-01	1.00E+00	protein-chromophore linkage	P
GO:0018342	10	7.69E-01	1.00E+00	4.46E-01	1.00E+00	8.22E-01	1.00E+00	4.70E-01	1.00E+00	6.12E-01	1.00E+00	6.31E-01	1.00E+00	7.50E-01	1.00E+00	1.95E-01	1.00E+00	protein prenylation	P
GO:0018958	83	6.14E-01	1.00E+00	9.55E-01	1.00E+00	6.19E-01	1.00E+00	8.60E-01	1.00E+00	9.41E-01	1.00E+00	9.67E-01	1.00E+00	4.99E-01	1.00E+00	8.84E-01	1.00E+00	phenol metabolism	P
GO:0019001	375	8.23E-05	7.00E-03	1.19E-04	2.80E-02	4.59E-04	1.61E-02	1.33E-03	4.40E-02	2.80E-04	8.00E-03	6.01E-04	2.00E-02	5.49E-02	1.00E+00	1.15E-01	1.00E+00	guanyl nucleotide binding	F
GO:0019012	15	3.85E-01	1.00E+00	5.78E-01	1.00E+00	3.84E-01	1.00E+00	7.42E-01	1.00E+00	3.17E-01	1.00E+00	3.18E-01	1.00E+00	4.75E-01	1.00E+00	8.10E-01	1.00E+00	virion	C
GO:0019028	14	4.06E-01	1.00E+00	5.36E-01	1.00E+00	4.60E-01	1.00E+00	7.10E-01	1.00E+00	3.18E-01	1.00E+00	2.86E-01	1.00E+00	4.65E-01	1.00E+00	7.62E-01	1.00E+00	viral capsid	C
GO:0019048	10	1.90E-01	1.00E+00	3.55E-01	1.00E+00	3.88E-01	1.00E+00	9.13E-01	1.00E+00	3.07E-01	1.00E+00	8.33E-01	1.00E+00	2.44E-02	5.60E-01	9.25E-02	1.00E+00	virus-host interaction	P
GO:0019058	17	7.24E-01	1.00E+00	9.56E-01	1.00E+00	9.71E-01	1.00E+00	9.51E-01	1.00E+00	1.94E-01	1.00E+00	7.57E-01	1.00E+00	9.36E-01	1.00E+00	9.59E-01	1.00E+00	viral infectious cycle	P
GO:0019098	17	9.94E-01	1.00E+00	9.99E-01	1.00E+00	9.81E-01	1.00E+00	9.97E-01	1.00E+00	8.75E-01	1.00E+00	9.94E-01	1.00E+00	8.93E-01	1.00E+00	9.89E-01	1.00E+00	reproductive behavior	P
GO:0019104	10	2.97E-01	1.00E+00	3.88E-01	1.00E+00	1.04E-01	1.00E+00	6.12E-01	1.00E+00	3.08E-01	1.00E+00	4.08E-01	1.00E+00	9.81E-01	1.00E+00	4.15E-01	1.00E+00	DNA N-glycosylase activity	F
GO:0019199	124	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	7.99E-01	1.00E+00	7.81E-01	1.00E+00	transmembrane receptor protein kinase acti	F
GO:0019200	36	1.08E-01	1.00E+00	5.98E-02	1.00E+00	1.14E-02	4.74E-01	1.11E-01	1.00E+00	6.20E-01	1.00E+00	4.03E-02	1.00E+00	2.44E-01	1.00E+00	3.09E-01	1.00E+00	carbohydrate kinase activity	F
GO:0019201	17	5.67E-02	1.00E+00	2.66E-02	1.00E+00	1.34E-01	1.00E+00	8.64E-02	1.00E+00	8.98E-02	1.00E+00	9.14E-03	3.55E-01	9.26E-02	1.00E+00	1.04E-01	1.00E+00	nucleotide kinase activity	F
GO:0019205	41	5.30E-03	3.48E-01	1.44E-03	7.50E-02	5.64E-03	1.88E-01	9.67E-03	3.78E-01	6.27E-03	1.65E-01	9.97E-04	4.80E-02	1.18E-01	1.00E+00	4.57E-02	1.00E+00	nucleobase, nucleoside, nucleotide kinase a	F
GO:0019207	93	2.47E-01	1.00E+00	2.79E-01	1.00E+00	4.50E-01	1.00E+00	1.38E-01	1.00E+00	4.19E-01	1.00E+00	6.50E-01	1.00E+00	3.60E-01	1.00E+00	5.81E-01	1.00E+00	kinase regulator activity	F
GO:0019208	46	1.67E-01	1.00E+00	2.43E-01	1.00E+00	9.71E-02	1.00E+00	2.72E-01	1.00E+00	3.77E-01	1.00E+00	4.29E-01	1.00E+00	5.75E-01	1.00E+00	1.82E-01	1.00E+00	phosphatase regulator activity	F
GO:0019209	16	7.40E-01	1.00E+00	3.51E-01	1.00E+00	3.55E-01	1.00E+00	5.40E-01	1.00E+00	5.45E-01	1.00E+00	2.09E-01	1.00E+00	1.00E+00	1.00E+00	9.57E-01	1.00E+00	kinase activator activity	F
GO:0019210	25	3.65E-01	1.00E+00	7.62E-01	1.00E+00	3.74E-01	1.00E+00	1.06E-01	1.00E+00	5.93E-01	1.00E+00	9.97E-01	1.00E+00	2.69E-01	1.00E+00	9.54E-01	1.00E+00	kinase inhibitor activity	F
GO:0019212	20	2.57E-01	1.00E+00	1.62E-01	1.00E+00	2.06E-01	1.00E+00	2.49E-01	1.00E+00	7.27E-01	1.00E+00	3.00E-01	1.00E+00	1.71E-01	1.00E+00	1.33E-01	1.00E+00	phosphatase inhibitor activity	F
GO:0019213	21	1.57E-02	9.83E-01	1.87E-02	1.00E+00	2.57E-02	1.00E+00	2.14E-02	7.69E-01	2.98E-02	1.00E+00	2.20E-01	1.00E+00	2.35E-01	1.00E+00	2.82E-02	1.00E+00	deacetylase activity	F
GO:0019216	38	1.87E-01	1.00E+00	7.17E-01	1.00E+00	5.33E-01	1.00E+00	8.13E-01	1.00E+00	2.03E-01	1.00E+00	8.91E-01	1.00E+00	1.60E-01	1.00E+00	2.16E-01	1.00E+00	regulation of lipid metabolism	P
GO:0019217	13	2.49E-01	1.00E+00	1.08E-01	1.00E+00	6.31E-01	1.00E+00	1.98E-01	1.00E+00	1.98E-01	1.00E+00	3.38E-01	1.00E+00	1.79E-01	1.00E+00	7.30E-02	1.00E+00	regulation of fatty acid metabolism	P
GO:0019218	17	6.77E-01	1.00E+00	9.99E-01	1.00E+00	6.49E-01	1.00E+00	1.00E+00	1.00E+00	6.14E-01	1.00E+00	1.00E+00	1.00E+00	6.53E-01	1.00E+00	8.29E-01	1.00E+00	regulation of steroid metabolism	P
GO:0019219	2464	3.08E-01	1.00E+00	2.63E-07	2.66E-03	8.24E-02	1.00E+00	5.39E-10	0.00E+00	1.36E-01	1.00E+00	5.91E-05	5.36E-03	9.66E-01	1.00E+00	5.42E-01	1.00E+00	regulation of nucleobase, nucleoside, nucle	P
GO:0019220	123	9.92E-01	1.00E+00	9.55E-01	1.00E+00	9.90E-01	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.15E-01	1.00E+00	4.99E-01	1.00E+00	regulation of phosphate metabolism	P
GO:0019221	45	9.26E-01	1.00E+00	8.71E-01	1.00E+00	9.69E-01	1.00E+00	6.22E-01	1.00E+00	9.18E-01	1.00E+00	9.69E-01	1.00E+00	4.63E-01	1.00E+00	6.88E-01	1.00E+00	cytokine and chemokine mediated signaling	P
GO:0019222	2865	1.46E-01	1.00E+00	1.17E-08	2.66E-03	5.34E-02	1.00E+00	6.59E-12	0.00E+00	8.88E-02	1.00E+00	2.91E-05	2.00E-03	9.04E-01	1.00E+00	2.98E-01	1.00E+00	regulation of metabolism	P
GO:0019226	286	9.53E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.99E-01	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	4.62E-01	1.00E+00	7.93E-01	1.00E+00	transmission of nerve impulse	P
GO:0019229	15	6.05E-01	1.00E+00	9.97E-01	1.00E+00	3.40E-01	1.00E+00	1.00E+00	1.00E+00	8.51E-01	1.00E+00	9.72E-01	1.00E+00	9.28E-01	1.00E+00	9.14E-01	1.00E+00	regulation of vasoconstriction	P
GO:0019233	29	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	3.79E-01	1.00E+00	9.99E-01	1.00E+00	sensory perception of pain	P
GO:0019239	22	2.84E-01	1.00E+00	2.16E-01	1.00E+00	6.98E-01	1.00E+00	3.92E-01	1.00E+00	2.81E-01	1.00E+00	3.43E-01	1.00E+00	1.31E-01	1.00E+00	3.61E-02	1.00E+00	deaminase activity	F
GO:0019290	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	siderophore biosynthesis	P
GO:0019318	174	4.64E-02	1.00E+00	1.66E-01	1.00E+00	2.25E-01	1.00E+00	6.30E-01	1.00E+00	1.08E-01	1.00E+00	1.04E-01	1.00E+00	7.28E-02	1.00E+00	3.35E-01	1.00E+00	hexose metabolism	P
GO:0019319	29	1.04E-01	1.00E+00	4.34E-01	1.00E+00	6.57E-01	1.00E+00	4.15E-01	1.00E+00	2.09E-01	1.00E+00	7.55E-01	1.00E+00	4.46E-02	8.34E-01	3.10E-01	1.00E+00	hexose biosynthesis	P
GO:0019320	68	1.40E-02	9.83E-01	1.64E-01	1.00E+00	5.59E-02	1.00E+00	3.92E-01	1.00E+00	1.16E-01	1.00E+00	5.44E-02	1.00E+00	2.89E-02	6.06E-01	5.10E-01	1.00E+00	hexose catabolism	P
GO:0019321	11	8.57E-02	1.00E+00	3.97E-01	1.00E+00	1.48E-01	1.00E+00	4.72E-01	1.00E+00	5.92E-02	1.00E+00	2.63E-01	1.00E+00	5.08E-01	1.00E+00	4.56E-01	1.00E+00	pentose metabolism	P
GO:0019362	26	8.05E-02	1.00E+00	4.70E-01	1.00E+00	1.40E-01	1.00E+00	4.32E-01	1.00E+00	2.51E-01	1.00E+00	7.28E-01	1.00E+00	9.43E-02	1.00E+00	5.45E-01	1.00E+00	pyridine nucleotide metabolism	P
GO:0019363	12	5.02E-01	1.00E+00	5.08E-01	1.00E+00	3.13E-01	1.00E+00	5.76E-01	1.00E+00	7.88E-01	1.00E+00	9.36E-01	1.00E+00	4.64E-01	1.00E+00	3.44E-01	1.00E+00	pyridine nucleotide biosynthesis	P
GO:0019370	17	8.95E-01	1.00E+00	9.31E-01	1.00E+00	9.13E-01	1.00E+00	8.52E-01	1.00E+00	8.86E-01	1.00E+00	9.62E-01	1.00E+00	5.76E-01	1.00E+00	5.28E-01	1.00E+00	leukotriene biosynthesis	P
GO:0019395	25	8.43E-04	9.30E-02	1.74E-06	2.66E-03	1.82E-03	1.18E-01	8.34E-04	2.70E-02	9.66E-03	3.69E-01	6.75E-03	3.55E-01	9.22E-02	1.00E+00	1.56E-05	3.91E-03	fatty acid oxidation	P
GO:0019438	58	2.00E-01	1.00E+00	3.98E-01	1.00E+00	2.68E-01	1.00E+00	7.22E-01	1.00E+00	5.08E-01	1.00E+00	1.65E-01	1.00E+00	1.01E-01	1.00E+00	4.60E-01	1.00E+00	aromatic compound biosynthesis	P
GO:0019439	15	5.93E-01	1.00E+00	6.14E-01	1.00E+00	9.12E-01	1.00E+00	9.98E-01	1.00E+00	4.79E-01	1.00E+00	3.06E-01	1.00E+00	2.83E-01	1.00E+00	3.30E-01	1.00E+00	aromatic compound catabolism	P
GO:0019538	3395	1.13E-12	6.62E-04	2.28E-29	0.00E+00	1.49E-09	0.00E+00	6.27E-18	0.00E+00	5.38E-08	0.00E+00	7.30E-17	0.00E+00	5.21E-03	9.40E-02	2.59E-13	0.00E+00	protein metabolism	P
GO:0019540	47	2.41E-01	1.00E+00	5.01E-01	1.00E+00	2.35E-01	1.00E+00	5.63E-01	1.00E+00	4.82E-01	1.00E+00	4.04E-01	1.00E+00	2.04E-01	1.00E+00	6.35E-01	1.00E+00	siderophore biosynthesis from catechol	P
GO:0019717	63	1.91E-01	1.00E+00	4.73E-01	1.00E+00	2.40E-01	1.00E+00	4.28E-01	1.00E+00	5.58E-01	1.00E+00	8.35E-01	1.00E+00	1.40E-01	1.00E+00	3.10E-01	1.00E+00	synaptosome	C
GO:0019722	33	5.82E-01	1.00E+00	3.54E-01	1.00E+00	9.37E-01	1.00E+00	1.63E-01	1.00E+00	2.42E-01	1.00E+00	7.97E-01	1.00E+00	4.60E-01	1.00E+00	5.22E-01	1.00E+00	calcium-mediated signaling	P
GO:0019724	120	7.99E-01	1.00E+00	8.94E-01	1.00E+00	8.13E-01	1.00E+00	8.58E-01	1.00E+00	9.75E-01	1.00E+00	7.24E-01	1.00E+00	4.57E-01	1.00E+00	9.48E-01	1.00E+00	B cell mediated immunity	P
GO:0019725	261	2.86E-03	1.39E-01	6.86E-01	1.00E+00	9.81E-02	1.00E+00	3.54E-01	1.00E+00	3.19E-02	1.00E+00	9.56E-01	1.00E+00	7.47E-03	2.01E-01	4.44E-01	1.00E+00	cell homeostasis	P
GO:0019748	95	1.05E-01	1.00E+00	2.27E-01	1.00E+00	9.66E-02	1.00E+00	3.72E-01	1.00E+00	1.87E-01	1.00E+00	2.43E-01	1.00E+00	1.45E-01	1.00E+00	3.15E-01	1.00E+00	secondary metabolism	P
GO:0019751	34	1.52E-02	9.83E-01	1.88E-01	1.00E+00	2.11E-02	1.00E+00	5.80E-02	1.00E+00	5.04E-01	1.00E+00	4.49E-01	1.00E+00	3.92E-02	7.83E-01	4.34E-01	1.00E+00	polyol metabolism	P
GO:0019752	633	2.79E-03	1.39E-01	1.26E-03	7.50E-02	5.66E-02	1.00E+00	5.11E-02	1.00E+00	3.24E-02	1.00E+00	2.23E-03	1.43E-01	3.45E-03	6.72E-02	4.81E-04	2.10E-02	carboxylic acid metabolism	P
GO:0019783	69	1.24E-02	9.83E-01	6.37E-05	2.80E-02	4.88E-02	1.00E+00	1.80E-05	1.92E-03	4.58E-03	1.35E-01	3.40E-03	1.43E-01	3.48E-01	1.00E+00	7.70E-03	4.48E-01	small conjugating protein-specific protease a	F
GO:0019787	167	4.43E-05	6.00E-03	1.81E-07	2.66E-03	5.63E-05	3.00E-03	1.84E-06	1.00E-03	3.69E-06	7.65E-04	2.84E-07	1.75E-03	2.70E-01	1.00E+00	1.01E-03	4.40E-02	small conjugating protein ligase activity	F
GO:0019825	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	oxygen binding	F
GO:0019827	16	4.66E-01	1.00E+00	2.55E-01	1.00E+00	4.39E-01	1.00E+00	2.25E-01	1.00E+00	7.93E-01	1.00E+00	2.81E-01	1.00E+00	1.83E-01	1.00E+00	4.07E-01	1.00E+00	stem cell maintenance	P
GO:0019829	50	7.19E-01	1.00E+00	2.26E-01	1.00E+00	9.97E-01	1.00E+00	6.61E-01	1.00E+00	2.94E-01	1.00E+00	2.41E-01	1.00E+00	9.16E-01	1.00E+00	2.14E-01	1.00E+00	cation-transporting ATPase activity	F
GO:0019835	26	5.39E-01	1.00E+00	8.56E-01	1.00E+00	3.69E-01	1.00E+00	9.40E-01	1.00E+00	9.88E-01	1.00E+00	7.32E-01	1.00E+00	4.67E-01	1.00E+00	8.14E-01	1.00E+00	cytolysis	P
GO:0019838	89	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.68E-01	1.00E+00	growth factor binding	F
GO:0019840	17	8.77E-01	1.00E+00	9.25E-01	1.00E+00	8.26E-01	1.00E+00	4.94E-01	1.00E+00	9.20E-01	1.00E+00	7.95E-01	1.00E+00	6.31E-01	1.00E+00	8.98E-01	1.00E+00	isoprenoid binding	F
GO:0019841	11	5.70E-01	1.00E+00	6.08E-01	1.00E+00	5.25E-01	1.00E+00	3.32E-01	1.00E+00	5.81E-01	1.00E+00	5.66E-01	1.00E+00	5.11E-01	1.00E+00	6.18E-01	1.00E+00	retinol binding	F
GO:0019842	149	9.39E-03	9.83E-01	1.98E-03	1.62E-01	5.97E-02	1.00E+00	2.90E-02	1.00E+00	2.91E-03	1.35E-01	1.22E-03	5.10E-02	4.58E-02	8.34E-01	1.85E-01	1.00E+00	vitamin binding	F
GO:0019843	19	6.09E-01	1.00E+00	5.78E-01	1.00E+00	6.19E-01	1.00E+00	1.15E-01	1.00E+00	5.69E-01	1.00E+00	4.53E-01	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	rRNA binding	F
GO:0019861	86	1.06E-01	1.00E+00	9.41E-01	1.00E+00	7.94E-01	1.00E+00	7.00E-01	1.00E+00	6.21E-02	1.00E+00	9.74E-01	1.00E+00	2.33E-01	1.00E+00	9.08E-01	1.00E+00	flagellum	C
GO:0019865	11	3.32E-01	1.00E+00	1.51E-01	1.00E+00	5.98E-01	1.00E+00	1.63E-01	1.00E+00	3.91E-01	1.00E+00	2.62E-01	1.00E+00	2.53E-01	1.00E+00	1.66E-01	1.00E+00	immunoglobulin binding	F
GO:0019866	314	5.43E-07	2.00E-03	1.34E-14	0.00E+00	1.31E-05	1.69E-03	1.47E-09	0.00E+00	1.30E-04	8.00E-03	2.61E-11	0.00E+00	1.48E-02	4.39E-01	1.49E-04	4.00E-03	organelle inner membrane	C

GO:0019867	79	2.02E-04	1.90E-02	6.19E-05	2.80E-02	2.37E-02	1.00E+00	3.73E-04	1.30E-02	3.62E-04	1.90E-02	3.07E-03	1.43E-01	1.68E-02	4.71E-01	5.32E-03	2.58E-01	outer membrane	C
GO:0019882	82	1.00E+00	1.00E+00	4.52E-01	1.00E+00	9.98E-01	1.00E+00	3.10E-01	1.00E+00	9.58E-01	1.00E+00	1.32E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	antigen processing and presentation	P
GO:0019884	23	8.01E-01	1.00E+00	9.48E-02	1.00E+00	6.86E-01	1.00E+00	5.96E-02	1.00E+00	2.38E-01	1.00E+00	2.67E-01	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019886	16	9.41E-01	1.00E+00	2.76E-01	1.00E+00	9.66E-01	1.00E+00	2.42E-01	1.00E+00	3.33E-01	1.00E+00	4.68E-01	1.00E+00	9.99E-01	1.00E+00	8.42E-01	1.00E+00	antigen processing and presentation of exo	P
GO:0019887	74	5.13E-01	1.00E+00	4.17E-01	1.00E+00	6.12E-01	1.00E+00	2.10E-01	1.00E+00	5.65E-01	1.00E+00	7.50E-01	1.00E+00	6.47E-01	1.00E+00	6.54E-01	1.00E+00	protein kinase regulator activity	F
GO:0019888	44	1.57E-01	1.00E+00	2.40E-01	1.00E+00	8.42E-02	1.00E+00	2.64E-01	1.00E+00	3.66E-01	1.00E+00	4.19E-01	1.00E+00	5.88E-01	1.00E+00	2.00E-01	1.00E+00	protein phosphatase regulator activity	F
GO:0019897	59	3.12E-01	1.00E+00	6.34E-01	1.00E+00	5.04E-01	1.00E+00	6.20E-01	1.00E+00	5.21E-01	1.00E+00	7.00E-01	1.00E+00	6.75E-02	1.00E+00	8.80E-01	1.00E+00	extrinsic to plasma membrane	C
GO:0019898	92	3.20E-01	1.00E+00	5.44E-01	1.00E+00	8.19E-01	1.00E+00	6.68E-01	1.00E+00	2.52E-01	1.00E+00	6.56E-01	1.00E+00	3.02E-02	7.53E-01	5.51E-01	1.00E+00	extrinsic to membrane	C
GO:0019899	247	2.55E-04	1.90E-02	1.81E-02	1.00E+00	9.10E-03	4.69E-01	7.12E-02	1.00E+00	2.19E-03	1.35E-01	5.43E-02	1.00E+00	4.77E-03	7.75E-02	4.14E-02	1.00E+00	enzyme binding	F
GO:0019900	94	1.18E-01	1.00E+00	5.09E-01	1.00E+00	1.44E-01	1.00E+00	7.26E-01	1.00E+00	1.44E-01	1.00E+00	5.66E-01	1.00E+00	2.39E-01	1.00E+00	3.92E-01	1.00E+00	kinase binding	F
GO:0019901	78	6.08E-02	1.00E+00	3.22E-01	1.00E+00	7.61E-02	1.00E+00	5.46E-01	1.00E+00	6.91E-02	1.00E+00	3.89E-01	1.00E+00	1.90E-01	1.00E+00	2.80E-01	1.00E+00	protein kinase binding	F
GO:0019902	16	3.40E-02	1.00E+00	3.64E-02	1.00E+00	9.03E-02	1.00E+00	2.62E-01	1.00E+00	1.79E-01	1.00E+00	6.51E-02	1.00E+00	1.36E-01	1.00E+00	6.75E-02	1.00E+00	phosphatase binding	F
GO:0019903	12	2.00E-01	1.00E+00	1.85E-02	1.00E+00	2.58E-01	1.00E+00	1.56E-01	1.00E+00	2.02E-01	1.00E+00	5.62E-02	1.00E+00	3.20E-01	1.00E+00	7.59E-02	1.00E+00	protein phosphatase binding	F
GO:0019904	139	9.77E-02	1.00E+00	1.79E-01	1.00E+00	2.14E-01	1.00E+00	7.33E-02	1.00E+00	2.38E-01	1.00E+00	3.97E-01	1.00E+00	2.04E-01	1.00E+00	5.94E-01	1.00E+00	protein domain specific binding	F
GO:0019905	25	6.90E-01	1.00E+00	7.66E-01	1.00E+00	8.65E-01	1.00E+00	5.98E-01	1.00E+00	4.45E-01	1.00E+00	9.08E-01	1.00E+00	5.52E-01	1.00E+00	5.21E-01	1.00E+00	syntaxin binding	F
GO:0019915	12	6.01E-02	1.00E+00	2.25E-01	1.00E+00	6.26E-02	1.00E+00	1.55E-01	1.00E+00	1.94E-01	1.00E+00	8.90E-01	1.00E+00	6.31E-01	1.00E+00	7.04E-02	1.00E+00	sequestering of lipid	P
GO:0019932	155	8.83E-01	1.00E+00	8.56E-01	1.00E+00	9.29E-01	1.00E+00	8.29E-01	1.00E+00	7.75E-01	1.00E+00	9.46E-01	1.00E+00	7.34E-01	1.00E+00	5.64E-01	1.00E+00	second-messenger-mediated signaling	P
GO:0019933	64	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	7.42E-01	1.00E+00	cAMP-mediated signaling	P
GO:0019935	69	9.98E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.98E-01	1.00E+00	8.64E-01	1.00E+00	7.86E-01	1.00E+00	cyclic-nucleotide-mediated signaling	P
GO:0019941	155	4.98E-06	2.00E-03	7.32E-11	2.66E-03	5.26E-05	3.00E-03	6.34E-08	0.00E+00	2.47E-06	7.65E-04	1.72E-07	1.75E-03	2.81E-01	1.00E+00	1.02E-04	4.00E-03	modification-dependent protein catabolism	P
GO:0019953	434	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.87E-01	1.00E+00	6.50E-01	1.00E+00	9.92E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	sexual reproduction	P
GO:0019955	105	8.66E-01	1.00E+00	9.71E-01	1.00E+00	9.37E-01	1.00E+00	9.92E-01	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	3.44E-01	1.00E+00	9.95E-02	1.00E+00	cytokine binding	F
GO:0019956	44	2.89E-01	1.00E+00	4.29E-01	1.00E+00	6.99E-01	1.00E+00	7.15E-01	1.00E+00	2.91E-01	1.00E+00	9.36E-01	1.00E+00	1.74E-01	1.00E+00	2.52E-02	1.00E+00	chemokine binding	F
GO:0019957	34	2.10E-01	1.00E+00	4.11E-01	1.00E+00	6.37E-01	1.00E+00	6.88E-01	1.00E+00	2.08E-01	1.00E+00	8.68E-01	1.00E+00	1.94E-01	1.00E+00	4.31E-02	1.00E+00	C-C chemokine binding	F
GO:0019958	29	3.00E-01	1.00E+00	3.46E-01	1.00E+00	7.74E-01	1.00E+00	7.48E-01	1.00E+00	8.49E-02	1.00E+00	7.51E-01	1.00E+00	4.11E-01	1.00E+00	2.97E-02	1.00E+00	C-X-C chemokine binding	F
GO:0019959	11	2.23E-01	1.00E+00	1.39E-01	1.00E+00	1.00E+00	1.00E+00	5.74E-01	1.00E+00	1.18E-01	1.00E+00	2.72E-01	1.00E+00	3.49E-01	1.00E+00	2.73E-02	1.00E+00	interleukin-8 binding	F
GO:0019965	58	9.63E-01	1.00E+00	9.22E-01	1.00E+00	9.97E-01	1.00E+00	9.98E-01	1.00E+00	7.98E-01	1.00E+00	9.67E-01	1.00E+00	5.93E-01	1.00E+00	1.68E-01	1.00E+00	interleukin binding	F
GO:0019966	30	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	interleukin-1 binding	F
GO:0019992	55	3.45E-03	1.86E-01	2.11E-02	1.00E+00	3.09E-02	1.00E+00	1.49E-01	1.00E+00	1.64E-02	7.19E-01	2.17E-01	1.00E+00	6.23E-03	2.01E-01	4.40E-04	2.10E-02	diacylglycerol binding	F
GO:0020037	194	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	6.04E-01	1.00E+00	7.12E-01	1.00E+00	heme binding	F
GO:0021510	37	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.93E-01	1.00E+00	spinal cord development	P
GO:0021515	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	9.98E-01	1.00E+00	cell differentiation in spinal cord	P
GO:0021516	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	dorsal spinal cord development	P
GO:0021517	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.67E-01	1.00E+00	9.63E-01	1.00E+00	ventral spinal cord development	P
GO:0021522	15	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.73E-01	1.00E+00	9.18E-01	1.00E+00	spinal cord motor neuron differentiation	P
GO:0021532	13	9.96E-01	1.00E+00	9.73E-01	1.00E+00	9.99E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	7.51E-01	1.00E+00	8.02E-01	1.00E+00	neural tube patterning	P
GO:0021533	14	9.64E-01	1.00E+00	9.64E-01	1.00E+00	9.76E-01	1.00E+00	9.31E-01	1.00E+00	9.96E-01	1.00E+00	9.93E-01	1.00E+00	7.49E-01	1.00E+00	7.70E-01	1.00E+00	cell differentiation in hindbrain	P
GO:0021534	10	9.64E-01	1.00E+00	9.86E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.40E-01	1.00E+00	7.43E-01	1.00E+00	6.97E-01	1.00E+00	cell proliferation in hindbrain	P
GO:0021536	28	1.00E+00	1.00E+00	5.86E-01	1.00E+00	1.00E+00	1.00E+00	2.97E-01	1.00E+00	9.97E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	diencephalon development	P
GO:0021537	50	6.50E-01	1.00E+00	6.42E-01	1.00E+00	6.37E-01	1.00E+00	6.47E-01	1.00E+00	5.08E-01	1.00E+00	4.30E-01	1.00E+00	8.09E-01	1.00E+00	8.99E-01	1.00E+00	telencephalon development	P
GO:0021543	35	2.33E-01	1.00E+00	4.51E-01	1.00E+00	1.82E-01	1.00E+00	5.03E-01	1.00E+00	1.61E-01	1.00E+00	2.52E-01	1.00E+00	6.51E-01	1.00E+00	8.05E-01	1.00E+00	pallium development	P
GO:0021545	13	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cranial nerve development	P
GO:0021549	26	7.31E-01	1.00E+00	9.72E-01	1.00E+00	9.10E-01	1.00E+00	9.94E-01	1.00E+00	6.10E-01	1.00E+00	9.51E-01	1.00E+00	4.08E-01	1.00E+00	4.89E-01	1.00E+00	cerebellum development	P
GO:0021575	19	5.41E-01	1.00E+00	9.10E-01	1.00E+00	7.26E-01	1.00E+00	9.72E-01	1.00E+00	5.99E-01	1.00E+00	8.87E-01	1.00E+00	2.66E-01	1.00E+00	3.48E-01	1.00E+00	hindbrain morphogenesis	P
GO:0021587	18	5.20E-01	1.00E+00	8.82E-01	1.00E+00	6.89E-01	1.00E+00	9.56E-01	1.00E+00	5.64E-01	1.00E+00	8.73E-01	1.00E+00	2.78E-01	1.00E+00	3.26E-01	1.00E+00	cerebellum morphogenesis	P
GO:0021675	19	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.46E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	nerve development	P
GO:0021680	11	7.35E-01	1.00E+00	8.54E-01	1.00E+00	9.64E-01	1.00E+00	9.29E-01	1.00E+00	7.87E-01	1.00E+00	9.04E-01	1.00E+00	3.33E-01	1.00E+00	4.91E-01	1.00E+00	cerebellar Purkinje cell layer development	P
GO:0021695	20	4.99E-01	1.00E+00	8.94E-01	1.00E+00	7.01E-01	1.00E+00	9.69E-01	1.00E+00	4.94E-01	1.00E+00	8.57E-01	1.00E+00	2.75E-01	1.00E+00	3.58E-01	1.00E+00	cerebellar cortex development	P
GO:0021696	17	4.48E-01	1.00E+00	8.24E-01	1.00E+00	6.14E-01	1.00E+00	9.28E-01	1.00E+00	5.13E-01	1.00E+00	8.24E-01	1.00E+00	2.44E-01	1.00E+00	2.78E-01	1.00E+00	cerebellar cortex morphogenesis	P
GO:0021697	13	5.84E-01	1.00E+00	9.28E-01	1.00E+00	7.04E-01	1.00E+00	8.82E-01	1.00E+00	5.30E-01	1.00E+00	9.83E-01	1.00E+00	4.35E-01	1.00E+00	6.71E-01	1.00E+00	cerebellar cortex formation	P
GO:0021700	90	8.41E-01	1.00E+00	1.00E+00	1.00E+00	7.08E-01	1.00E+00	9.89E-01	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	5.79E-01	1.00E+00	9.98E-01	1.00E+00	developmental maturation	P
GO:0021761	20	3.56E-01	1.00E+00	4.58E-01	1.00E+00	2.01E-01	1.00E+00	4.26E-01	1.00E+00	3.68E-01	1.00E+00	3.93E-01	1.00E+00	6.65E-01	1.00E+00	5.84E-01	1.00E+00	limbic system development	P
GO:0021766	16	1.07E-01	1.00E+00	2.19E-01	1.00E+00	5.41E-02	1.00E+00	2.05E-01	1.00E+00	1.65E-01	1.00E+00	1.65E-01	1.00E+00	3.24E-01	1.00E+00	3.90E-01	1.00E+00	hippocampus development	P
GO:0021782	14	2.63E-01	1.00E+00	5.60E-01	1.00E+00	1.31E-01	1.00E+00	5.99E-01	1.00E+00	2.26E-01	1.00E+00	4.62E-01	1.00E+00	7.55E-01	1.00E+00	5.99E-01	1.00E+00	glial cell development	P
GO:0021795	11	1.70E-01	1.00E+00	5.10E-01	1.00E+00	3.27E-01	1.00E+00	7.43E-01	1.00E+00	6.74E-02	1.00E+00	4.72E-01	1.00E+00	3.86E-01	1.00E+00	4.68E-01	1.00E+00	cerebral cortex cell migration	P
GO:0021872	11	9.68E-01	1.00E+00	9.59E-01	1.00E+00	9.50E-01	1.00E+00	9.93E-01	1.00E+00	9.68E-01	1.00E+00	9.56E-01	1.00E+00	9.13E-01	1.00E+00	8.59E-01	1.00E+00	generation of neurons in the forebrain	P
GO:0021885	14	3.62E-01	1.00E+00	7.57E-01	1.00E+00	5.49E-01	1.00E+00	9.27E-01	1.00E+00	1.84E-01	1.00E+00	6.90E-01	1.00E+00	5.64E-01	1.00E+00	6.76E-01	1.00E+00	forebrain cell migration	P
GO:0021895	13	8.96E-01	1.00E+00	7.14E-01	1.00E+00	9.42E-01	1.00E+00	7.99E-01	1.00E+00	8.33E-01	1.00E+00	6.79E-01	1.00E+00	8.67E-01	1.00E+00	6.38E-01	1.00E+00	cerebral cortex neuron differentiation	P
GO:0021915	62	9.49E-01	1.00E+00	5.40E-01	1.00E+00	9.40E-01	1.00E+00	4.86E-01	1.00E+00	8.22E-01	1.00E+00	7.14E-01	1.00E+00	9.85E-01	1.00E+00	5.02E-01	1.00E+00	neural tube development	P
GO:0021924	10	9.64E-01	1.00E+00	9.86E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.40E-01	1.00E+00	7.43E-01	1.00E+00	6.97E-01	1.00E+00	cell proliferation in the external granule laye	P
GO:0021930	10	9.64E-01	1.00E+00	9.86E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.40E-01	1.00E+00	7.43E-01	1.00E+00	6.97E-01	1.00E+00	granule cell precursor proliferation	P
GO:0021953	33	6.67E-01	1.00E+00	8.13E-01	1.00E+00	8.16E-01	1.00E+00	8.87E-01	1.00E+00	5.86E-01	1.00E+00	8.16E-01	1.00E+00	5.47E-01	1.00E+00	5.53E-01	1.00E+00	central nervous system neuron differentiatio	P
GO:0021954	29	7.34E-01	1.00E+00	7.21E-01	1.00E+00	8.49E-01	1.00E+00	8.22E-01	1.00E+00	5.81E-01	1.00E+00	7.27E-01	1.00E+00	6.50E-01	1.00E+00	4.76E-01	1.00E+00	central nervous system neuron developmen	P
GO:0021955	14	5.83E-01	1.00E+00	3.06E-01	1.00E+00	7.24E-01	1.00E+00	3.46E-01	1.00E+00	5.20E-01	1.00E+00	4.05E-01	1.00E+00	5.28E-01	1.00E+00	2.67E-01	1.00E+00	central nervous system neuron axonogenes	P
GO:0021983	22	1.00E+00	1.00E+00	4.38E-01	1.00E+00	1.00E+00	1.00E+00	2.57E-01	1.00E+00	1.00E+00	1.00E+00	9.78E-01	1.00E+00	9.97E-01	1.00E+00	9.54E-01	1.00E+00	pituitary gland development	P
GO:0021987	26	3.13E-02	1.00E+00	1.20E-01	1.00E+00	2.32E-02	1.00E+00	1.24E-01	1.00E+00	4.75E-02	1.00E+00	8.52E-02	1.00E+00	2.94E-01	1.00E+00	4.28E-01	1.00E+00	cerebral cortex development	P
GO:0022008	420	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	1.00E+00	1.00E+00	neurogenesis	P
GO:0022029	13	2.73E-01	1.00E+00	6.68E-01	1.00E+00	4.56E-01	1.00E+00	8.80E-01	1.00E+00	1.33E-01	1.00E+00	6.07E-01	1.00E+00	4.53E-01	1.00E+00	5.72E-01	1.00E+00	telencephalon cell migration	P
GO:0022037	31	8.25E-01	1.00E+00	9.98E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	5.02E-01	1.00E+00	9.94E-01	1.00E+00	6.04E-01	1.00E+00	7.45E-01	1.00E+00	metencephalon development	P
GO:0030001	575	4.74E-01	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	9.35E-01	1.00E+00	8.72E-01	1.00E+00	1.00E+00	1.00E+00	7.67E-03	2.01E-01	7.19E-01	1.00E+00	metal ion transport	P
GO:0030003	144	8.20E-02	1.00E+00	9.14E-01	1.00E+00	1.97E-01	1.00E+00	5.44E-01	1.00E+00	1.82E-01	1.00E+00	9.97E-01	1.00E+00	1.02E-01	1.00E+00	8.30E-01	1.00E+00	cation homeostasis	P
GO:0030004	18	4.66E-01	1.00E+00	5.55E-01	1.00E+00	5.42E-01	1.00E+00	5.16E-01	1.00E+00	9.78E-01	1.00E+00	7.63E-01	1.00E+00	3.73E-01	1.00E+00	2.40E-01	1.00E+00	monovalent inorganic cation homeostasis	P
GO:0030005	126	7.05E-02	1.00E+00	8.67E-01	1.00E+00	1.86E-01	1.00E+00	4.71E-01	1.00E+00	9.48E-02	1.00E+00	9.90E-01	1.00E+00	1.13E-01	1.00E+00	8.74E-01	1.00E+00	di-, tri-valent inorganic cation homeostasis	P
GO:0030010	12	5.26E-01	1.00E+00	7.29E-01	1.00E+00	3.93E-01	1.00E+00	8.36E-01	1.00E+00	8.50E-01	1.00E+00	8.11E-01	1.00E+00	8.29E-01	1.00E+00	3.70E-01	1.00E+00	establishment of cell polarity	P
GO:0030016	83	6.55E-01	1.00E+00	9.99E-01	1.00E+00	3.98E-01	1.00E+00	9.98E-01	1.00E+00	6.76E-01	1.00E+00	9.95E-01	1.00E+00	4.69E-01	1.00E+00	9.71E-01	1.00E+00	myofibril	C

GO:0030017	74	5.45E-01	1.00E+00	9.95E-01	1.00E+00	3.38E-01	1.00E+00	9.93E-01	1.00E+00	5.41E-01	1.00E+00	9.81E-01	1.00E+00	5.04E-01	1.00E+00	9.56E-01	1.00E+00	sarcomere	C
GO:0030018	36	3.14E-01	1.00E+00	8.00E-01	1.00E+00	9.35E-02	1.00E+00	9.01E-01	1.00E+00	4.99E-01	1.00E+00	6.03E-01	1.00E+00	5.45E-01	1.00E+00	9.23E-01	1.00E+00	Z disc	C
GO:0030027	56	1.09E-01	1.00E+00	4.23E-02	1.00E+00	1.68E-01	1.00E+00	1.34E-01	1.00E+00	1.37E-01	1.00E+00	1.89E-01	1.00E+00	7.04E-02	1.00E+00	5.87E-02	1.00E+00	lamellipodium	C
GO:0030029	226	3.35E-02	1.00E+00	7.03E-02	1.00E+00	1.25E-01	1.00E+00	1.45E-01	1.00E+00	2.98E-01	1.00E+00	5.24E-01	1.00E+00	3.23E-02	7.53E-01	2.94E-02	1.00E+00	actin filament-based process	P
GO:0030030	323	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.02E-01	1.00E+00	9.68E-01	1.00E+00	cell projection organization and biogenesis	P
GO:0030031	82	6.65E-01	1.00E+00	2.85E-03	1.87E-01	5.27E-01	1.00E+00	9.68E-03	3.78E-01	8.01E-01	1.00E+00	1.28E-02	1.00E+00	6.96E-01	1.00E+00	3.14E-02	1.00E+00	cell projection biogenesis	P
GO:0030032	18	9.38E-01	1.00E+00	5.08E-02	1.00E+00	9.01E-01	1.00E+00	7.06E-02	1.00E+00	8.13E-01	1.00E+00	8.44E-02	1.00E+00	9.98E-01	1.00E+00	1.08E-01	1.00E+00	lamellipodium biogenesis	P
GO:0030035	15	6.21E-02	1.00E+00	6.76E-02	1.00E+00	1.99E-01	1.00E+00	4.43E-01	1.00E+00	1.03E-01	1.00E+00	1.72E-01	1.00E+00	1.26E-01	1.00E+00	1.64E-02	9.40E-01	microspike biogenesis	P
GO:0030036	206	3.67E-02	1.00E+00	6.42E-02	1.00E+00	1.84E-01	1.00E+00	1.64E-01	1.00E+00	1.77E-01	1.00E+00	4.89E-01	1.00E+00	4.43E-02	8.34E-01	2.96E-02	1.00E+00	actin cytoskeleton organization and biogene	P
GO:0030041	36	2.21E-01	1.00E+00	6.05E-02	1.00E+00	3.54E-01	1.00E+00	6.07E-02	1.00E+00	4.67E-01	1.00E+00	3.99E-01	1.00E+00	1.59E-01	1.00E+00	7.72E-02	1.00E+00	actin filament polymerization	P
GO:0030042	22	3.26E-02	1.00E+00	6.67E-02	1.00E+00	2.10E-01	1.00E+00	1.57E-01	1.00E+00	1.23E-01	1.00E+00	1.47E-01	1.00E+00	1.87E-02	4.71E-01	4.25E-02	1.00E+00	actin filament depolymerization	P
GO:0030048	15	1.42E-01	1.00E+00	2.00E-01	1.00E+00	3.94E-01	1.00E+00	1.13E-01	1.00E+00	1.83E-01	1.00E+00	4.38E-01	1.00E+00	1.08E-01	1.00E+00	1.08E-01	1.00E+00	actin filament-based movement	P
GO:0030054	455	5.61E-01	1.00E+00	9.58E-01	1.00E+00	8.03E-01	1.00E+00	8.39E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	1.55E-03	4.40E-02	2.10E-01	1.00E+00	cell junction	C
GO:0030055	49	1.07E-01	1.00E+00	4.96E-01	1.00E+00	2.04E-01	1.00E+00	4.66E-01	1.00E+00	5.40E-01	1.00E+00	8.12E-01	1.00E+00	2.92E-02	6.06E-01	3.66E-01	1.00E+00	cell-matrix junction	C
GO:0030057	15	5.53E-01	1.00E+00	4.17E-01	1.00E+00	9.35E-01	1.00E+00	3.25E-01	1.00E+00	3.70E-01	1.00E+00	4.61E-01	1.00E+00	2.07E-01	1.00E+00	5.58E-01	1.00E+00	desmosome	C
GO:0030072	43	6.54E-01	1.00E+00	6.29E-01	1.00E+00	8.55E-01	1.00E+00	8.56E-01	1.00E+00	1.99E-01	1.00E+00	5.07E-01	1.00E+00	9.00E-01	1.00E+00	2.82E-01	1.00E+00	peptide hormone secretion	P
GO:0030073	37	5.60E-01	1.00E+00	4.76E-01	1.00E+00	8.07E-01	1.00E+00	7.41E-01	1.00E+00	1.65E-01	1.00E+00	3.84E-01	1.00E+00	8.84E-01	1.00E+00	2.08E-01	1.00E+00	insulin secretion	P
GO:0030097	262	8.88E-01	1.00E+00	5.96E-01	1.00E+00	8.43E-01	1.00E+00	2.48E-01	1.00E+00	7.85E-01	1.00E+00	9.52E-01	1.00E+00	9.79E-01	1.00E+00	9.52E-01	1.00E+00	hemopoiesis	P
GO:0030098	109	2.44E-01	1.00E+00	1.79E-01	1.00E+00	4.53E-01	1.00E+00	1.02E-01	1.00E+00	6.83E-01	1.00E+00	9.72E-01	1.00E+00	1.72E-01	1.00E+00	2.62E-01	1.00E+00	lymphocyte differentiation	P
GO:0030099	129	8.33E-01	1.00E+00	8.61E-01	1.00E+00	8.32E-01	1.00E+00	7.74E-01	1.00E+00	4.20E-01	1.00E+00	9.15E-01	1.00E+00	9.90E-01	1.00E+00	9.47E-01	1.00E+00	myeloid cell differentiation	P
GO:0030100	46	2.74E-01	1.00E+00	8.24E-01	1.00E+00	6.57E-01	1.00E+00	7.66E-01	1.00E+00	1.92E-01	1.00E+00	7.85E-01	1.00E+00	1.85E-01	1.00E+00	8.66E-01	1.00E+00	regulation of endocytosis	P
GO:0030101	12	2.69E-02	1.00E+00	2.29E-01	1.00E+00	1.28E-01	1.00E+00	2.58E-01	1.00E+00	5.99E-02	1.00E+00	1.98E-01	1.00E+00	9.93E-02	1.00E+00	3.67E-01	1.00E+00	natural killer cell activation	P
GO:0030111	28	7.07E-01	1.00E+00	9.28E-01	1.00E+00	6.97E-01	1.00E+00	9.31E-01	1.00E+00	5.45E-01	1.00E+00	8.81E-01	1.00E+00	7.11E-01	1.00E+00	8.29E-01	1.00E+00	regulation of Wnt receptor signaling pathwa	P
GO:0030117	61	8.77E-07	2.00E-03	2.14E-07	2.66E-03	1.47E-03	7.90E-02	4.34E-07	1.00E-03	3.60E-05	1.56E-03	1.24E-04	1.36E-02	8.63E-04	2.40E-02	1.94E-03	6.30E-02	membrane coat	C
GO:0030118	39	1.23E-04	1.90E-02	7.32E-05	2.80E-02	1.04E-02	4.74E-01	4.57E-05	5.41E-03	1.33E-02	4.81E-01	6.75E-03	3.55E-01	2.65E-03	5.54E-02	7.21E-03	2.58E-01	clathrin coat	C
GO:0030119	28	2.41E-04	1.90E-02	3.88E-04	4.30E-02	8.68E-03	4.69E-01	1.95E-04	1.10E-02	3.53E-02	1.00E+00	3.06E-02	1.00E+00	4.85E-03	7.75E-02	5.89E-03	2.58E-01	membrane coat adaptor complex	C
GO:0030120	30	1.98E-04	1.90E-02	4.25E-05	2.80E-02	2.46E-02	1.00E+00	1.78E-04	1.10E-02	1.68E-04	8.00E-03	2.17E-03	1.43E-01	1.99E-03	5.54E-02	1.68E-02	9.40E-01	vesicle coat	C
GO:0030125	16	1.36E-02	9.83E-01	2.09E-03	1.62E-01	1.14E-01	1.00E+00	1.60E-03	4.40E-02	3.62E-02	1.00E+00	3.95E-02	1.00E+00	1.14E-02	4.39E-01	4.73E-02	1.00E+00	clathrin vesicle coat	C
GO:0030131	28	2.41E-04	1.90E-02	3.88E-04	4.30E-02	8.68E-03	4.69E-01	1.95E-04	1.10E-02	3.53E-02	1.00E+00	3.06E-02	1.00E+00	4.85E-03	7.75E-02	5.89E-03	2.58E-01	clathrin adaptor complex	C
GO:0030133	41	7.17E-02	1.00E+00	1.01E-01	1.00E+00	2.31E-01	1.00E+00	1.28E-01	1.00E+00	9.87E-02	1.00E+00	1.30E-01	1.00E+00	1.29E-01	1.00E+00	2.12E-01	1.00E+00	transport vesicle	C
GO:0030135	120	2.86E-03	1.39E-01	1.44E-01	1.00E+00	1.81E-01	1.00E+00	3.13E-01	1.00E+00	5.91E-03	1.65E-01	1.91E-01	1.00E+00	1.05E-03	2.40E-02	1.68E-01	1.00E+00	coated vesicle	C
GO:0030136	103	3.83E-02	1.00E+00	5.11E-01	1.00E+00	4.44E-01	1.00E+00	6.89E-01	1.00E+00	8.70E-02	1.00E+00	5.07E-01	1.00E+00	4.01E-03	7.75E-02	3.37E-01	1.00E+00	clathrin-coated vesicle	C
GO:0030137	11	2.57E-04	1.90E-02	1.96E-03	1.62E-01	3.03E-02	1.00E+00	4.16E-03	1.42E-01	1.16E-05	1.56E-03	2.28E-02	1.00E+00	1.46E-02	4.39E-01	1.90E-01	1.00E+00	COPI-coated vesicle	C
GO:0030139	23	2.85E-01	1.00E+00	3.44E-01	1.00E+00	5.06E-01	1.00E+00	3.26E-01	1.00E+00	7.28E-01	1.00E+00	4.80E-01	1.00E+00	1.02E-01	1.00E+00	5.40E-01	1.00E+00	endocytic vesicle	C
GO:0030140	19	8.08E-02	1.00E+00	1.30E-01	1.00E+00	5.09E-01	1.00E+00	2.53E-02	7.69E-01	8.41E-02	1.00E+00	1.99E-01	1.00E+00	2.93E-02	6.06E-01	4.95E-01	1.00E+00	trans-Golgi network transport vesicle	C
GO:0030141	55	1.36E-01	1.00E+00	2.22E-01	1.00E+00	9.22E-01	1.00E+00	2.18E-01	1.00E+00	1.60E-01	1.00E+00	5.65E-01	1.00E+00	6.40E-02	1.00E+00	9.69E-02	1.00E+00	secretory granule	C
GO:0030145	139	7.71E-03	6.18E-01	1.02E-03	7.30E-02	1.53E-02	8.10E-01	1.80E-02	7.69E-01	7.74E-02	1.00E+00	2.28E-03	1.43E-01	2.10E-02	5.29E-01	1.09E-02	6.43E-01	manganese ion binding	F
GO:0030148	20	3.94E-01	1.00E+00	3.41E-02	1.00E+00	3.30E-01	1.00E+00	2.43E-02	7.69E-01	7.83E-01	1.00E+00	5.01E-01	1.00E+00	3.24E-01	1.00E+00	1.03E-01	1.00E+00	sphingolipid biosynthesis	P
GO:0030149	11	6.72E-02	1.00E+00	1.67E-01	1.00E+00	9.92E-03	4.74E-01	2.16E-01	1.00E+00	5.99E-01	1.00E+00	4.53E-01	1.00E+00	7.51E-01	1.00E+00	2.32E-01	1.00E+00	sphingolipid catabolism	P
GO:0030154	1347	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	cell differentiation	P
GO:0030155	65	7.39E-01	1.00E+00	6.74E-01	1.00E+00	8.71E-01	1.00E+00	8.50E-01	1.00E+00	7.56E-01	1.00E+00	6.93E-01	1.00E+00	3.75E-01	1.00E+00	2.48E-01	1.00E+00	regulation of cell adhesion	P
GO:0030162	14	5.90E-01	1.00E+00	3.62E-01	1.00E+00	6.25E-01	1.00E+00	1.60E-01	1.00E+00	6.37E-01	1.00E+00	8.99E-01	1.00E+00	5.46E-01	1.00E+00	7.97E-01	1.00E+00	regulation of proteolysis	P
GO:0030163	221	4.79E-08	9.73E-04	1.83E-12	0.00E+00	6.78E-07	9.88E-04	3.69E-10	0.00E+00	3.66E-07	7.65E-04	3.56E-08	7.71E-04	1.89E-01	1.00E+00	1.12E-05	3.91E-03	protein catabolism	P
GO:0030165	29	6.71E-01	1.00E+00	9.79E-01	1.00E+00	8.80E-01	1.00E+00	9.16E-01	1.00E+00	8.18E-01	1.00E+00	9.81E-01	1.00E+00	2.45E-01	1.00E+00	9.57E-01	1.00E+00	PDZ domain binding	F
GO:0030166	22	9.44E-01	1.00E+00	8.48E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	4.71E-01	1.00E+00	9.84E-01	1.00E+00	7.46E-01	1.00E+00	2.86E-01	1.00E+00	proteoglycan biosynthesis	P
GO:0030168	16	8.84E-01	1.00E+00	4.18E-01	1.00E+00	9.22E-01	1.00E+00	4.90E-01	1.00E+00	8.09E-01	1.00E+00	8.49E-01	1.00E+00	7.69E-01	1.00E+00	1.58E-01	1.00E+00	platelet activation	P
GO:0030169	14	4.53E-02	1.00E+00	2.71E-01	1.00E+00	1.79E-02	8.10E-01	5.06E-01	1.00E+00	7.68E-02	1.00E+00	2.50E-01	1.00E+00	6.88E-01	1.00E+00	6.08E-01	1.00E+00	low-density lipoprotein binding	F
GO:0030170	63	3.82E-02	1.00E+00	1.64E-02	1.00E+00	7.84E-02	1.00E+00	2.78E-01	1.00E+00	9.47E-03	3.69E-01	2.04E-03	1.43E-01	1.44E-01	1.00E+00	1.02E-01	1.00E+00	pyridoxal phosphate binding	F
GO:0030173	32	1.63E-01	1.00E+00	6.13E-01	1.00E+00	3.33E-01	1.00E+00	8.19E-01	1.00E+00	9.50E-01	1.00E+00	7.62E-01	1.00E+00	1.82E-02	4.71E-01	7.76E-02	1.00E+00	integral to Golgi membrane	C
GO:0030175	18	3.89E-02	1.00E+00	2.11E-01	1.00E+00	2.23E-01	1.00E+00	2.14E-01	1.00E+00	1.42E-02	4.81E-01	5.05E-01	1.00E+00	1.65E-01	1.00E+00	2.29E-01	1.00E+00	filopodium	C
GO:0030176	33	2.69E-01	1.00E+00	3.08E-02	1.00E+00	5.33E-01	1.00E+00	6.28E-02	1.00E+00	1.23E-01	1.00E+00	8.02E-02	1.00E+00	7.41E-01	1.00E+00	1.21E-01	1.00E+00	integral to endoplasmic reticulum membrane	C
GO:0030178	20	3.05E-01	1.00E+00	7.71E-01	1.00E+00	2.35E-01	1.00E+00	8.88E-01	1.00E+00	2.68E-01	1.00E+00	6.78E-01	1.00E+00	4.15E-01	1.00E+00	5.54E-01	1.00E+00	negative regulation of Wnt receptor signalin	P
GO:0030182	342	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	neuron differentiation	P
GO:0030183	47	4.04E-01	1.00E+00	9.91E-02	1.00E+00	3.54E-01	1.00E+00	1.01E-01	1.00E+00	9.48E-01	1.00E+00	8.30E-01	1.00E+00	2.48E-01	1.00E+00	1.87E-01	1.00E+00	B cell differentiation	P
GO:0030193	13	7.62E-01	1.00E+00	3.76E-01	1.00E+00	8.86E-01	1.00E+00	6.70E-01	1.00E+00	5.13E-01	1.00E+00	5.96E-01	1.00E+00	5.33E-01	1.00E+00	1.17E-01	1.00E+00	regulation of blood coagulation	P
GO:0030198	78	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.39E-01	1.00E+00	8.90E-01	1.00E+00	extracellular matrix organization and biogen	P
GO:0030199	12	9.14E-01	1.00E+00	8.47E-01	1.00E+00	9.92E-01	1.00E+00	9.74E-01	1.00E+00	4.93E-01	1.00E+00	9.05E-01	1.00E+00	8.01E-01	1.00E+00	2.62E-01	1.00E+00	collagen fibril organization	P
GO:0030203	29	7.19E-01	1.00E+00	5.94E-01	1.00E+00	8.77E-01	1.00E+00	6.46E-01	1.00E+00	2.70E-01	1.00E+00	8.25E-01	1.00E+00	9.40E-01	1.00E+00	3.95E-01	1.00E+00	glycosaminoglycan metabolism	P
GO:0030216	35	5.12E-01	1.00E+00	5.66E-01	1.00E+00	3.88E-01	1.00E+00	2.71E-01	1.00E+00	2.39E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	keratinocyte differentiation	P
GO:0030217	71	3.23E-01	1.00E+00	8.33E-01	1.00E+00	8.44E-01	1.00E+00	4.71E-01	1.00E+00	6.62E-01	1.00E+00	9.99E-01	1.00E+00	1.18E-01	1.00E+00	4.46E-01	1.00E+00	T cell differentiation	P
GO:0030218	50	5.99E-01	1.00E+00	3.69E-01	1.00E+00	4.95E-01	1.00E+00	3.40E-01	1.00E+00	3.73E-01	1.00E+00	5.95E-01	1.00E+00	9.62E-01	1.00E+00	8.70E-01	1.00E+00	erythrocyte differentiation	P
GO:0030225	11	9.82E-01	1.00E+00	8.82E-01	1.00E+00	7.77E-01	1.00E+00	8.86E-01	1.00E+00	9.91E-01	1.00E+00	7.69E-01	1.00E+00	9.91E-01	1.00E+00	9.60E-01	1.00E+00	macrophage differentiation	P
GO:0030234	815	3.40E-01	1.00E+00	8.02E-01	1.00E+00	7.59E-01	1.00E+00	9.17E-01	1.00E+00	2.92E-01	1.00E+00	9.75E-01	1.00E+00	2.83E-01	1.00E+00	1.12E-01	1.00E+00	enzyme regulator activity	F
GO:0030238	10	9.16E-01	1.00E+00	9.78E-01	1.00E+00	9.99E-01	1.00E+00	9.24E-01	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	3.89E-01	1.00E+00	5.89E-01	1.00E+00	male sex determination	P
GO:0030239	18	4.64E-01	1.00E+00	5.20E-01	1.00E+00	3.38E-01	1.00E+00	2.43E-01	1.00E+00	9.99E-01	1.00E+00	7.46E-01	1.00E+00	3.11E-01	1.00E+00	7.42E-01	1.00E+00	myofibril assembly	P
GO:0030246	311	9.97E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.65E-02	1.00E+00	4.00E-01	1.00E+00	carbohydrate binding	F
GO:0030247	95	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.72E-01	1.00E+00	8.95E-01	1.00E+00	polysaccharide binding	F
GO:0030258	37	4.56E-02	1.00E+00	4.16E-03	3.82E-01	4.50E-02	1.00E+00	8.11E-03	3.78E-01	9.61E-02	1.00E+00	4.73E-02	1.00E+00	3.30E-01	1.00E+00	9.92E-04	4.40E-02	lipid modification	P
GO:0030261	21	6.47E-03	3.64E-01	7.23E-03	5.59E-01	1.94E-02	8.10E-01	1.90E-02	7.69E-01	3.31E-03	1.35E-01	1.05E-02	4.01E-01	2.97E-01	1.00E+00	1.38E-01	1.00E+00	chromosome condensation	P
GO:0030262	16	2.20E-02	1.00E+00	5.29E-04	7.30E-02	2.55E-02	1.00E+00	1.58E-04	5.80E-03	9.39E-02	1.00E+00	6.90E-02	1.00E+00	2.36E-01	1.00E+00	4.65E-02	1.00E+00	apoptotic nuclear changes	P
GO:0030278	38	9.53E-01	1.00E+00	9.96E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	6.04E-01	1.00E+00	9.96E-01	1.00E+00	8.57E-01	1.00E+00	7.52E-01	1.00E+00	regulation of ossification	P
GO:0030279	12	3.92E-01	1.00E+00	8.39E-01	1.00E+00	5.82E-01	1.00E+00	9.04E-01	1.00E+00	1.45E-01	1.00E+00	9.86E-01	1.00E+00	5.04E-01	1.00E+00	4.90E-01	1.00E+00	negative regulation of ossification	P
GO:0030282	36	9.23E-01	1.00E+00	9.42E-01	1.00E+00	9.95E-01	1.00E+00	8.77E-01	1.00E+00	5.77E-01	1.00E+00	9.96E-01	1.00E+00	5.15E-01	1.00E+00	5.10E-01	1.00E+00	bone mineralization	P
GO:0030286	37	1.19E-01	1.00E+00	3.88E-01	1.00E+00	1.13E-01	1.00E+00	4.30E-01	1.00E+00	2.14E-01	1.00E+00	3.13E-01	1.00E+00	1.56E-01	1.00E+00	5.48E-01	1.00E+00	dynein complex	C
GO:0030288	20	6.95E-01	1.00E+00	9.98E-01	1.00E+00	9.67E-01	1.00E+00	7.73E-01	1.00E+00	6.71E-01	1.00E+00	1.00E+00	1.00E+00	1.18E-01	1.00E+00	9.55E-01	1.00E+00	periplasmic space (sensu Proteobacteria)	C

GO:0030295	11	9.51E-01	1.00E+00	4.78E-01	1.00E+00	8.60E-01	1.00E+00	7.80E-01	1.00E+00	5.52E-01	1.00E+00	4.03E-01	1.00E+00	1.00E+00	1.00E+00	8.07E-01	1.00E+00	protein kinase activator activity	F
GO:0030301	15	2.32E-01	1.00E+00	5.26E-01	1.00E+00	2.78E-01	1.00E+00	6.49E-01	1.00E+00	2.42E-01	1.00E+00	4.43E-01	1.00E+00	2.87E-01	1.00E+00	4.43E-01	1.00E+00	cholesterol transport	P
GO:0030308	48	8.89E-02	1.00E+00	3.89E-01	1.00E+00	6.06E-02	1.00E+00	1.19E-01	1.00E+00	4.98E-01	1.00E+00	8.57E-01	1.00E+00	6.85E-02	1.00E+00	3.35E-01	1.00E+00	negative regulation of cell growth	P
GO:0030312	24	5.81E-01	1.00E+00	9.94E-01	1.00E+00	8.29E-01	1.00E+00	7.74E-01	1.00E+00	6.00E-01	1.00E+00	9.97E-01	1.00E+00	1.62E-01	1.00E+00	9.73E-01	1.00E+00	external encapsulating structure	C
GO:0030313	22	5.93E-01	1.00E+00	9.96E-01	1.00E+00	9.29E-01	1.00E+00	7.87E-01	1.00E+00	5.64E-01	1.00E+00	1.00E+00	1.00E+00	1.23E-01	1.00E+00	9.64E-01	1.00E+00	cell envelope	C
GO:0030315	16	9.22E-01	1.00E+00	9.91E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	9.55E-01	1.00E+00	5.16E-01	1.00E+00	8.66E-01	1.00E+00	T-tubule	C
GO:0030316	21	9.39E-01	1.00E+00	7.05E-01	1.00E+00	7.70E-01	1.00E+00	6.65E-01	1.00E+00	8.21E-01	1.00E+00	6.79E-01	1.00E+00	1.00E+00	1.00E+00	5.42E-01	1.00E+00	osteoclast differentiation	P
GO:0030317	29	6.84E-01	1.00E+00	7.37E-01	1.00E+00	6.54E-01	1.00E+00	3.04E-01	1.00E+00	8.53E-01	1.00E+00	9.94E-01	1.00E+00	4.85E-01	1.00E+00	9.98E-01	1.00E+00	sperm motility	P
GO:0030318	18	9.66E-01	1.00E+00	9.33E-01	1.00E+00	9.73E-01	1.00E+00	9.73E-01	1.00E+00	9.44E-01	1.00E+00	9.74E-01	1.00E+00	7.85E-01	1.00E+00	3.58E-01	1.00E+00	melanocyte differentiation	P
GO:0030321	10	7.69E-01	1.00E+00	9.93E-01	1.00E+00	6.14E-01	1.00E+00	9.82E-01	1.00E+00	9.95E-01	1.00E+00	8.79E-01	1.00E+00	2.65E-01	1.00E+00	9.87E-01	1.00E+00	transepithelial chloride transport	P
GO:0030323	90	1.00E+00	1.00E+00	9.38E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	8.24E-01	1.00E+00	5.15E-01	1.00E+00	respiratory tube development	P
GO:0030324	88	1.00E+00	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	7.87E-01	1.00E+00	4.71E-01	1.00E+00	lung development	P
GO:0030325	10	9.98E-01	1.00E+00	1.00E+00	1.00E+00	7.53E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	adrenal gland development	P
GO:0030326	85	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	embryonic limb morphogenesis	P
GO:0030330	17	2.12E-01	1.00E+00	5.60E-01	1.00E+00	1.70E-01	1.00E+00	1.21E-01	1.00E+00	8.03E-01	1.00E+00	9.27E-01	1.00E+00	6.93E-01	1.00E+00	3.94E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0030334	85	7.85E-01	1.00E+00	9.84E-01	1.00E+00	7.23E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	9.82E-01	1.00E+00	3.94E-01	1.00E+00	6.31E-01	1.00E+00	regulation of cell migration	P
GO:0030335	36	5.43E-01	1.00E+00	9.39E-01	1.00E+00	6.60E-01	1.00E+00	1.00E+00	1.00E+00	6.87E-01	1.00E+00	9.84E-01	1.00E+00	2.43E-01	1.00E+00	1.46E-01	1.00E+00	positive regulation of cell migration	P
GO:0030336	24	7.74E-01	1.00E+00	8.29E-01	1.00E+00	3.70E-01	1.00E+00	6.46E-01	1.00E+00	9.79E-01	1.00E+00	8.13E-01	1.00E+00	5.70E-01	1.00E+00	9.98E-01	1.00E+00	negative regulation of cell migration	P
GO:0030374	19	1.65E-01	1.00E+00	3.94E-01	1.00E+00	4.73E-02	1.00E+00	9.23E-02	1.00E+00	4.27E-01	1.00E+00	8.66E-01	1.00E+00	4.86E-01	1.00E+00	9.05E-01	1.00E+00	ligand-dependent nuclear receptor transcrip	F
GO:0030375	11	2.89E-01	1.00E+00	6.42E-01	1.00E+00	2.99E-01	1.00E+00	1.94E-01	1.00E+00	3.89E-01	1.00E+00	9.73E-01	1.00E+00	3.43E-01	1.00E+00	9.47E-01	1.00E+00	thyroid hormone receptor coactivator activity	F
GO:0030384	60	1.36E-03	9.30E-02	7.25E-05	2.80E-02	6.81E-04	3.00E-02	8.14E-04	2.70E-02	6.75E-02	1.00E+00	1.27E-03	5.10E-02	2.64E-02	6.06E-01	3.18E-03	2.16E-01	phosphoinositide metabolism	P
GO:0030414	219	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.37E-01	1.00E+00	9.98E-01	1.00E+00	protease inhibitor activity	F
GO:0030424	80	9.33E-01	1.00E+00	9.99E-01	1.00E+00	9.71E-01	1.00E+00	1.00E+00	1.00E+00	6.49E-01	1.00E+00	9.99E-01	1.00E+00	8.35E-01	1.00E+00	7.35E-01	1.00E+00	axon	C
GO:0030425	76	4.45E-01	1.00E+00	9.94E-01	1.00E+00	8.60E-01	1.00E+00	9.62E-01	1.00E+00	1.73E-01	1.00E+00	1.00E+00	1.00E+00	3.49E-01	1.00E+00	6.38E-01	1.00E+00	dendrite	C
GO:0030426	34	3.55E-01	1.00E+00	7.42E-01	1.00E+00	1.51E-01	1.00E+00	9.62E-01	1.00E+00	5.87E-01	1.00E+00	7.21E-01	1.00E+00	6.67E-01	1.00E+00	3.31E-01	1.00E+00	growth cone	C
GO:0030427	34	3.55E-01	1.00E+00	7.42E-01	1.00E+00	1.51E-01	1.00E+00	9.62E-01	1.00E+00	5.87E-01	1.00E+00	7.21E-01	1.00E+00	6.67E-01	1.00E+00	3.31E-01	1.00E+00	site of polarized growth	C
GO:0030433	11	1.90E-01	1.00E+00	2.15E-03	1.62E-01	1.10E-01	1.00E+00	3.24E-03	1.42E-01	1.97E-01	1.00E+00	7.31E-02	1.00E+00	7.97E-01	1.00E+00	4.64E-02	1.00E+00	ER-associated protein catabolism	P
GO:0030496	10	1.42E-01	1.00E+00	5.20E-02	1.00E+00	9.81E-02	1.00E+00	3.82E-02	1.00E+00	4.96E-01	1.00E+00	5.61E-01	1.00E+00	2.64E-01	1.00E+00	1.27E-01	1.00E+00	midbody	C
GO:0030500	24	9.68E-01	1.00E+00	9.73E-01	1.00E+00	9.99E-01	1.00E+00	9.93E-01	1.00E+00	4.78E-01	1.00E+00	9.97E-01	1.00E+00	8.31E-01	1.00E+00	6.03E-01	1.00E+00	regulation of bone mineralization	P
GO:0030501	12	8.91E-01	1.00E+00	7.01E-01	1.00E+00	9.98E-01	1.00E+00	7.82E-01	1.00E+00	6.93E-01	1.00E+00	8.20E-01	1.00E+00	4.85E-01	1.00E+00	3.56E-01	1.00E+00	positive regulation of bone mineralization	P
GO:0030509	41	9.84E-01	1.00E+00	9.81E-01	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	9.63E-01	1.00E+00	8.85E-01	1.00E+00	8.17E-01	1.00E+00	9.54E-01	1.00E+00	BMP signaling pathway	P
GO:0030510	20	9.39E-01	1.00E+00	8.63E-01	1.00E+00	9.87E-01	1.00E+00	8.91E-01	1.00E+00	9.22E-01	1.00E+00	6.14E-01	1.00E+00	3.78E-01	1.00E+00	9.97E-01	1.00E+00	regulation of BMP signaling pathway	P
GO:0030512	10	2.04E-01	1.00E+00	1.27E-01	1.00E+00	2.72E-01	1.00E+00	1.92E-01	1.00E+00	7.48E-02	1.00E+00	6.87E-02	1.00E+00	5.09E-01	1.00E+00	1.32E-01	1.00E+00	negative regulation of transforming growth f	P
GO:0030514	13	9.99E-01	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	9.35E-01	1.00E+00	8.93E-01	1.00E+00	5.35E-01	1.00E+00	5.51E-01	1.00E+00	9.90E-01	1.00E+00	negative regulation of BMP signaling pathwa	P
GO:0030516	15	4.86E-01	1.00E+00	7.14E-01	1.00E+00	8.77E-01	1.00E+00	7.60E-01	1.00E+00	7.34E-01	1.00E+00	8.17E-01	1.00E+00	1.53E-01	1.00E+00	4.18E-01	1.00E+00	regulation of axon extension	P
GO:0030518	24	3.31E-02	1.00E+00	8.17E-02	1.00E+00	9.73E-03	4.74E-01	3.38E-02	1.00E+00	1.70E-01	1.00E+00	2.44E-01	1.00E+00	8.89E-01	1.00E+00	4.71E-01	1.00E+00	steroid hormone receptor signaling pathway	P
GO:0030521	13	2.01E-02	1.00E+00	4.84E-02	1.00E+00	5.32E-03	1.88E-01	1.05E-02	3.78E-01	5.78E-02	1.00E+00	2.33E-01	1.00E+00	9.78E-01	1.00E+00	6.71E-01	1.00E+00	androgen receptor signaling pathway	P
GO:0030522	34	2.93E-01	1.00E+00	4.42E-01	1.00E+00	4.51E-02	1.00E+00	2.60E-01	1.00E+00	5.57E-01	1.00E+00	4.86E-01	1.00E+00	9.96E-01	1.00E+00	8.07E-01	1.00E+00	intracellular receptor-mediated signaling pat	P
GO:0030528	1329	8.95E-01	1.00E+00	4.96E-01	1.00E+00	7.65E-01	1.00E+00	4.82E-02	1.00E+00	9.91E-01	1.00E+00	9.47E-01	1.00E+00	7.62E-01	1.00E+00	8.30E-01	1.00E+00	transcription regulator activity	F
GO:0030529	490	9.26E-03	9.83E-01	3.53E-12	0.00E+00	2.38E-03	1.18E-01	6.34E-12	0.00E+00	7.72E-02	1.00E+00	2.50E-06	2.00E-03	9.96E-01	1.00E+00	1.78E-01	1.00E+00	ribonucleoprotein complex	C
GO:0030532	15	1.11E-03	9.30E-02	1.56E-04	2.80E-02	2.08E-02	1.00E+00	2.08E-03	4.50E-02	1.45E-01	1.00E+00	8.04E-02	1.00E+00	1.05E-01	1.00E+00	7.19E-02	1.00E+00	small nuclear ribonucleoprotein complex	C
GO:0030534	82	6.30E-01	1.00E+00	9.98E-01	1.00E+00	6.23E-01	1.00E+00	9.73E-01	1.00E+00	6.26E-01	1.00E+00	1.00E+00	1.00E+00	5.64E-01	1.00E+00	9.45E-01	1.00E+00	adult behavior	P
GO:0030539	11	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.56E-01	1.00E+00	8.66E-01	1.00E+00	1.00E+00	1.00E+00	6.53E-01	1.00E+00	male genitalia development	P
GO:0030545	10	7.14E-01	1.00E+00	9.98E-01	1.00E+00	6.53E-01	1.00E+00	9.71E-01	1.00E+00	7.61E-01	1.00E+00	9.98E-01	1.00E+00	4.52E-01	1.00E+00	9.56E-01	1.00E+00	receptor regulator activity	F
GO:0030551	26	9.64E-01	1.00E+00	4.47E-01	1.00E+00	9.92E-01	1.00E+00	9.55E-01	1.00E+00	3.82E-01	1.00E+00	1.82E-01	1.00E+00	9.52E-01	1.00E+00	2.09E-01	1.00E+00	cyclic nucleotide binding	F
GO:0030552	18	9.89E-01	1.00E+00	3.58E-01	1.00E+00	1.00E+00	1.00E+00	7.13E-01	1.00E+00	5.80E-01	1.00E+00	3.52E-01	1.00E+00	9.33E-01	1.00E+00	1.43E-01	1.00E+00	cAMP binding	F
GO:0030554	1620	2.36E-17	0.00E+00	1.28E-24	0.00E+00	1.79E-10	0.00E+00	1.81E-14	0.00E+00	3.63E-13	0.00E+00	1.11E-16	0.00E+00	5.07E-08	6.33E-04	1.37E-12	0.00E+00	adenyl nucleotide binding	F
GO:0030574	17	9.78E-01	1.00E+00	8.91E-01	1.00E+00	7.30E-01	1.00E+00	8.58E-01	1.00E+00	9.69E-01	1.00E+00	9.16E-01	1.00E+00	1.00E+00	1.00E+00	3.45E-01	1.00E+00	collagen catabolism	P
GO:0030593	16	9.10E-01	1.00E+00	5.47E-01	1.00E+00	5.81E-01	1.00E+00	7.67E-01	1.00E+00	9.32E-01	1.00E+00	6.90E-01	1.00E+00	9.00E-01	1.00E+00	1.44E-01	1.00E+00	neutrophil chemotaxis	P
GO:0030594	210	9.99E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.34E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	5.29E-01	1.00E+00	4.45E-01	1.00E+00	neurotransmitter receptor activity	F
GO:0030595	32	1.00E+00	1.00E+00	9.13E-01	1.00E+00	9.18E-01	1.00E+00	8.58E-01	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	9.99E-01	1.00E+00	6.31E-01	1.00E+00	leukocyte chemotaxis	P
GO:0030641	13	2.44E-01	1.00E+00	3.95E-01	1.00E+00	3.05E-01	1.00E+00	3.41E-01	1.00E+00	8.66E-01	1.00E+00	5.71E-01	1.00E+00	3.70E-01	1.00E+00	2.15E-01	1.00E+00	hydrogen ion homeostasis	P
GO:0030658	17	1.10E-02	9.83E-01	1.77E-02	1.00E+00	1.90E-01	1.00E+00	6.18E-03	3.78E-01	1.46E-02	4.81E-01	2.33E-02	1.00E+00	1.20E-02	4.39E-01	1.27E-01	1.00E+00	transport vesicle membrane	C
GO:0030659	93	5.94E-03	3.64E-01	2.05E-02	1.00E+00	3.73E-02	1.00E+00	6.34E-02	1.00E+00	4.23E-02	1.00E+00	5.85E-02	1.00E+00	3.88E-02	7.83E-01	7.98E-02	1.00E+00	cytoplasmic vesicle membrane	C
GO:0030660	19	3.03E-03	1.39E-01	6.27E-03	5.59E-01	6.84E-02	1.00E+00	2.21E-03	4.50E-02	1.05E-02	4.14E-01	1.08E-02	4.01E-01	4.05E-03	7.75E-02	9.70E-02	1.00E+00	Golgi-associated vesicle membrane	C
GO:0030662	33	1.76E-04	1.90E-02	1.30E-04	2.80E-02	3.00E-02	1.00E+00	2.86E-04	1.30E-02	5.96E-04	4.40E-02	2.54E-03	1.43E-01	1.73E-03	5.54E-02	2.48E-02	1.00E+00	coated vesicle membrane	C
GO:0030665	19	1.05E-02	9.83E-01	6.10E-03	5.59E-01	1.38E-01	1.00E+00	3.35E-03	1.42E-01	3.59E-02	1.00E+00	4.18E-02	1.00E+00	1.02E-02	2.17E-01	7.24E-02	1.00E+00	clathrin coated vesicle membrane	C
GO:0030667	10	7.31E-01	1.00E+00	1.23E-01	1.00E+00	8.74E-01	1.00E+00	4.13E-01	1.00E+00	6.36E-01	1.00E+00	1.70E-01	1.00E+00	9.89E-01	1.00E+00	1.26E-01	1.00E+00	secretory granule membrane	C
GO:0030672	16	5.33E-01	1.00E+00	9.32E-01	1.00E+00	5.51E-01	1.00E+00	8.85E-01	1.00E+00	8.66E-01	1.00E+00	9.84E-01	1.00E+00	3.72E-01	1.00E+00	8.81E-01	1.00E+00	synaptic vesicle membrane	C
GO:0030674	34	6.79E-02	1.00E+00	2.07E-01	1.00E+00	5.43E-02	1.00E+00	1.70E-01	1.00E+00	2.56E-01	1.00E+00	5.67E-01	1.00E+00	1.08E-01	1.00E+00	2.10E-01	1.00E+00	protein binding, bridging	F
GO:0030693	16	8.71E-01	1.00E+00	8.68E-01	1.00E+00	6.45E-01	1.00E+00	5.50E-01	1.00E+00	9.92E-01	1.00E+00	6.29E-01	1.00E+00	6.03E-01	1.00E+00	1.00E+00	1.00E+00	caspase activity	F
GO:0030695	367	6.47E-03	3.64E-01	1.81E-01	1.00E+00	6.28E-02	1.00E+00	8.15E-01	1.00E+00	2.49E-02	1.00E+00	4.79E-01	1.00E+00	1.24E-02	4.39E-01	2.13E-03	6.30E-02	GTPase regulator activity	F
GO:0030705	131	7.38E-05	7.00E-03	1.95E-03	1.62E-01	5.15E-04	1.61E-02	6.99E-03	3.78E-01	9.74E-04	4.40E-02	1.98E-02	1.00E+00	2.32E-02	5.60E-01	2.90E-02	1.00E+00	cytoskeleton-dependent intracellular transpo	P
GO:0030728	11	6.09E-01	1.00E+00	8.70E-01	1.00E+00	8.75E-01	1.00E+00	9.98E-01	1.00E+00	7.31E-01	1.00E+00	1.00E+00	1.00E+00	1.10E-01	1.00E+00	1.57E-01	1.00E+00	ovulation	P
GO:0030799	16	6.16E-01	1.00E+00	9.35E-01	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	9.65E-01	1.00E+00	9.82E-01	1.00E+00	4.62E-01	1.00E+00	8.25E-01	1.00E+00	regulation of cyclic nucleotide metabolism	P
GO:0030801	10	5.36E-01	1.00E+00	9.97E-01	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	4.63E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of cyclic nucleotide meta	P
GO:0030802	12	4.82E-01	1.00E+00	9.29E-01	1.00E+00	8.43E-01	1.00E+00	9.98E-01	1.00E+00	9.51E-01	1.00E+00	9.80E-01	1.00E+00	3.79E-01	1.00E+00	9.96E-01	1.00E+00	regulation of cyclic nucleotide biosynthesis	P
GO:0030808	12	4.82E-01	1.00E+00	9.29E-01	1.00E+00	8.43E-01	1.00E+00	9.98E-01	1.00E+00	9.51E-01	1.00E+00	9.80E-01	1.00E+00	3.79E-01	1.00E+00	9.96E-01	1.00E+00	regulation of nucleotide biosynthesis	P
GO:0030814	11	6.46E-01	1.00E+00	9.48E-01	1.00E+00	9.50E-01	1.00E+00	9.99E-01	1.00E+00	8.66E-01	1.00E+00	9.23E-01	1.00E+00	9.24E-01	1.00E+00	8.39E-01	1.00E+00	regulation of cAMP metabolism	P
GO:0030832	52	6.51E-02	1.00E+00	4.36E-02	1.00E+00	2.38E-01	1.00E+00	4.06E-02	1.00E+00	1.84E-01	1.00E+00	2.72E-01	1.00E+00	5.40E-02	1.00E+00	4.07E-02	1.00E+00	regulation of actin filament length	P
GO:0030833	27	1.81E-01	1.00E+00	8.41E-02	1.00E+00	3.00E-01	1.00E+00	3.58E-02	1.00E+00	3.38E-01	1.00E+00	5.12E-01	1.00E+00	1.36E-01	1.00E+00	1.30E-01	1.00E+00	regulation of actin filament polymerization	P
GO:0030834	22	3.26E-02	1.00E+00	6.67E-02	1.00E+00	2.10E-01	1.00E+00	1.57E-01	1.00E+00	1.23E-01	1.00E+00	1.47E-01	1.00E+00	1.87E-02	4.71E-01	4.25E-02	1.00E+00	regulation of actin filament depolymerizatior	P
GO:0030835	20	2.50E-02	1.00E+00	9.26E-02	1.00E+00	1.21E-01	1.00E+00	3.48E-01	1.00E+00	8.15E-02	1.00E+00	1.54E-01	1.00E+00	3.05E-03	5.54E-02	3.06E-02	1.00E+00	negative regulation of actin filament depolyr	P
GO:0030855	53	9.94E-01	1.00E+00	9.93E-01	1.00E+00	9.69E-01	1.00E+00	9.94E-01	1.00E+00	9.89E-01	1.00E+00	9.86E-01	1.00E+00	9.91E-01	1.00E+00	9.76E-01	1.00E+00	epithelial cell differentiation	P
GO:0030856	10	9.72E-01	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	8.88E-01	1.00E+00	7.65E-01	1.00E+00	regulation of epithelial cell differentiation	P

GO:0030863	32	1.44E-01	1.00E+00	1.55E-01	1.00E+00	2.23E-01	1.00E+00	2.24E-01	1.00E+00	6.83E-01	1.00E+00	2.78E-01	1.00E+00	1.62E-01	1.00E+00	2.52E-01	1.00E+00	cortical cytoskeleton	C
GO:0030864	22	3.51E-01	1.00E+00	6.27E-01	1.00E+00	3.12E-01	1.00E+00	5.07E-01	1.00E+00	6.87E-01	1.00E+00	6.78E-01	1.00E+00	3.67E-01	1.00E+00	7.19E-01	1.00E+00	cortical actin cytoskeleton	C
GO:0030865	14	4.79E-01	1.00E+00	3.20E-01	1.00E+00	7.48E-01	1.00E+00	6.86E-01	1.00E+00	1.97E-01	1.00E+00	6.49E-01	1.00E+00	7.22E-01	1.00E+00	2.41E-01	1.00E+00	cortical cytoskeleton organization and biogo	P
GO:0030866	11	4.65E-01	1.00E+00	5.77E-01	1.00E+00	8.82E-01	1.00E+00	9.71E-01	1.00E+00	1.92E-01	1.00E+00	8.67E-01	1.00E+00	5.92E-01	1.00E+00	2.42E-01	1.00E+00	cortical actin cytoskeleton organization and	P
GO:0030867	10	5.43E-02	1.00E+00	3.81E-01	1.00E+00	2.13E-01	1.00E+00	7.33E-01	1.00E+00	3.84E-01	1.00E+00	2.04E-01	1.00E+00	8.83E-03	2.17E-01	4.14E-01	1.00E+00	rough endoplasmic reticulum membrane	C
GO:0030878	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.86E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	thyroid gland development	P
GO:0030879	28	6.46E-01	1.00E+00	9.48E-01	1.00E+00	8.28E-01	1.00E+00	9.98E-01	1.00E+00	4.84E-01	1.00E+00	8.88E-01	1.00E+00	3.86E-01	1.00E+00	5.48E-01	1.00E+00	mammary gland development	P
GO:0030880	16	6.42E-03	3.64E-01	1.79E-03	1.62E-01	7.93E-03	3.43E-01	5.30E-04	2.70E-02	3.05E-02	1.00E+00	1.07E-02	4.01E-01	9.57E-01	1.00E+00	3.70E-02	1.00E+00	RNA polymerase complex	C
GO:0030888	28	9.71E-01	1.00E+00	9.47E-01	1.00E+00	9.94E-01	1.00E+00	4.09E-01	1.00E+00	7.77E-01	1.00E+00	1.00E+00	1.00E+00	8.21E-01	1.00E+00	8.08E-01	1.00E+00	regulation of B cell proliferation	P
GO:0030890	19	9.61E-01	1.00E+00	9.72E-01	1.00E+00	9.90E-01	1.00E+00	5.22E-01	1.00E+00	7.71E-01	1.00E+00	1.00E+00	1.00E+00	7.48E-01	1.00E+00	5.60E-01	1.00E+00	positive regulation of B cell proliferation	P
GO:0030900	134	1.00E+00	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	4.89E-01	1.00E+00	9.86E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	forebrain development	P
GO:0030901	14	9.96E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.22E-01	1.00E+00	5.97E-01	1.00E+00	9.19E-01	1.00E+00	8.45E-01	1.00E+00	midbrain development	P
GO:0030902	54	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.98E-01	1.00E+00	hindbrain development	P
GO:0030955	103	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	9.00E-01	1.00E+00	1.00E+00	1.00E+00	9.26E-01	1.00E+00	9.74E-01	1.00E+00	potassium ion binding	F
GO:0030968	16	6.70E-02	1.00E+00	5.63E-01	1.00E+00	1.50E-01	1.00E+00	5.03E-01	1.00E+00	5.85E-02	1.00E+00	6.99E-01	1.00E+00	1.51E-01	1.00E+00	5.89E-01	1.00E+00	unfolded protein response	P
GO:0030983	12	1.06E-01	1.00E+00	5.45E-03	5.59E-01	3.11E-01	1.00E+00	1.14E-02	3.78E-01	9.98E-02	1.00E+00	3.39E-03	1.43E-01	1.05E-01	1.00E+00	1.22E-01	1.00E+00	mismatched DNA binding	F
GO:0031012	321	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	2.54E-01	1.00E+00	9.99E-01	1.00E+00	extracellular matrix	C
GO:0031016	25	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	pancreas development	P
GO:0031018	15	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	8.72E-01	1.00E+00	9.98E-01	1.00E+00	endocrine pancreas development	P
GO:0031023	16	1.79E-03	1.02E-01	3.28E-04	4.20E-02	8.53E-04	3.05E-02	3.37E-03	1.42E-01	3.10E-02	1.00E+00	1.27E-02	1.00E+00	1.97E-01	1.00E+00	2.69E-02	1.00E+00	microtubule organizing center organization a	P
GO:0031032	12	2.09E-01	1.00E+00	1.60E-01	1.00E+00	5.16E-01	1.00E+00	5.04E-01	1.00E+00	5.23E-01	1.00E+00	9.32E-02	1.00E+00	1.48E-01	1.00E+00	2.26E-01	1.00E+00	actomyosin structure organization and biogo	P
GO:0031047	12	4.22E-01	1.00E+00	1.40E-01	1.00E+00	6.02E-01	1.00E+00	3.26E-01	1.00E+00	1.51E-01	1.00E+00	7.28E-02	1.00E+00	7.75E-01	1.00E+00	2.60E-01	1.00E+00	RNA-mediated gene silencing	P
GO:0031069	15	9.60E-01	1.00E+00	8.65E-01	1.00E+00	9.20E-01	1.00E+00	9.88E-01	1.00E+00	6.20E-01	1.00E+00	8.89E-01	1.00E+00	9.99E-01	1.00E+00	3.82E-01	1.00E+00	hair follicle morphogenesis	P
GO:0031072	59	4.20E-04	5.20E-02	1.88E-04	2.80E-02	6.84E-03	2.83E-01	9.79E-04	3.60E-02	4.67E-03	1.35E-01	8.70E-04	4.80E-02	1.94E-01	1.00E+00	2.83E-01	1.00E+00	heat shock protein binding	F
GO:0031090	1396	3.01E-18	0.00E+00	7.92E-30	0.00E+00	1.85E-09	0.00E+00	5.48E-20	0.00E+00	8.17E-11	0.00E+00	7.68E-16	0.00E+00	2.62E-08	6.33E-04	5.43E-14	0.00E+00	organelle membrane	C
GO:0031098	53	9.41E-01	1.00E+00	9.86E-01	1.00E+00	9.88E-01	1.00E+00	9.91E-01	1.00E+00	9.32E-01	1.00E+00	8.55E-01	1.00E+00	6.00E-01	1.00E+00	9.67E-01	1.00E+00	stress-activated protein kinase signaling pat	P
GO:0031099	28	8.86E-01	1.00E+00	9.95E-01	1.00E+00	9.98E-01	1.00E+00	9.83E-01	1.00E+00	7.65E-01	1.00E+00	1.00E+00	1.00E+00	4.09E-01	1.00E+00	4.47E-01	1.00E+00	regeneration	P
GO:0031105	13	4.40E-01	1.00E+00	2.06E-01	1.00E+00	5.02E-01	1.00E+00	1.08E-01	1.00E+00	7.31E-01	1.00E+00	7.79E-01	1.00E+00	2.59E-01	1.00E+00	7.26E-01	1.00E+00	septin complex	C
GO:0031109	31	1.68E-01	1.00E+00	6.84E-01	1.00E+00	3.49E-01	1.00E+00	4.72E-01	1.00E+00	4.29E-01	1.00E+00	7.58E-01	1.00E+00	9.11E-02	1.00E+00	8.89E-01	1.00E+00	microtubule polymerization or depolymeriza	P
GO:0031110	28	9.53E-02	1.00E+00	6.50E-01	1.00E+00	2.49E-01	1.00E+00	4.22E-01	1.00E+00	3.04E-01	1.00E+00	7.08E-01	1.00E+00	5.98E-02	1.00E+00	9.16E-01	1.00E+00	regulation of microtubule polymerization or d	P
GO:0031111	18	2.08E-02	1.00E+00	1.46E-01	1.00E+00	1.96E-01	1.00E+00	1.48E-01	1.00E+00	4.55E-02	1.00E+00	1.81E-01	1.00E+00	2.06E-02	5.29E-01	3.88E-01	1.00E+00	negative regulation of microtubule polymeriz	P
GO:0031112	11	4.06E-01	1.00E+00	1.00E+00	1.00E+00	3.68E-01	1.00E+00	9.36E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	2.34E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031113	12	1.92E-01	1.00E+00	9.08E-01	1.00E+00	3.32E-01	1.00E+00	8.13E-01	1.00E+00	6.07E-01	1.00E+00	9.15E-01	1.00E+00	1.10E-01	1.00E+00	9.74E-01	1.00E+00	regulation of microtubule polymerization	P
GO:0031114	16	6.06E-02	1.00E+00	1.73E-01	1.00E+00	1.59E-01	1.00E+00	1.73E-01	1.00E+00	7.50E-02	1.00E+00	2.16E-01	1.00E+00	6.31E-02	1.00E+00	4.61E-01	1.00E+00	regulation of microtubule depolymerization	P
GO:0031116	10	3.49E-01	1.00E+00	1.00E+00	1.00E+00	3.10E-01	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	2.16E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of microtubule polymeriz	P
GO:0031123	13	6.88E-02	1.00E+00	2.06E-03	1.62E-01	1.08E-01	1.00E+00	1.20E-03	4.40E-02	7.12E-01	1.00E+00	6.37E-02	1.00E+00	1.41E-01	1.00E+00	2.37E-01	1.00E+00	RNA 3'-end processing	P
GO:0031124	10	7.20E-02	1.00E+00	6.21E-03	5.59E-01	9.78E-02	1.00E+00	2.14E-03	4.50E-02	6.42E-01	1.00E+00	9.20E-02	1.00E+00	2.55E-01	1.00E+00	3.00E-01	1.00E+00	mRNA 3'-end processing	P
GO:0031128	15	9.98E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	9.25E-01	1.00E+00	8.60E-01	1.00E+00	9.56E-01	1.00E+00	9.90E-01	1.00E+00	induction	P
GO:0031175	223	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.50E-01	1.00E+00	1.00E+00	1.00E+00	neurite development	P
GO:0031177	20	5.09E-01	1.00E+00	1.96E-02	1.00E+00	3.72E-01	1.00E+00	4.61E-02	1.00E+00	3.61E-01	1.00E+00	1.41E-01	1.00E+00	7.19E-01	1.00E+00	1.89E-01	1.00E+00	phosphopantetheine binding	F
GO:0031202	13	6.46E-02	1.00E+00	1.11E-03	7.30E-02	6.53E-02	1.00E+00	4.34E-02	1.00E+00	1.46E-01	1.00E+00	5.63E-03	2.02E-01	5.52E-01	1.00E+00	1.50E-01	1.00E+00	RNA splicing factor activity, transesterificatic	F
GO:0031214	144	1.00E+00	1.00E+00	9.68E-01	1.00E+00	9.96E-01	1.00E+00	9.40E-01	1.00E+00	9.95E-01	1.00E+00	9.43E-01	1.00E+00	9.96E-01	1.00E+00	7.40E-01	1.00E+00	biomineral formation	P
GO:0031224	4901	7.67E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	1.00E+00	1.00E+00	1.36E-04	6.45E-03	1.15E-03	4.40E-02	intrinsic to membrane	C
GO:0031225	124	9.17E-01	1.00E+00	7.95E-01	1.00E+00	7.26E-01	1.00E+00	9.37E-01	1.00E+00	9.69E-01	1.00E+00	8.44E-01	1.00E+00	6.79E-01	1.00E+00	3.78E-01	1.00E+00	anchored to membrane	C
GO:0031226	506	9.45E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.63E-01	1.00E+00	1.00E+00	1.00E+00	1.62E-01	1.00E+00	9.14E-01	1.00E+00	intrinsic to plasma membrane	C
GO:0031227	44	3.63E-01	1.00E+00	2.64E-01	1.00E+00	7.83E-01	1.00E+00	3.99E-01	1.00E+00	1.60E-01	1.00E+00	2.29E-01	1.00E+00	4.98E-01	1.00E+00	2.48E-01	1.00E+00	intrinsic to endoplasmic reticulum membran	C
GO:0031228	32	1.63E-01	1.00E+00	6.13E-01	1.00E+00	3.33E-01	1.00E+00	8.19E-01	1.00E+00	9.50E-01	1.00E+00	7.62E-01	1.00E+00	1.82E-02	4.71E-01	7.76E-02	1.00E+00	intrinsic to Golgi membrane	C
GO:0031252	93	6.74E-02	1.00E+00	3.81E-02	1.00E+00	1.00E-01	1.00E+00	8.64E-02	1.00E+00	7.77E-02	1.00E+00	3.45E-01	1.00E+00	1.58E-01	1.00E+00	1.14E-01	1.00E+00	leading edge	C
GO:0031253	17	5.44E-01	1.00E+00	4.03E-01	1.00E+00	6.05E-01	1.00E+00	7.96E-01	1.00E+00	5.16E-01	1.00E+00	2.90E-01	1.00E+00	5.30E-01	1.00E+00	5.08E-01	1.00E+00	cell projection membrane	C
GO:0031267	61	1.90E-02	9.83E-01	6.60E-02	1.00E+00	2.28E-01	1.00E+00	1.52E-01	1.00E+00	4.32E-02	1.00E+00	1.95E-01	1.00E+00	1.49E-02	4.39E-01	7.01E-02	1.00E+00	small GTPase binding	F
GO:0031279	22	7.61E-01	1.00E+00	8.84E-01	1.00E+00	7.15E-01	1.00E+00	9.61E-01	1.00E+00	6.26E-01	1.00E+00	6.52E-01	1.00E+00	9.92E-01	1.00E+00	9.44E-01	1.00E+00	regulation of cyclase activity	P
GO:0031281	16	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.93E-01	1.00E+00	positive regulation of cyclase activity	P
GO:0031290	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	retinal ganglion cell axon guidance	P
GO:0031300	94	1.45E-02	9.83E-01	1.93E-01	1.00E+00	1.94E-01	1.00E+00	5.72E-01	1.00E+00	4.02E-02	1.00E+00	3.01E-01	1.00E+00	2.30E-02	5.60E-01	2.16E-02	1.00E+00	intrinsic to organelle membrane	C
GO:0031301	80	1.30E-02	9.83E-01	3.65E-02	1.00E+00	7.35E-02	1.00E+00	2.52E-01	1.00E+00	5.44E-02	1.00E+00	1.38E-01	1.00E+00	5.85E-02	1.00E+00	7.25E-03	2.58E-01	integral to organelle membrane	C
GO:0031323	2703	3.37E-01	1.00E+00	4.50E-07	2.66E-03	1.01E-01	1.00E+00	4.76E-10	0.00E+00	1.88E-01	1.00E+00	1.98E-04	1.36E-02	9.61E-01	1.00E+00	4.54E-01	1.00E+00	regulation of cellular metabolism	P
GO:0031324	403	1.06E-01	1.00E+00	3.81E-03	3.82E-01	1.92E-01	1.00E+00	1.31E-03	4.40E-02	1.66E-01	1.00E+00	8.51E-02	1.00E+00	1.73E-01	1.00E+00	7.84E-02	1.00E+00	negative regulation of cellular metabolism	P
GO:0031325	537	6.06E-01	1.00E+00	9.86E-01	1.00E+00	6.33E-01	1.00E+00	9.18E-01	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	2.53E-01	1.00E+00	4.77E-01	1.00E+00	positive regulation of cellular metabolism	P
GO:0031326	178	1.01E-01	1.00E+00	1.65E-01	1.00E+00	5.10E-02	1.00E+00	1.66E-01	1.00E+00	2.64E-01	1.00E+00	2.12E-01	1.00E+00	4.29E-01	1.00E+00	2.44E-01	1.00E+00	regulation of cellular biosynthesis	P
GO:0031327	41	3.51E-02	1.00E+00	1.54E-02	1.00E+00	2.47E-02	1.00E+00	5.39E-02	1.00E+00	1.31E-01	1.00E+00	1.34E-01	1.00E+00	1.77E-01	1.00E+00	3.95E-03	2.16E-01	negative regulation of cellular biosynthesis	P
GO:0031328	70	5.96E-01	1.00E+00	9.86E-01	1.00E+00	8.67E-01	1.00E+00	9.94E-01	1.00E+00	8.93E-01	1.00E+00	9.51E-01	1.00E+00	1.13E-01	1.00E+00	4.99E-01	1.00E+00	positive regulation of cellular biosynthesis	P
GO:0031341	24	7.32E-01	1.00E+00	9.72E-01	1.00E+00	9.16E-01	1.00E+00	9.34E-01	1.00E+00	1.00E+00	1.00E+00	8.53E-01	1.00E+00	3.32E-02	7.53E-01	7.96E-01	1.00E+00	regulation of cell killing	P
GO:0031344	10	1.40E-01	1.00E+00	1.07E-02	7.51E-01	9.43E-02	1.00E+00	9.93E-02	1.00E+00	2.95E-02	1.00E+00	8.48E-02	1.00E+00	9.87E-01	1.00E+00	2.80E-02	1.00E+00	regulation of cell projection organization and	P
GO:0031396	15	4.91E-02	1.00E+00	5.33E-01	1.00E+00	5.90E-02	1.00E+00	7.00E-01	1.00E+00	1.34E-02	4.81E-01	4.48E-01	1.00E+00	3.54E-01	1.00E+00	4.34E-01	1.00E+00	regulation of protein ubiquitination	P
GO:0031399	16	6.21E-02	1.00E+00	5.84E-01	1.00E+00	7.58E-02	1.00E+00	7.43E-01	1.00E+00	1.88E-02	7.19E-01	5.01E-01	1.00E+00	3.68E-01	1.00E+00	4.62E-01	1.00E+00	regulation of protein modification	P
GO:0031402	98	9.34E-01	1.00E+00	9.59E-01	1.00E+00	9.99E-01	1.00E+00	9.62E-01	1.00E+00	9.29E-01	1.00E+00	9.98E-01	1.00E+00	2.76E-01	1.00E+00	3.45E-01	1.00E+00	sodium ion binding	F
GO:0031404	62	8.10E-01	1.00E+00	1.00E+00	1.00E+00	8.00E-01	1.00E+00	1.00E+00	1.00E+00	6.08E-01	1.00E+00	1.00E+00	1.00E+00	7.74E-01	1.00E+00	1.00E+00	1.00E+00	chloride ion binding	F
GO:0031410	437	4.84E-04	5.20E-02	2.66E-03	1.87E-01	1.72E-02	8.10E-01	2.34E-02	7.69E-01	8.00E-03	3.18E-01	2.79E-02	1.00E+00	1.39E-02	4.39E-01	5.83E-03	2.58E-01	cytoplasmic vesicle	C
GO:0031418	19	1.26E-01	1.00E+00	6.48E-01	1.00E+00	3.24E-01	1.00E+00	5.26E-01	1.00E+00	2.17E-01	1.00E+00	5.74E-01	1.00E+00	4.00E-02	8.34E-01	8.92E-01	1.00E+00	L-ascorbic acid binding	F
GO:0031420	188	9.81E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	6.99E-01	1.00E+00	8.82E-01	1.00E+00	alkali metal ion binding	F
GO:0031424	34	8.83E-01	1.00E+00	1.00E+00	1.00E+00	4.26E-01	1.00E+00	1.00E+00	1.00E+00	6.04E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.96E-01	1.00E+00	keratinization	P
GO:0031461	13	1.95E-03	1.02E-01	9.04E-04	7.30E-02	2.08E-02	1.00E+00	4.04E-03	1.42E-01	5.80E-05	1.56E-03	3.56E-04	1.36E-02	1.54E-01	1.00E+00	9.43E-02	1.00E+00	cullin-RING ubiquitin ligase complex	C
GO:0031497	102	2.26E-02	1.00E+00	4.15E-03	3.82E-01	3.26E-02	1.00E+00	5.02E-03	1.42E-01	7.87E-02	1.00E+00	2.70E-02	1.00E+00	5.55E-01	1.00E+00	2.96E-01	1.00E+00	chromatin assembly	P
GO:0031507	15	6.59E-02	1.00E+00	3.09E-04	4.20E-02	8.87E-02	1.00E+00	5.02E-02	1.00E+00	1.49E-01	1.00E+00	1.09E-02	4.01E-01	2.26E-01	1.00E+00	4.04E-03	2.16E-01	heterochromatin formation	P
GO:0031513	22	7.49E-01	1.00E+00	6.20E-01	1.00E+00	9.41E-01	1.00E+00	5.18E-01	1.00E+00	6.62E-01	1.00E+00	9.25E-01	1.00E+00	3.58E-01	1.00E+00	1.07E-01	1.00E+00	nonmotile primary cilium	C

GO:0031519	11	4.27E-01	1.00E+00	3.50E-01	1.00E+00	3.15E-01	1.00E+00	2.49E-01	1.00E+00	7.25E-01	1.00E+00	3.98E-01	1.00E+00	3.78E-01	1.00E+00	7.58E-01	1.00E+00	PcG protein complex	C
GO:0031526	12	3.85E-01	1.00E+00	4.74E-01	1.00E+00	3.87E-01	1.00E+00	8.18E-01	1.00E+00	4.97E-01	1.00E+00	2.98E-01	1.00E+00	3.90E-01	1.00E+00	2.69E-01	1.00E+00	brush border membrane	C
GO:0031570	26	1.86E-03	1.02E-01	3.79E-03	3.82E-01	1.39E-02	8.10E-01	2.48E-03	8.70E-02	1.83E-02	7.19E-01	2.93E-02	1.00E+00	2.87E-02	6.06E-01	1.10E-02	6.43E-01	DNA integrity checkpoint	P
GO:0031589	92	2.77E-01	1.00E+00	2.63E-01	1.00E+00	1.26E-01	1.00E+00	4.68E-01	1.00E+00	5.46E-01	1.00E+00	5.65E-01	1.00E+00	4.81E-01	1.00E+00	1.17E-01	1.00E+00	cell-substrate adhesion	P
GO:0031594	20	1.78E-01	1.00E+00	6.24E-01	1.00E+00	5.07E-01	1.00E+00	8.66E-01	1.00E+00	3.87E-01	1.00E+00	3.60E-01	1.00E+00	3.98E-02	8.34E-01	3.91E-01	1.00E+00	neuromuscular junction	C
GO:0031625	13	1.22E-02	9.83E-01	1.17E-02	7.51E-01	2.66E-02	1.00E+00	7.01E-02	1.00E+00	1.26E-02	4.81E-01	2.25E-03	1.43E-01	6.56E-02	1.00E+00	3.59E-01	1.00E+00	ubiquitin protein ligase binding	F
GO:0031644	80	8.02E-01	1.00E+00	1.00E+00	1.00E+00	9.19E-01	1.00E+00	9.65E-01	1.00E+00	8.69E-01	1.00E+00	1.00E+00	1.00E+00	3.55E-01	1.00E+00	9.06E-01	1.00E+00	regulation of neurophysiological process	P
GO:0031645	15	2.71E-01	1.00E+00	1.00E+00	1.00E+00	9.11E-01	1.00E+00	1.00E+00	1.00E+00	2.59E-01	1.00E+00	1.00E+00	1.00E+00	1.09E-01	1.00E+00	5.81E-01	1.00E+00	negative regulation of neurophysiological pr	P
GO:0031646	16	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	7.40E-01	1.00E+00	9.97E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	positive regulation of neurophysiological prc	P
GO:0031647	23	2.44E-01	1.00E+00	8.73E-02	1.00E+00	1.16E-01	1.00E+00	1.11E-01	1.00E+00	2.33E-01	1.00E+00	1.17E-01	1.00E+00	7.01E-01	1.00E+00	4.42E-01	1.00E+00	regulation of protein stability	P
GO:0031663	13	1.86E-01	1.00E+00	2.13E-01	1.00E+00	1.41E-01	1.00E+00	2.41E-01	1.00E+00	2.75E-01	1.00E+00	1.71E-01	1.00E+00	3.62E-01	1.00E+00	8.73E-01	1.00E+00	lipopolysaccharide-mediated signaling pathv	P
GO:0031667	71	1.79E-02	9.83E-01	4.25E-01	1.00E+00	1.36E-02	8.10E-01	3.34E-01	1.00E+00	2.18E-01	1.00E+00	4.86E-01	1.00E+00	9.84E-02	1.00E+00	3.78E-01	1.00E+00	response to nutrient levels	P
GO:0031668	19	3.97E-01	1.00E+00	9.22E-01	1.00E+00	6.16E-01	1.00E+00	1.99E-01	1.00E+00	7.39E-01	1.00E+00	1.00E+00	1.00E+00	2.93E-01	1.00E+00	8.92E-01	1.00E+00	cellular response to extracellular stimulus	P
GO:0031669	15	3.35E-01	1.00E+00	8.81E-01	1.00E+00	4.92E-01	1.00E+00	2.67E-01	1.00E+00	7.08E-01	1.00E+00	9.99E-01	1.00E+00	2.66E-01	1.00E+00	8.47E-01	1.00E+00	cellular response to nutrient levels	P
GO:0031672	20	8.05E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	8.58E-01	1.00E+00	8.74E-01	1.00E+00	1.00E+00	1.00E+00	1.67E-01	1.00E+00	9.08E-01	1.00E+00	A band	C
GO:0031901	15	1.08E-01	1.00E+00	3.53E-02	1.00E+00	3.44E-01	1.00E+00	4.36E-02	1.00E+00	1.59E-01	1.00E+00	1.61E-01	1.00E+00	1.10E-01	1.00E+00	1.64E-02	9.40E-01	early endosome membrane	C
GO:0031902	31	1.27E-01	1.00E+00	1.69E-02	1.00E+00	3.77E-01	1.00E+00	5.23E-02	1.00E+00	3.29E-01	1.00E+00	2.15E-01	1.00E+00	2.19E-01	1.00E+00	1.52E-02	9.40E-01	late endosome membrane	C
GO:0031903	40	1.50E-03	9.30E-02	6.85E-03	5.59E-01	7.79E-03	3.43E-01	1.15E-01	1.00E+00	7.84E-03	3.18E-01	2.01E-02	1.00E+00	5.03E-02	1.00E+00	5.40E-02	1.00E+00	microbody membrane	C
GO:0031941	17	1.20E-01	1.00E+00	3.50E-01	1.00E+00	2.58E-01	1.00E+00	5.80E-01	1.00E+00	1.83E-01	1.00E+00	4.66E-01	1.00E+00	1.55E-01	1.00E+00	3.01E-01	1.00E+00	filamentous actin	C
GO:0031965	129	1.54E-06	2.00E-03	7.21E-18	0.00E+00	5.67E-07	9.88E-04	1.95E-11	0.00E+00	2.43E-04	8.00E-03	4.34E-12	0.00E+00	2.90E-02	6.06E-01	1.85E-06	3.91E-03	nuclear membrane	C
GO:0031966	379	2.05E-08	9.73E-04	3.05E-15	0.00E+00	1.56E-05	1.69E-03	1.28E-10	0.00E+00	6.44E-06	1.56E-03	1.41E-10	7.71E-04	3.54E-03	6.72E-02	1.14E-05	3.91E-03	mitochondrial membrane	C
GO:0031967	558	2.82E-13	6.62E-04	2.67E-26	0.00E+00	1.48E-09	0.00E+00	5.26E-18	0.00E+00	3.79E-09	0.00E+00	7.44E-18	0.00E+00	9.72E-04	2.40E-02	3.71E-09	0.00E+00	organelle envelope	C
GO:0031968	76	2.48E-04	1.90E-02	5.44E-05	2.80E-02	2.50E-02	1.00E+00	2.60E-04	1.15E-02	4.40E-04	1.90E-02	3.74E-03	1.43E-01	1.85E-02	4.71E-01	4.00E-03	2.16E-01	organelle outer membrane	C
GO:0031970	33	7.11E-02	1.00E+00	6.00E-03	5.59E-01	1.13E-01	1.00E+00	5.58E-02	1.00E+00	4.90E-02	1.00E+00	1.77E-02	1.00E+00	8.61E-01	1.00E+00	2.60E-02	1.00E+00	organelle envelope lumen	C
GO:0031974	924	5.43E-16	0.00E+00	1.51E-34	0.00E+00	2.01E-14	0.00E+00	8.23E-27	0.00E+00	1.51E-08	0.00E+00	9.20E-22	0.00E+00	7.18E-03	2.01E-01	8.22E-10	0.00E+00	membrane-enclosed lumen	C
GO:0031975	579	5.27E-13	6.62E-04	1.77E-24	0.00E+00	4.67E-09	0.00E+00	4.26E-17	0.00E+00	7.56E-09	0.00E+00	1.20E-16	0.00E+00	5.28E-04	1.89E-02	1.34E-08	0.00E+00	envelope	C
GO:0031980	153	4.48E-05	6.00E-03	4.53E-08	2.66E-03	1.54E-04	1.61E-02	1.66E-03	4.40E-02	6.86E-03	1.65E-01	1.99E-06	2.00E-03	7.80E-02	1.00E+00	1.37E-04	4.00E-03	mitochondrial lumen	C
GO:0031981	670	1.20E-11	6.62E-04	3.19E-24	0.00E+00	2.82E-11	0.00E+00	4.28E-23	0.00E+00	2.83E-06	7.65E-04	2.76E-14	0.00E+00	1.98E-02	4.71E-01	1.99E-05	3.91E-03	nuclear lumen	C
GO:0031982	451	8.83E-04	9.30E-02	2.53E-03	1.87E-01	2.28E-02	1.00E+00	1.80E-02	7.69E-01	8.83E-03	3.69E-01	3.13E-02	1.00E+00	2.06E-02	5.29E-01	5.82E-03	2.58E-01	vesicle	C
GO:0031988	358	1.03E-03	9.30E-02	4.79E-03	3.82E-01	2.66E-02	1.00E+00	2.73E-02	1.00E+00	1.86E-02	7.19E-01	2.08E-02	1.00E+00	1.53E-02	4.39E-01	2.51E-02	1.00E+00	membrane-bound vesicle	C
GO:0032011	16	8.39E-01	1.00E+00	7.65E-01	1.00E+00	9.59E-01	1.00E+00	7.32E-01	1.00E+00	7.04E-01	1.00E+00	9.07E-01	1.00E+00	8.00E-01	1.00E+00	5.03E-01	1.00E+00	ARF protein signal transduction	P
GO:0032012	16	8.39E-01	1.00E+00	7.65E-01	1.00E+00	9.59E-01	1.00E+00	7.32E-01	1.00E+00	7.04E-01	1.00E+00	9.07E-01	1.00E+00	8.00E-01	1.00E+00	5.03E-01	1.00E+00	regulation of ARF protein signal transductior	P
GO:0032039	13	2.65E-01	1.00E+00	7.84E-03	5.59E-01	4.87E-01	1.00E+00	8.08E-03	3.78E-01	2.61E-01	1.00E+00	2.94E-01	1.00E+00	2.40E-01	1.00E+00	2.15E-01	1.00E+00	integrator complex	C
GO:0032094	11	9.47E-01	1.00E+00	7.13E-01	1.00E+00	9.95E-01	1.00E+00	6.97E-01	1.00E+00	9.44E-01	1.00E+00	9.98E-01	1.00E+00	5.69E-01	1.00E+00	2.94E-01	1.00E+00	response to food	P
GO:0032147	50	8.24E-01	1.00E+00	8.04E-01	1.00E+00	5.71E-01	1.00E+00	6.20E-01	1.00E+00	6.74E-01	1.00E+00	6.79E-01	1.00E+00	9.08E-01	1.00E+00	8.64E-01	1.00E+00	activation of protein kinase activity	P
GO:0032156	13	4.40E-01	1.00E+00	2.06E-01	1.00E+00	5.02E-01	1.00E+00	1.08E-01	1.00E+00	7.31E-01	1.00E+00	7.79E-01	1.00E+00	2.59E-01	1.00E+00	7.26E-01	1.00E+00	septin cytoskeleton	C
GO:0032182	10	5.18E-02	1.00E+00	1.14E-01	1.00E+00	9.29E-02	1.00E+00	4.60E-01	1.00E+00	4.47E-02	1.00E+00	1.52E-02	1.00E+00	1.78E-01	1.00E+00	5.47E-01	1.00E+00	small conjugating protein binding	F
GO:0032200	24	1.57E-02	9.83E-01	2.55E-03	1.87E-01	4.15E-02	1.00E+00	1.42E-03	4.40E-02	7.39E-03	3.18E-01	8.46E-02	1.00E+00	6.14E-02	1.00E+00	4.03E-02	1.00E+00	telomere organization and biogenesis	P
GO:0032259	82	2.06E-02	1.00E+00	7.23E-03	5.59E-01	1.36E-02	8.10E-01	5.48E-02	1.00E+00	1.50E-02	4.81E-01	7.16E-03	3.55E-01	2.96E-01	1.00E+00	3.03E-02	1.00E+00	methylation	P
GO:0032312	23	2.21E-02	1.00E+00	1.47E-01	1.00E+00	4.92E-02	1.00E+00	2.90E-01	1.00E+00	2.38E-01	1.00E+00	1.91E-01	1.00E+00	2.84E-02	6.06E-01	9.23E-02	1.00E+00	regulation of ARF GTPase activity	P
GO:0032313	41	3.46E-03	1.86E-01	3.66E-03	3.82E-01	2.27E-02	1.00E+00	4.89E-02	1.00E+00	4.28E-02	1.00E+00	8.95E-03	3.55E-01	1.24E-02	4.39E-01	5.60E-03	2.58E-01	regulation of Rab GTPase activity	P
GO:0032318	72	7.83E-05	7.00E-03	4.54E-03	3.82E-01	2.33E-03	1.18E-01	4.08E-02	1.00E+00	6.64E-03	1.65E-01	1.03E-02	4.01E-01	5.14E-04	1.89E-02	4.70E-03	2.58E-01	regulation of Ras GTPase activity	P
GO:0032392	11	5.09E-02	1.00E+00	1.24E-02	7.51E-01	4.87E-01	1.00E+00	2.54E-02	7.69E-01	1.50E-02	4.81E-01	4.07E-02	1.00E+00	2.47E-01	1.00E+00	2.16E-01	1.00E+00	DNA geometric change	P
GO:0032403	74	3.51E-01	1.00E+00	3.46E-01	1.00E+00	6.45E-01	1.00E+00	2.49E-01	1.00E+00	4.84E-01	1.00E+00	8.01E-01	1.00E+00	3.25E-01	1.00E+00	2.04E-01	1.00E+00	protein complex binding	F
GO:0032432	25	4.20E-01	1.00E+00	7.55E-02	1.00E+00	8.09E-01	1.00E+00	1.73E-01	1.00E+00	4.12E-01	1.00E+00	1.81E-01	1.00E+00	2.14E-01	1.00E+00	6.67E-02	1.00E+00	actin filament bundle	C
GO:0035004	11	1.40E-01	1.00E+00	1.72E-01	1.00E+00	3.09E-01	1.00E+00	3.87E-01	1.00E+00	2.46E-01	1.00E+00	1.15E-01	1.00E+00	1.74E-01	1.00E+00	1.30E-01	1.00E+00	phosphoinositide 3-kinase activity	F
GO:0035014	11	4.41E-02	1.00E+00	2.61E-01	1.00E+00	3.43E-01	1.00E+00	2.88E-01	1.00E+00	1.13E-01	1.00E+00	5.10E-01	1.00E+00	7.43E-02	1.00E+00	2.08E-01	1.00E+00	phosphoinositide 3-kinase regulator activity	F
GO:0035023	73	2.55E-01	1.00E+00	6.02E-01	1.00E+00	7.95E-01	1.00E+00	9.93E-01	1.00E+00	4.40E-01	1.00E+00	2.58E-01	1.00E+00	2.77E-02	6.06E-01	2.78E-01	1.00E+00	regulation of Rho protein signal transductior	P
GO:0035036	20	7.54E-01	1.00E+00	6.49E-01	1.00E+00	4.75E-01	1.00E+00	5.78E-01	1.00E+00	1.00E+00	1.00E+00	6.36E-01	1.00E+00	4.72E-01	1.00E+00	6.46E-01	1.00E+00	sperm-egg recognition	P
GO:0035050	13	9.57E-01	1.00E+00	8.06E-01	1.00E+00	9.51E-01	1.00E+00	7.98E-01	1.00E+00	6.43E-01	1.00E+00	5.80E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	embryonic heart tube development	P
GO:0035051	21	5.32E-01	1.00E+00	6.31E-01	1.00E+00	3.23E-01	1.00E+00	7.81E-01	1.00E+00	5.66E-01	1.00E+00	4.48E-01	1.00E+00	6.19E-01	1.00E+00	6.49E-01	1.00E+00	cardiac cell differentiation	P
GO:0035088	12	6.64E-01	1.00E+00	6.96E-01	1.00E+00	4.39E-01	1.00E+00	9.19E-01	1.00E+00	8.81E-01	1.00E+00	8.50E-01	1.00E+00	9.84E-01	1.00E+00	2.97E-01	1.00E+00	establishment and/or maintenance of apical	P
GO:0035091	76	1.06E-02	9.83E-01	6.46E-04	7.30E-02	7.28E-02	1.00E+00	1.68E-02	7.69E-01	8.25E-02	1.00E+00	4.40E-03	1.52E-01	3.73E-02	7.83E-01	2.56E-02	1.00E+00	phosphoinositide binding	F
GO:0035094	10	9.79E-01	1.00E+00	8.07E-01	1.00E+00	8.10E-01	1.00E+00	7.78E-01	1.00E+00	9.95E-01	1.00E+00	9.56E-01	1.00E+00	8.20E-01	1.00E+00	3.13E-01	1.00E+00	response to nicotine	P
GO:0035107	91	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	appendage morphogenesis	P
GO:0035108	91	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	limb morphogenesis	P
GO:0035113	85	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	embryonic appendage morphogenesis	P
GO:0035115	17	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	embryonic forelimb morphogenesis	P
GO:0035116	20	1.00E+00	1.00E+00	7.90E-01	1.00E+00	9.98E-01	1.00E+00	9.37E-01	1.00E+00	9.92E-01	1.00E+00	5.19E-01	1.00E+00	1.00E+00	1.00E+00	8.14E-01	1.00E+00	embryonic hindlimb morphogenesis	P
GO:0035136	20	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	forelimb morphogenesis	P
GO:0035137	27	1.00E+00	1.00E+00	8.66E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	9.97E-01	1.00E+00	6.70E-01	1.00E+00	1.00E+00	1.00E+00	8.72E-01	1.00E+00	hindlimb morphogenesis	P
GO:0035176	12	9.46E-01	1.00E+00	1.00E+00	1.00E+00	9.63E-01	1.00E+00	9.57E-01	1.00E+00	5.60E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	social behavior	P
GO:0035239	116	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.93E-01	1.00E+00	9.45E-01	1.00E+00	tube morphogenesis	P
GO:0035240	53	8.74E-01	1.00E+00	6.54E-01	1.00E+00	8.61E-01	1.00E+00	3.55E-01	1.00E+00	9.73E-01	1.00E+00	8.81E-01	1.00E+00	7.35E-01	1.00E+00	5.42E-01	1.00E+00	dopamine binding	F
GO:0035249	26	6.46E-01	1.00E+00	9.99E-01	1.00E+00	9.41E-01	1.00E+00	1.00E+00	1.00E+00	3.99E-01	1.00E+00	1.00E+00	1.00E+00	4.19E-01	1.00E+00	8.97E-01	1.00E+00	synaptic transmission, glutamatergic	P
GO:0035250	21	8.69E-01	1.00E+00	3.82E-01	1.00E+00	8.61E-01	1.00E+00	4.71E-01	1.00E+00	9.59E-01	1.00E+00	9.77E-02	1.00E+00	6.38E-01	1.00E+00	4.00E-01	1.00E+00	UDP-galactosyltransferase activity	F
GO:0035257	43	2.02E-03	1.02E-01	1.87E-02	1.00E+00	4.99E-04	1.61E-02	1.25E-02	3.78E-01	6.04E-02	1.00E+00	5.38E-02	1.00E+00	2.56E-01	1.00E+00	4.17E-01	1.00E+00	nuclear hormone receptor binding	F
GO:0035258	11	5.14E-03	3.48E-01	8.94E-02	1.00E+00	1.16E-02	4.74E-01	8.74E-02	1.00E+00	3.26E-02	1.00E+00	9.51E-02	1.00E+00	3.62E-01	1.00E+00	3.71E-01	1.00E+00	steroid hormone receptor binding	F
GO:0035264	69	1.75E-01	1.00E+00	3.25E-01	1.00E+00	9.03E-01	1.00E+00	6.71E-01	1.00E+00	1.31E-01	1.00E+00	6.49E-01	1.00E+00	1.12E-01	1.00E+00	1.34E-01	1.00E+00	body growth	P
GO:0035265	24	6.50E-01	1.00E+00	8.19E-01	1.00E+00	8.65E-01	1.00E+00	8.99E-01	1.00E+00	7.30E-01	1.00E+00	9.05E-01	1.00E+00	6.52E-01	1.00E+00	4.75E-01	1.00E+00	organ growth	P
GO:0035270	57	1.00E+00	1.00E+00	9.61E-01	1.00E+00	1.00E+00	1.00E+00	4.87E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	endocrine system development	P
GO:0035272	17	9.83E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	7.65E-01	1.00E+00	9.97E-01	1.00E+00	8.33E-01	1.00E+00	9.71E-01	1.00E+00	exocrine system development	P
GO:0035282	45	9.91E-01	1.00E+00	7.41E-01	1.00E+00	9.87E-01	1.00E+00	7.33E-01	1.00E+00	9.70E-01	1.00E+00	5.85E-01	1.00E+00	9.99E-01	1.00E+00	7.33E-01	1.00E+00	segmentation	P
GO:0035295	194	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	8.99E-01	1.00E+00	tube development	P
GO:0035315	18	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	5.32E-01	1.00E+00	hair cell differentiation	P

GO:0040007	306	2.48E-01	1.00E+00	7.35E-01	1.00E+00	8.02E-01	1.00E+00	6.45E-01	1.00E+00	9.44E-01	1.00E+00	9.87E-01	1.00E+00	5.20E-03	9.40E-02	2.31E-01	1.00E+00	growth	P
GO:0040008	200	3.64E-01	1.00E+00	8.41E-01	1.00E+00	8.15E-01	1.00E+00	7.67E-01	1.00E+00	9.16E-01	1.00E+00	9.81E-01	1.00E+00	3.39E-02	7.53E-01	5.72E-01	1.00E+00	regulation of growth	P
GO:0040011	447	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.22E-01	1.00E+00	9.39E-01	1.00E+00	locomotion	P
GO:0040012	99	7.49E-01	1.00E+00	9.96E-01	1.00E+00	8.71E-01	1.00E+00	1.00E+00	1.00E+00	7.57E-01	1.00E+00	9.94E-01	1.00E+00	3.48E-01	1.00E+00	7.89E-01	1.00E+00	regulation of locomotion	P
GO:0040013	32	9.44E-01	1.00E+00	8.96E-01	1.00E+00	6.60E-01	1.00E+00	5.65E-01	1.00E+00	9.88E-01	1.00E+00	9.07E-01	1.00E+00	7.86E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of locomotion	P
GO:0040014	55	3.45E-01	1.00E+00	6.73E-01	1.00E+00	9.09E-01	1.00E+00	9.54E-01	1.00E+00	3.00E-01	1.00E+00	7.72E-01	1.00E+00	2.84E-01	1.00E+00	3.30E-01	1.00E+00	regulation of body size	P
GO:0040017	39	4.06E-01	1.00E+00	9.69E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	3.97E-01	1.00E+00	9.93E-01	1.00E+00	1.59E-01	1.00E+00	2.12E-01	1.00E+00	positive regulation of locomotion	P
GO:0040018	22	9.38E-01	1.00E+00	7.68E-01	1.00E+00	9.35E-01	1.00E+00	9.85E-01	1.00E+00	5.49E-01	1.00E+00	8.37E-01	1.00E+00	9.86E-01	1.00E+00	2.99E-01	1.00E+00	positive regulation of body size	P
GO:0040029	60	2.60E-01	1.00E+00	5.16E-02	1.00E+00	4.28E-01	1.00E+00	1.65E-01	1.00E+00	1.28E-01	1.00E+00	1.25E-01	1.00E+00	3.29E-01	1.00E+00	5.91E-02	1.00E+00	regulation of gene expression, epigenetic	P
GO:0042035	67	5.91E-01	1.00E+00	9.96E-01	1.00E+00	7.56E-01	1.00E+00	9.95E-01	1.00E+00	8.20E-01	1.00E+00	9.74E-01	1.00E+00	2.04E-01	1.00E+00	8.38E-01	1.00E+00	regulation of cytokine biosynthesis	P
GO:0042036	15	3.88E-01	1.00E+00	8.30E-01	1.00E+00	4.72E-01	1.00E+00	8.73E-01	1.00E+00	4.18E-01	1.00E+00	7.79E-01	1.00E+00	4.92E-01	1.00E+00	6.10E-01	1.00E+00	negative regulation of cytokine biosynthesis	P
GO:0042044	11	7.14E-01	1.00E+00	6.63E-01	1.00E+00	7.32E-01	1.00E+00	3.64E-01	1.00E+00	8.18E-01	1.00E+00	8.15E-01	1.00E+00	4.39E-01	1.00E+00	6.54E-01	1.00E+00	fluid transport	P
GO:0042054	32	8.16E-05	7.00E-03	2.54E-07	2.66E-03	1.56E-04	1.61E-02	3.67E-05	5.41E-03	1.44E-03	4.80E-02	3.46E-06	2.00E-03	1.34E-01	1.00E+00	3.39E-03	2.16E-01	histone methyltransferase activity	F
GO:0042060	160	8.94E-01	1.00E+00	9.93E-01	1.00E+00	7.92E-01	1.00E+00	9.99E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	4.88E-01	1.00E+00	2.89E-01	1.00E+00	wound healing	P
GO:0042063	47	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.57E-01	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gliogenesis	P
GO:0042088	14	1.25E-01	1.00E+00	6.27E-01	1.00E+00	5.32E-01	1.00E+00	5.04E-01	1.00E+00	7.06E-02	1.00E+00	9.31E-01	1.00E+00	3.62E-01	1.00E+00	5.19E-01	1.00E+00	T-helper 1 type immune response	P
GO:0042089	79	6.29E-01	1.00E+00	9.99E-01	1.00E+00	5.99E-01	1.00E+00	9.99E-01	1.00E+00	7.15E-01	1.00E+00	9.75E-01	1.00E+00	4.51E-01	1.00E+00	9.05E-01	1.00E+00	cytokine biosynthesis	P
GO:0042093	12	3.41E-02	1.00E+00	4.94E-01	1.00E+00	1.44E-01	1.00E+00	2.69E-01	1.00E+00	7.67E-02	1.00E+00	9.22E-01	1.00E+00	1.05E-01	1.00E+00	3.38E-01	1.00E+00	T-helper cell differentiation	P
GO:0042094	17	3.89E-01	1.00E+00	6.91E-01	1.00E+00	7.41E-01	1.00E+00	9.88E-01	1.00E+00	5.70E-01	1.00E+00	4.78E-01	1.00E+00	9.83E-02	1.00E+00	2.75E-01	1.00E+00	interleukin-2 biosynthesis	P
GO:0042095	14	2.54E-01	1.00E+00	1.00E+00	1.00E+00	3.45E-01	1.00E+00	9.99E-01	1.00E+00	2.79E-01	1.00E+00	9.69E-01	1.00E+00	4.02E-01	1.00E+00	1.00E+00	1.00E+00	interferon-gamma biosynthesis	P
GO:0042098	68	1.35E-01	1.00E+00	9.40E-01	1.00E+00	2.99E-01	1.00E+00	8.21E-01	1.00E+00	2.69E-01	1.00E+00	9.79E-01	1.00E+00	1.31E-01	1.00E+00	8.26E-01	1.00E+00	T cell proliferation	P
GO:0042100	36	8.00E-01	1.00E+00	7.80E-01	1.00E+00	8.18E-01	1.00E+00	2.36E-01	1.00E+00	9.66E-01	1.00E+00	9.97E-01	1.00E+00	5.68E-01	1.00E+00	6.07E-01	1.00E+00	B cell proliferation	P
GO:0042101	11	1.05E-01	1.00E+00	8.76E-01	1.00E+00	3.35E-01	1.00E+00	4.27E-01	1.00E+00	4.24E-01	1.00E+00	9.92E-01	1.00E+00	9.90E-03	2.17E-01	4.93E-01	1.00E+00	T cell receptor complex	C
GO:0042102	34	3.64E-01	1.00E+00	5.12E-01	1.00E+00	6.49E-01	1.00E+00	4.73E-01	1.00E+00	5.92E-01	1.00E+00	8.31E-01	1.00E+00	8.78E-02	1.00E+00	2.21E-01	1.00E+00	positive regulation of T cell proliferation	P
GO:0042107	80	6.37E-01	1.00E+00	9.99E-01	1.00E+00	6.34E-01	1.00E+00	1.00E+00	1.00E+00	7.40E-01	1.00E+00	9.77E-01	1.00E+00	3.96E-01	1.00E+00	9.19E-01	1.00E+00	cytokine metabolism	P
GO:0042108	45	5.03E-01	1.00E+00	9.85E-01	1.00E+00	7.48E-01	1.00E+00	9.68E-01	1.00E+00	8.05E-01	1.00E+00	9.83E-01	1.00E+00	1.22E-01	1.00E+00	7.06E-01	1.00E+00	positive regulation of cytokine biosynthesis	P
GO:0042110	148	1.01E-01	1.00E+00	7.01E-01	1.00E+00	4.59E-01	1.00E+00	5.50E-01	1.00E+00	5.46E-01	1.00E+00	9.78E-01	1.00E+00	5.74E-02	1.00E+00	2.93E-01	1.00E+00	T cell activation	P
GO:0042113	105	1.90E-01	1.00E+00	1.52E-01	1.00E+00	4.06E-01	1.00E+00	6.73E-02	1.00E+00	6.56E-01	1.00E+00	9.83E-01	1.00E+00	9.80E-02	1.00E+00	1.90E-01	1.00E+00	B cell activation	P
GO:0042127	461	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	regulation of cell proliferation	P
GO:0042129	49	1.59E-01	1.00E+00	8.04E-01	1.00E+00	5.30E-01	1.00E+00	5.82E-01	1.00E+00	2.09E-01	1.00E+00	9.57E-01	1.00E+00	4.12E-02	8.34E-01	5.49E-01	1.00E+00	regulation of T cell proliferation	P
GO:0042130	17	5.30E-01	1.00E+00	9.43E-01	1.00E+00	8.14E-01	1.00E+00	6.93E-01	1.00E+00	5.69E-01	1.00E+00	9.99E-01	1.00E+00	2.42E-01	1.00E+00	9.91E-01	1.00E+00	negative regulation of T cell proliferation	P
GO:0042133	46	9.67E-01	1.00E+00	9.69E-01	1.00E+00	9.80E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.33E-01	1.00E+00	4.23E-01	1.00E+00	3.10E-01	1.00E+00	neurotransmitter metabolism	P
GO:0042135	10	5.72E-01	1.00E+00	6.52E-01	1.00E+00	8.44E-01	1.00E+00	7.07E-01	1.00E+00	9.16E-01	1.00E+00	9.33E-01	1.00E+00	3.39E-01	1.00E+00	1.43E-01	1.00E+00	neurotransmitter catabolism	P
GO:0042136	17	1.00E+00	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	8.41E-01	1.00E+00	7.43E-01	1.00E+00	2.72E-01	1.00E+00	neurotransmitter biosynthesis	P
GO:0042157	74	1.72E-01	1.00E+00	6.96E-02	1.00E+00	3.68E-02	1.00E+00	1.02E-01	1.00E+00	1.28E-01	1.00E+00	1.45E-01	1.00E+00	8.45E-01	1.00E+00	2.64E-01	1.00E+00	lipoprotein metabolism	P
GO:0042158	53	1.97E-01	1.00E+00	5.35E-02	1.00E+00	4.59E-02	1.00E+00	1.09E-01	1.00E+00	4.40E-01	1.00E+00	1.33E-01	1.00E+00	6.65E-01	1.00E+00	3.62E-01	1.00E+00	lipoprotein biosynthesis	P
GO:0042165	211	9.99E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	5.44E-01	1.00E+00	4.51E-01	1.00E+00	neurotransmitter binding	F
GO:0042166	21	3.78E-01	1.00E+00	6.73E-01	1.00E+00	5.92E-01	1.00E+00	8.20E-01	1.00E+00	9.00E-01	1.00E+00	5.92E-01	1.00E+00	2.76E-02	6.06E-01	2.05E-01	1.00E+00	acetylcholine binding	F
GO:0042168	18	6.14E-02	1.00E+00	1.19E-01	1.00E+00	1.46E-01	1.00E+00	1.09E-01	1.00E+00	3.05E-02	1.00E+00	2.85E-01	1.00E+00	2.26E-01	1.00E+00	2.48E-01	1.00E+00	heme metabolism	P
GO:0042169	16	1.42E-02	9.83E-01	3.45E-02	1.00E+00	1.39E-01	1.00E+00	9.27E-02	1.00E+00	3.06E-01	1.00E+00	9.01E-02	1.00E+00	2.67E-03	5.54E-02	3.76E-02	1.00E+00	SH2 domain binding	F
GO:0042175	472	1.16E-04	1.90E-02	1.52E-04	2.80E-02	3.34E-02	1.00E+00	1.73E-03	4.40E-02	6.83E-04	4.40E-02	3.59E-02	1.00E+00	7.59E-04	2.40E-02	1.75E-03	6.30E-02	nuclear envelope-endoplasmic reticulum ne	C
GO:0042176	24	2.81E-02	1.00E+00	1.30E-01	1.00E+00	3.94E-02	1.00E+00	2.58E-02	7.69E-01	5.11E-02	1.00E+00	8.00E-02	1.00E+00	1.95E-01	1.00E+00	8.46E-01	1.00E+00	regulation of protein catabolism	P
GO:0042219	17	2.64E-01	1.00E+00	3.67E-01	1.00E+00	7.42E-01	1.00E+00	2.38E-01	1.00E+00	2.19E-01	1.00E+00	5.25E-01	1.00E+00	1.63E-01	1.00E+00	3.61E-01	1.00E+00	amino acid derivative catabolism	P
GO:0042221	616	2.29E-01	1.00E+00	6.90E-01	1.00E+00	4.92E-01	1.00E+00	9.74E-01	1.00E+00	6.39E-01	1.00E+00	6.77E-01	1.00E+00	5.19E-02	1.00E+00	1.14E-01	1.00E+00	response to chemical stimulus	P
GO:0042226	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.55E-01	1.00E+00	9.96E-01	1.00E+00	interleukin-6 biosynthesis	P
GO:0042228	10	6.18E-01	1.00E+00	8.75E-01	1.00E+00	8.28E-01	1.00E+00	8.36E-01	1.00E+00	8.62E-01	1.00E+00	5.45E-01	1.00E+00	3.68E-01	1.00E+00	7.41E-01	1.00E+00	interleukin-8 biosynthesis	P
GO:0042246	22	7.19E-01	1.00E+00	9.95E-01	1.00E+00	9.85E-01	1.00E+00	9.93E-01	1.00E+00	7.44E-01	1.00E+00	1.00E+00	1.00E+00	2.37E-01	1.00E+00	4.18E-01	1.00E+00	tissue regeneration	P
GO:0042254	98	5.36E-04	5.20E-02	1.70E-06	2.66E-03	4.93E-02	1.00E+00	4.17E-07	1.00E-03	1.41E-03	4.80E-02	3.20E-03	1.43E-01	1.52E-01	1.00E+00	3.34E-01	1.00E+00	ribosome biogenesis and assembly	P
GO:0042267	21	2.94E-01	1.00E+00	6.18E-01	1.00E+00	2.65E-01	1.00E+00	7.20E-01	1.00E+00	9.19E-01	1.00E+00	3.80E-01	1.00E+00	7.01E-02	1.00E+00	5.21E-01	1.00E+00	natural killer cell mediated cytotoxicity	P
GO:0042269	17	7.03E-01	1.00E+00	9.68E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.37E-01	1.00E+00	5.03E-02	1.00E+00	7.04E-01	1.00E+00	regulation of natural killer cell mediated cytc	P
GO:0042277	345	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	7.39E-01	1.00E+00	7.33E-01	1.00E+00	peptide binding	F
GO:0042287	15	6.33E-01	1.00E+00	2.72E-01	1.00E+00	7.71E-01	1.00E+00	9.43E-01	1.00E+00	9.28E-01	1.00E+00	1.60E-01	1.00E+00	4.24E-01	1.00E+00	2.71E-01	1.00E+00	MHC protein binding	F
GO:0042288	13	7.60E-01	1.00E+00	4.40E-01	1.00E+00	9.14E-01	1.00E+00	9.88E-01	1.00E+00	9.36E-01	1.00E+00	2.20E-01	1.00E+00	4.96E-01	1.00E+00	3.99E-01	1.00E+00	MHC class I protein binding	F
GO:0042303	42	5.10E-01	1.00E+00	3.61E-01	1.00E+00	4.77E-01	1.00E+00	2.37E-01	1.00E+00	3.85E-01	1.00E+00	9.60E-01	1.00E+00	4.58E-01	1.00E+00	3.95E-01	1.00E+00	molting cycle	P
GO:0042306	23	1.03E-01	1.00E+00	7.27E-02	1.00E+00	3.82E-01	1.00E+00	3.77E-01	1.00E+00	4.35E-01	1.00E+00	2.05E-01	1.00E+00	3.82E-02	7.83E-01	3.35E-02	1.00E+00	regulation of protein import into nucleus	P
GO:0042307	11	6.17E-01	1.00E+00	7.02E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	9.94E-01	1.00E+00	1.13E-01	1.00E+00	1.30E-01	1.00E+00	positive regulation of protein import into nuc	P
GO:0042309	170	1.00E+00	1.00E+00	9.34E-01	1.00E+00	9.96E-01	1.00E+00	3.04E-01	1.00E+00	9.96E-01	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	homoiothermy	P
GO:0042310	21	6.16E-01	1.00E+00	9.96E-01	1.00E+00	3.99E-01	1.00E+00	1.00E+00	1.00E+00	8.83E-01	1.00E+00	9.98E-01	1.00E+00	7.80E-01	1.00E+00	7.53E-01	1.00E+00	vasoconstriction	P
GO:0042311	22	7.32E-01	1.00E+00	9.99E-01	1.00E+00	8.12E-01	1.00E+00	1.00E+00	1.00E+00	9.41E-01	1.00E+00	1.00E+00	1.00E+00	5.82E-01	1.00E+00	1.00E+00	1.00E+00	vasodilation	P
GO:0042325	118	1.00E+00	1.00E+00	9.83E-01	1.00E+00	9.99E-01	1.00E+00	9.26E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.99E-01	1.00E+00	5.29E-01	1.00E+00	regulation of phosphorylation	P
GO:0042326	15	6.63E-01	1.00E+00	7.08E-01	1.00E+00	7.70E-01	1.00E+00	4.73E-02	1.00E+00	8.64E-01	1.00E+00	9.95E-01	1.00E+00	2.87E-01	1.00E+00	8.91E-01	1.00E+00	negative regulation of phosphorylation	P
GO:0042327	35	8.59E-01	1.00E+00	8.38E-01	1.00E+00	8.91E-01	1.00E+00	7.75E-01	1.00E+00	1.00E+00	1.00E+00	9.71E-01	1.00E+00	2.94E-01	1.00E+00	4.13E-01	1.00E+00	positive regulation of phosphorylation	P
GO:0042330	157	9.94E-01	1.00E+00	9.03E-01	1.00E+00	9.81E-01	1.00E+00	9.98E-01	1.00E+00	9.93E-01	1.00E+00	9.65E-01	1.00E+00	7.23E-01	1.00E+00	7.80E-02	1.00E+00	taxis	P
GO:0042345	10	1.55E-01	1.00E+00	7.92E-02	1.00E+00	8.84E-01	1.00E+00	4.46E-01	1.00E+00	7.03E-01	1.00E+00	3.46E-01	1.00E+00	6.20E-02	1.00E+00	2.27E-02	1.00E+00	regulation of NF-kappaB import into nucleus	P
GO:0042348	10	1.55E-01	1.00E+00	7.92E-02	1.00E+00	8.84E-01	1.00E+00	4.46E-01	1.00E+00	7.03E-01	1.00E+00	3.46E-01	1.00E+00	6.20E-02	1.00E+00	2.27E-02	1.00E+00	NF-kappaB import into nucleus	P
GO:0042364	23	3.83E-01	1.00E+00	2.11E-01	1.00E+00	1.68E-01	1.00E+00	3.61E-01	1.00E+00	6.38E-01	1.00E+00	2.96E-01	1.00E+00	6.41E-01	1.00E+00	3.43E-01	1.00E+00	water-soluble vitamin biosynthesis	P
GO:0042375	12	8.08E-03	6.18E-01	3.39E-03	2.13E-01	3.85E-03	1.88E-01	1.54E-02	7.69E-01	1.78E-02	7.19E-01	8.52E-02	1.00E+00	5.44E-02	1.00E+00	2.56E-02	1.00E+00	quinone cofactor metabolism	P
GO:0042379	57	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	7.38E-01	1.00E+00	chemokine receptor binding	F
GO:0042383	24	1.41E-01	1.00E+00	2.08E-01	1.00E+00	3.68E-01	1.00E+00	4.99E-01	1.00E+00	1.44E-01	1.00E+00	1.81E-01	1.00E+00	2.43E-01	1.00E+00	1.05E-01	1.00E+00	sarcolemma	C
GO:0042384	20	9.87E-01	1.00E+00	1.62E-01	1.00E+00	8.55E-01	1.00E+00	2.82E-01	1.00E+00	9.89E-01	1.00E+00	4.06E-02	1.00E+00	9.15E-01	1.00E+00	5.41E-01	1.00E+00	cilium biogenesis	P
GO:0042391	52	4.65E-02	1.00E+00	5.61E-01	1.00E+00	4.76E-01	1.00E+00	7.94E-01	1.00E+00	5.34E-01	1.00E+00	5.63E-01	1.00E+00	7.69E-04	2.40E-02	1.61E-01	1.00E+00	regulation of membrane potential	P
GO:0042393	11	5.33E-03	3.48E-01	1.76E-04	2.80E-02	5.52E-03	1.88E-01	1.17E-03	4.40E-02	7.86E-03	3.18E-01	2.26E-04	1.36E-02	2.11E-01	1.00E+00	1.57E-02	9.40E-01	histone binding	F
GO:0042398	35	4.36E-01	1.00E+00	8.43E-01	1.00E+00	9.75E-01	1.00E+00	7.41E-01	1.00E+00	6.97E-01	1.00E+00	9.99E-01	1.00E+00	3.41E-01	1.00E+00	2.84E-01	1.00E+00	amino acid derivative biosynthesis	P
GO:0042401	30	5.59E-01	1.00E+00	8.64E-01	1.00E+00	9.59E-01	1.00E+00	9.33E-01	1.00E+00	9.30E-01	1.00E+00	9.86E-01	1.00E+00	4.60E-01	1.00E+00	2.53E-01	1.00E+00	biogenic amine biosynthesis	P
GO:0042402	15	4.71E-01	1.00E+00	7.56E-01	1.00E+00	8.38E-01	1.00E+00	2.39E-01	1.00E+00	3.50E-01	1.00E+00	9.73E-01	1.00E+00	3.46E-01	1.00E+00	6.50E-01	1.00E+00	biogenic amine catabolism	P

GO:0042403	11	4.40E-01	1.00E+00	6.32E-01	1.00E+00	7.63E-01	1.00E+00	7.61E-01	1.00E+00	4.92E-01	1.00E+00	6.81E-01	1.00E+00	6.98E-02	1.00E+00	3.23E-01	1.00E+00	thyroid hormone metabolism	P
GO:0042417	25	9.39E-01	1.00E+00	9.81E-01	1.00E+00	9.15E-01	1.00E+00	9.87E-01	1.00E+00	9.92E-01	1.00E+00	9.89E-01	1.00E+00	5.79E-01	1.00E+00	6.85E-01	1.00E+00	dopamine metabolism	P
GO:0042423	12	8.25E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.19E-01	1.00E+00	catecholamine biosynthesis	P
GO:0042430	11	2.03E-01	1.00E+00	4.60E-01	1.00E+00	7.62E-01	1.00E+00	9.35E-01	1.00E+00	1.76E-01	1.00E+00	4.99E-01	1.00E+00	3.16E-02	7.53E-01	1.29E-01	1.00E+00	indole and derivative metabolism	P
GO:0042434	11	2.03E-01	1.00E+00	4.60E-01	1.00E+00	7.62E-01	1.00E+00	9.35E-01	1.00E+00	1.76E-01	1.00E+00	4.99E-01	1.00E+00	3.16E-02	7.53E-01	1.29E-01	1.00E+00	indole derivative metabolism	P
GO:0042440	38	1.19E-01	1.00E+00	9.79E-02	1.00E+00	1.07E-01	1.00E+00	1.04E-01	1.00E+00	5.99E-02	1.00E+00	2.03E-01	1.00E+00	3.84E-01	1.00E+00	1.73E-01	1.00E+00	pigment metabolism	P
GO:0042445	108	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	9.55E-01	1.00E+00	hormone metabolism	P
GO:0042446	41	8.40E-01	1.00E+00	1.00E+00	1.00E+00	8.46E-01	1.00E+00	9.99E-01	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	7.47E-01	1.00E+00	9.71E-01	1.00E+00	hormone biosynthesis	P
GO:0042461	18	6.79E-01	1.00E+00	5.74E-01	1.00E+00	3.29E-01	1.00E+00	3.05E-01	1.00E+00	7.97E-01	1.00E+00	5.36E-01	1.00E+00	6.36E-01	1.00E+00	8.90E-01	1.00E+00	photoreceptor cell development	P
GO:0042462	13	8.87E-01	1.00E+00	4.99E-01	1.00E+00	4.17E-01	1.00E+00	2.42E-01	1.00E+00	8.10E-01	1.00E+00	4.24E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	eye photoreceptor cell development	P
GO:0042470	75	2.03E-03	1.02E-01	3.88E-05	2.80E-02	2.79E-02	1.00E+00	7.61E-03	3.78E-01	2.56E-02	1.00E+00	1.62E-04	1.36E-02	8.75E-02	1.00E+00	3.07E-03	2.16E-01	melanosome	C
GO:0042471	58	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ear morphogenesis	P
GO:0042472	50	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	inner ear morphogenesis	P
GO:0042474	11	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.56E-01	1.00E+00	9.97E-01	1.00E+00	middle ear morphogenesis	P
GO:0042475	40	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.93E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	9.51E-01	1.00E+00	odontogenesis (sensu Vertebrata)	P
GO:0042476	43	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.80E-01	1.00E+00	9.65E-01	1.00E+00	odontogenesis	P
GO:0042490	21	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	8.60E-01	1.00E+00	mechanoreceptor differentiation	P
GO:0042491	15	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.36E-01	1.00E+00	7.27E-01	1.00E+00	auditory receptor cell differentiation	P
GO:0042493	121	3.91E-02	1.00E+00	8.68E-01	1.00E+00	5.12E-01	1.00E+00	9.80E-01	1.00E+00	2.99E-01	1.00E+00	8.32E-01	1.00E+00	1.18E-03	2.40E-02	2.91E-01	1.00E+00	response to drug	P
GO:0042509	15	9.39E-01	1.00E+00	9.88E-01	1.00E+00	9.86E-01	1.00E+00	9.54E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	4.94E-01	1.00E+00	5.29E-01	1.00E+00	regulation of tyrosine phosphorylation of ST/	P
GO:0042533	10	3.39E-01	1.00E+00	5.75E-01	1.00E+00	4.54E-01	1.00E+00	5.53E-01	1.00E+00	9.97E-01	1.00E+00	7.91E-01	1.00E+00	7.13E-02	1.00E+00	3.11E-01	1.00E+00	tumor necrosis factor-alpha biosynthesis	P
GO:0042534	10	3.39E-01	1.00E+00	5.75E-01	1.00E+00	4.54E-01	1.00E+00	5.53E-01	1.00E+00	9.97E-01	1.00E+00	7.91E-01	1.00E+00	7.13E-02	1.00E+00	3.11E-01	1.00E+00	regulation of tumor necrosis factor-alpha bic	P
GO:0042542	23	4.91E-02	1.00E+00	1.03E-01	1.00E+00	9.32E-02	1.00E+00	7.49E-02	1.00E+00	6.48E-02	1.00E+00	1.20E-01	1.00E+00	2.04E-01	1.00E+00	2.89E-01	1.00E+00	response to hydrogen peroxide	P
GO:0042551	16	4.44E-01	1.00E+00	9.93E-01	1.00E+00	6.07E-01	1.00E+00	9.98E-01	1.00E+00	5.33E-01	1.00E+00	9.81E-01	1.00E+00	3.12E-01	1.00E+00	1.00E+00	1.00E+00	neuron maturation	P
GO:0042552	36	4.17E-01	1.00E+00	6.00E-01	1.00E+00	4.49E-01	1.00E+00	7.45E-01	1.00E+00	4.26E-01	1.00E+00	6.84E-01	1.00E+00	5.15E-01	1.00E+00	2.75E-01	1.00E+00	myelination	P
GO:0042558	14	6.44E-02	1.00E+00	3.92E-02	1.00E+00	2.27E-01	1.00E+00	4.97E-01	1.00E+00	3.25E-01	1.00E+00	1.62E-02	1.00E+00	7.17E-03	2.01E-01	7.09E-02	1.00E+00	pteridine and derivative metabolism	P
GO:0042559	11	1.85E-01	1.00E+00	1.18E-01	1.00E+00	6.50E-01	1.00E+00	9.40E-01	1.00E+00	5.96E-01	1.00E+00	3.60E-02	1.00E+00	2.36E-02	5.60E-01	7.21E-02	1.00E+00	pteridine and derivative biosynthesis	P
GO:0042562	22	7.91E-01	1.00E+00	9.29E-01	1.00E+00	9.86E-01	1.00E+00	9.14E-01	1.00E+00	9.59E-01	1.00E+00	9.82E-01	1.00E+00	7.51E-01	1.00E+00	3.65E-01	1.00E+00	hormone binding	F
GO:0042573	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.41E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	retinoic acid metabolism	P
GO:0042577	11	4.51E-01	1.00E+00	3.02E-01	1.00E+00	4.14E-01	1.00E+00	3.24E-01	1.00E+00	9.43E-01	1.00E+00	3.97E-01	1.00E+00	2.61E-01	1.00E+00	2.14E-01	1.00E+00	lipid phosphatase activity	F
GO:0042578	321	1.94E-03	1.02E-01	4.43E-04	4.30E-02	2.36E-02	1.00E+00	2.83E-02	1.00E+00	4.12E-02	1.00E+00	4.40E-03	1.52E-01	2.21E-03	5.54E-02	3.04E-04	1.70E-02	phosphoric ester hydrolase activity	F
GO:0042579	99	5.30E-03	3.48E-01	9.95E-05	2.80E-02	2.88E-03	1.27E-01	1.49E-02	7.69E-01	1.33E-02	4.81E-01	2.04E-04	1.36E-02	1.48E-01	1.00E+00	2.11E-02	1.00E+00	microbody	C
GO:0042592	559	5.19E-01	1.00E+00	9.85E-01	1.00E+00	9.00E-01	1.00E+00	5.65E-01	1.00E+00	5.23E-01	1.00E+00	1.00E+00	1.00E+00	3.04E-01	1.00E+00	9.77E-01	1.00E+00	homeostasis	P
GO:0042593	38	5.89E-01	1.00E+00	5.26E-01	1.00E+00	9.77E-01	1.00E+00	3.58E-01	1.00E+00	8.08E-01	1.00E+00	9.10E-01	1.00E+00	8.43E-02	1.00E+00	1.54E-01	1.00E+00	glucose homeostasis	P
GO:0042594	18	1.25E-01	1.00E+00	5.14E-01	1.00E+00	3.29E-01	1.00E+00	4.68E-01	1.00E+00	1.95E-01	1.00E+00	6.27E-01	1.00E+00	1.60E-01	1.00E+00	3.31E-01	1.00E+00	response to starvation	P
GO:0042596	15	9.97E-01	1.00E+00	7.10E-01	1.00E+00	9.99E-01	1.00E+00	9.28E-01	1.00E+00	9.94E-01	1.00E+00	6.85E-01	1.00E+00	9.57E-01	1.00E+00	4.87E-01	1.00E+00	fear response	P
GO:0042597	20	6.95E-01	1.00E+00	9.98E-01	1.00E+00	9.67E-01	1.00E+00	7.73E-01	1.00E+00	6.71E-01	1.00E+00	1.00E+00	1.00E+00	1.18E-01	1.00E+00	9.55E-01	1.00E+00	periplasmic space	C
GO:0042598	178	8.43E-01	1.00E+00	4.85E-01	1.00E+00	1.00E+00	1.00E+00	8.90E-01	1.00E+00	3.47E-01	1.00E+00	5.84E-01	1.00E+00	1.30E-01	1.00E+00	9.11E-02	1.00E+00	vesicular fraction	C
GO:0042611	49	1.00E+00	1.00E+00	7.68E-01	1.00E+00	1.00E+00	1.00E+00	7.00E-01	1.00E+00	1.00E+00	1.00E+00	1.68E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	MHC protein complex	C
GO:0042612	39	1.00E+00	1.00E+00	8.13E-01	1.00E+00	1.00E+00	1.00E+00	6.60E-01	1.00E+00	9.97E-01	1.00E+00	1.99E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	MHC class I protein complex	C
GO:0042613	10	9.98E-01	1.00E+00	3.48E-01	1.00E+00	9.97E-01	1.00E+00	6.56E-01	1.00E+00	1.00E+00	1.00E+00	3.23E-01	1.00E+00	9.78E-01	1.00E+00	9.16E-01	1.00E+00	MHC class II protein complex	C
GO:0042623	262	4.05E-05	6.00E-03	1.02E-06	2.66E-03	2.50E-03	1.18E-01	3.21E-04	1.30E-02	1.72E-03	5.40E-02	9.92E-06	2.00E-03	8.28E-03	2.17E-01	9.19E-04	3.30E-02	ATPase activity, coupled	F
GO:0042625	90	5.77E-01	1.00E+00	3.33E-01	1.00E+00	9.97E-01	1.00E+00	8.61E-01	1.00E+00	3.17E-01	1.00E+00	2.19E-01	1.00E+00	4.73E-01	1.00E+00	3.16E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042626	129	3.68E-01	1.00E+00	3.51E-01	1.00E+00	9.67E-01	1.00E+00	9.16E-01	1.00E+00	2.43E-01	1.00E+00	1.35E-01	1.00E+00	2.54E-01	1.00E+00	3.24E-01	1.00E+00	ATPase activity, coupled to transmembrane	F
GO:0042627	10	7.32E-01	1.00E+00	5.87E-01	1.00E+00	8.52E-01	1.00E+00	7.31E-01	1.00E+00	8.94E-01	1.00E+00	8.37E-01	1.00E+00	2.77E-01	1.00E+00	6.08E-01	1.00E+00	chylomicron	C
GO:0042632	25	4.74E-01	1.00E+00	6.42E-01	1.00E+00	6.70E-01	1.00E+00	8.03E-01	1.00E+00	6.22E-01	1.00E+00	7.67E-01	1.00E+00	1.56E-01	1.00E+00	6.45E-01	1.00E+00	cholesterol homeostasis	P
GO:0042633	42	5.10E-01	1.00E+00	3.61E-01	1.00E+00	4.77E-01	1.00E+00	2.37E-01	1.00E+00	3.85E-01	1.00E+00	9.60E-01	1.00E+00	4.58E-01	1.00E+00	3.95E-01	1.00E+00	hair cycle	P
GO:0042692	84	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	8.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	muscle cell differentiation	P
GO:0042698	38	5.03E-01	1.00E+00	2.96E-01	1.00E+00	2.17E-01	1.00E+00	7.04E-01	1.00E+00	8.15E-01	1.00E+00	4.51E-01	1.00E+00	5.54E-01	1.00E+00	6.51E-02	1.00E+00	menstrual cycle	P
GO:0042733	18	8.19E-01	1.00E+00	9.14E-01	1.00E+00	9.74E-01	1.00E+00	9.89E-01	1.00E+00	7.31E-01	1.00E+00	9.67E-01	1.00E+00	6.51E-01	1.00E+00	5.58E-01	1.00E+00	embryonic digit morphogenesis	P
GO:0042734	24	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.31E-01	1.00E+00	9.34E-01	1.00E+00	presynaptic membrane	C
GO:0042742	84	5.77E-01	1.00E+00	9.61E-01	1.00E+00	8.81E-01	1.00E+00	5.88E-01	1.00E+00	8.37E-01	1.00E+00	9.52E-01	1.00E+00	6.21E-02	1.00E+00	1.00E+00	1.00E+00	defense response to bacterium	P
GO:0042743	18	2.41E-01	1.00E+00	9.69E-02	1.00E+00	7.44E-01	1.00E+00	8.27E-02	1.00E+00	3.48E-01	1.00E+00	1.72E-01	1.00E+00	7.94E-02	1.00E+00	2.47E-01	1.00E+00	hydrogen peroxide metabolism	P
GO:0042744	12	2.37E-01	1.00E+00	9.91E-02	1.00E+00	9.12E-01	1.00E+00	7.40E-02	1.00E+00	2.17E-01	1.00E+00	1.56E-01	1.00E+00	8.42E-02	1.00E+00	2.69E-01	1.00E+00	hydrogen peroxide catabolism	P
GO:0042755	13	8.45E-01	1.00E+00	7.95E-01	1.00E+00	9.56E-01	1.00E+00	8.94E-01	1.00E+00	7.53E-01	1.00E+00	9.83E-01	1.00E+00	6.00E-01	1.00E+00	3.74E-01	1.00E+00	eating behavior	P
GO:0042770	48	3.66E-03	1.86E-01	2.23E-04	2.80E-02	1.18E-02	4.74E-01	1.18E-04	5.80E-03	4.72E-02	1.00E+00	1.49E-02	1.00E+00	4.20E-02	8.34E-01	1.10E-03	4.40E-02	DNA damage response, signal transduction	P
GO:0042771	11	1.75E-01	1.00E+00	3.00E-01	1.00E+00	2.43E-01	1.00E+00	3.76E-02	1.00E+00	4.78E-01	1.00E+00	5.67E-01	1.00E+00	3.15E-01	1.00E+00	5.19E-01	1.00E+00	DNA damage response, signal transduction	P
GO:0042773	24	1.23E-02	9.83E-01	7.71E-03	5.59E-01	2.09E-01	1.00E+00	3.27E-02	1.00E+00	9.77E-02	1.00E+00	3.82E-02	1.00E+00	5.84E-02	1.00E+00	6.26E-02	1.00E+00	ATP synthesis coupled electron transport	P
GO:0042775	18	1.01E-02	9.83E-01	8.77E-03	5.59E-01	1.91E-01	1.00E+00	6.06E-02	1.00E+00	1.57E-01	1.00E+00	6.15E-02	1.00E+00	5.74E-02	1.00E+00	5.54E-02	1.00E+00	ATP synthesis coupled electron transport (s	P
GO:0042802	383	7.39E-06	5.00E-03	1.21E-03	7.50E-02	4.71E-04	1.61E-02	2.36E-03	6.52E-02	2.80E-04	8.00E-03	3.19E-03	1.43E-01	5.14E-03	9.40E-02	1.12E-01	1.00E+00	identical protein binding	F
GO:0042803	187	1.38E-02	9.83E-01	7.90E-02	1.00E+00	5.01E-02	1.00E+00	1.85E-01	1.00E+00	8.74E-02	1.00E+00	1.13E-01	1.00E+00	6.41E-02	1.00E+00	2.82E-01	1.00E+00	protein homodimerization activity	F
GO:0042809	10	5.08E-01	1.00E+00	4.86E-01	1.00E+00	4.12E-01	1.00E+00	2.29E-01	1.00E+00	5.29E-01	1.00E+00	5.39E-01	1.00E+00	5.67E-01	1.00E+00	9.50E-01	1.00E+00	vitamin D receptor binding	F
GO:0042826	10	1.00E-01	1.00E+00	5.37E-01	1.00E+00	1.51E-01	1.00E+00	9.32E-01	1.00E+00	1.67E-01	1.00E+00	6.21E-01	1.00E+00	8.07E-02	1.00E+00	2.11E-01	1.00E+00	histone deacetylase binding	F
GO:0042895	22	1.99E-01	1.00E+00	2.20E-01	1.00E+00	8.99E-01	1.00E+00	5.43E-01	1.00E+00	3.16E-01	1.00E+00	2.38E-01	1.00E+00	6.77E-02	1.00E+00	1.77E-01	1.00E+00	antibiotic transporter activity	F
GO:0042923	123	9.99E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.03E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	6.58E-01	1.00E+00	4.01E-01	1.00E+00	neuropeptide binding	F
GO:0042974	15	2.86E-01	1.00E+00	4.67E-01	1.00E+00	2.69E-01	1.00E+00	1.51E-01	1.00E+00	4.14E-01	1.00E+00	7.32E-01	1.00E+00	3.11E-01	1.00E+00	8.07E-01	1.00E+00	retinoic acid receptor binding	F
GO:0042981	527	1.23E-02	9.83E-01	3.34E-01	1.00E+00	1.09E-01	1.00E+00	2.00E-01	1.00E+00	2.79E-02	1.00E+00	5.27E-01	1.00E+00	5.70E-02	1.00E+00	3.86E-01	1.00E+00	regulation of apoptosis	P
GO:0042990	17	1.43E-01	1.00E+00	3.41E-02	1.00E+00	6.49E-01	1.00E+00	3.62E-01	1.00E+00	6.68E-01	1.00E+00	1.12E-01	1.00E+00	5.24E-02	1.00E+00	1.98E-02	1.00E+00	regulation of transcription factor import into	P
GO:0042991	17	1.43E-01	1.00E+00	3.41E-02	1.00E+00	6.49E-01	1.00E+00	3.62E-01	1.00E+00	6.68E-01	1.00E+00	1.12E-01	1.00E+00	5.24E-02	1.00E+00	1.98E-02	1.00E+00	transcription factor import into nucleus	P
GO:0042995	524	5.05E-02	1.00E+00	9.82E-01	1.00E+00	3.86E-01	1.00E+00	9.76E-01	1.00E+00	3.42E-02	1.00E+00	9.94E-01	1.00E+00	5.38E-02	1.00E+00	7.00E-01	1.00E+00	cell projection	C
GO:0043005	171	6.61E-01	1.00E+00	1.00E+00	1.00E+00	8.34E-01	1.00E+00	1.00E+00	1.00E+00	4.07E-01	1.00E+00	1.00E+00	1.00E+00	4.93E-01	1.00E+00	8.70E-01	1.00E+00	neuron projection	C
GO:0043009	234	1.00E+00	1.00E+00	8.94E-01	1.00E+00	9.99E-01	1.00E+00	6.57E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	1.00E+00	1.00E+00	9.27E-01	1.00E+00	embryonic development (sensu Vertebrata)	P
GO:0043010	66	4.21E-01	1.00E+00	9.07E-01	1.00E+00	5.39E-01	1.00E+00	8.85E-01	1.00E+00	4.90E-01	1.00E+00	8.58E-01	1.00E+00	2.30E-01	1.00E+00	7.49E-01	1.00E+00	eye development (sensu Vertebrata)	P
GO:0043021	24	7.05E-02	1.00E+00	1.10E-02	7.51E-01	6.67E-02	1.00E+00	8.69E-03	3.78E-01	6.37E-02	1.00E+00	8.36E-03	3.55E-01	2.74E-01	1.00E+00	5.66E-01	1.00E+00	ribonucleoprotein binding	F
GO:0043025	99	5.83E-01	1.00E+00	9.98E-01	1.00E+00	7.85E-01	1.00E+00	9.90E-01	1.00E+00	5.47E-01	1.00E+00	1.00E+00	1.00E+00	2.73E-01	1.00E+00	7.36E-01	1.00E+00	cell soma	C

GO:0043028	11	1.04E-03	9.30E-02	1.91E-02	1.00E+00	4.84E-02	1.00E+00	1.81E-01	1.00E+00	2.63E-01	1.00E+00	2.97E-01	1.00E+00	4.94E-02	1.00E+00	4.56E-02	1.00E+00	caspase regulator activity	F
GO:0043029	18	1.39E-01	1.00E+00	4.19E-02	1.00E+00	1.30E-01	1.00E+00	1.05E-01	1.00E+00	3.14E-01	1.00E+00	1.02E-01	1.00E+00	1.73E-01	1.00E+00	1.09E-01	1.00E+00	T cell homeostasis	P
GO:0043037	156	3.21E-05	6.00E-03	2.05E-10	2.66E-03	2.66E-04	1.61E-02	4.42E-06	1.00E-03	8.12E-06	1.56E-03	2.68E-08	7.71E-04	5.04E-01	1.00E+00	2.32E-02	1.00E+00	translation	P
GO:0043038	67	2.01E-03	1.02E-01	1.09E-04	2.80E-02	7.30E-03	2.83E-01	1.05E-04	5.80E-03	4.65E-03	1.35E-01	3.49E-03	1.43E-01	8.33E-02	1.00E+00	8.97E-02	1.00E+00	amino acid activation	P
GO:0043039	67	2.01E-03	1.02E-01	1.09E-04	2.80E-02	7.30E-03	2.83E-01	1.05E-04	5.80E-03	4.65E-03	1.35E-01	3.49E-03	1.43E-01	8.33E-02	1.00E+00	8.97E-02	1.00E+00	tRNA aminoacylation	P
GO:0043062	78	9.84E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.84E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	5.39E-01	1.00E+00	8.90E-01	1.00E+00	extracellular structure organization and biog	P
GO:0043064	15	1.42E-02	9.83E-01	1.23E-02	7.51E-01	5.56E-02	1.00E+00	3.83E-03	1.42E-01	4.51E-01	1.00E+00	1.41E-02	1.00E+00	8.10E-02	1.00E+00	6.11E-01	1.00E+00	flagellum organization and biogenesis	P
GO:0043065	246	7.84E-03	6.18E-01	1.64E-01	1.00E+00	7.74E-02	1.00E+00	1.36E-01	1.00E+00	5.26E-02	1.00E+00	4.20E-01	1.00E+00	4.78E-03	7.75E-02	1.96E-01	1.00E+00	positive regulation of apoptosis	P
GO:0043066	222	4.66E-01	1.00E+00	7.11E-01	1.00E+00	6.99E-01	1.00E+00	3.75E-01	1.00E+00	6.37E-01	1.00E+00	7.52E-01	1.00E+00	6.28E-01	1.00E+00	8.67E-01	1.00E+00	negative regulation of apoptosis	P
GO:0043067	533	1.86E-02	9.83E-01	3.82E-01	1.00E+00	1.42E-01	1.00E+00	2.35E-01	1.00E+00	3.84E-02	1.00E+00	5.69E-01	1.00E+00	6.91E-02	1.00E+00	4.20E-01	1.00E+00	regulation of programmed cell death	P
GO:0043068	248	8.22E-03	6.18E-01	1.57E-01	1.00E+00	9.21E-02	1.00E+00	1.03E-01	1.00E+00	4.92E-02	1.00E+00	4.40E-01	1.00E+00	5.04E-03	9.40E-02	1.95E-01	1.00E+00	positive regulation of programmed cell death	P
GO:0043069	226	5.39E-01	1.00E+00	7.54E-01	1.00E+00	7.53E-01	1.00E+00	4.33E-01	1.00E+00	6.97E-01	1.00E+00	7.78E-01	1.00E+00	6.72E-01	1.00E+00	8.75E-01	1.00E+00	negative regulation of programmed cell dea	P
GO:0043085	215	5.01E-01	1.00E+00	7.57E-01	1.00E+00	8.03E-01	1.00E+00	9.52E-01	1.00E+00	1.89E-01	1.00E+00	8.34E-01	1.00E+00	6.38E-01	1.00E+00	1.37E-01	1.00E+00	positive regulation of enzyme activity	P
GO:0043086	76	5.28E-02	1.00E+00	8.96E-02	1.00E+00	1.90E-01	1.00E+00	6.16E-02	1.00E+00	1.63E-01	1.00E+00	3.65E-01	1.00E+00	4.18E-02	8.34E-01	2.75E-01	1.00E+00	negative regulation of enzyme activity	P
GO:0043087	88	5.59E-04	5.20E-02	1.64E-02	1.00E+00	1.05E-02	4.74E-01	7.02E-02	1.00E+00	2.11E-02	8.49E-01	1.46E-01	1.00E+00	4.85E-03	7.75E-02	2.25E-03	6.30E-02	regulation of GTPase activity	P
GO:0043112	28	1.53E-01	1.00E+00	3.47E-01	1.00E+00	2.15E-01	1.00E+00	4.15E-01	1.00E+00	1.84E-01	1.00E+00	2.53E-01	1.00E+00	3.50E-01	1.00E+00	5.88E-01	1.00E+00	receptor metabolism	P
GO:0043113	11	2.74E-01	1.00E+00	8.23E-01	1.00E+00	5.12E-01	1.00E+00	9.82E-01	1.00E+00	2.66E-01	1.00E+00	5.70E-01	1.00E+00	1.61E-01	1.00E+00	4.81E-01	1.00E+00	receptor clustering	P
GO:0043118	997	3.60E-02	1.00E+00	6.58E-02	1.00E+00	2.45E-01	1.00E+00	6.05E-03	3.78E-01	1.75E-01	1.00E+00	6.39E-01	1.00E+00	3.03E-02	7.53E-01	4.56E-01	1.00E+00	negative regulation of physiological process	P
GO:0043119	1082	4.68E-01	1.00E+00	9.56E-01	1.00E+00	7.23E-01	1.00E+00	5.41E-01	1.00E+00	8.88E-01	1.00E+00	1.00E+00	1.00E+00	1.52E-01	1.00E+00	6.18E-01	1.00E+00	positive regulation of physiological process	P
GO:0043122	80	5.32E-01	1.00E+00	1.01E-01	1.00E+00	2.79E-01	1.00E+00	2.38E-02	7.69E-01	8.40E-01	1.00E+00	2.95E-01	1.00E+00	4.91E-01	1.00E+00	4.19E-01	1.00E+00	regulation of I-kappaB kinase/NF-kappaB ca	P
GO:0043123	74	5.18E-01	1.00E+00	1.12E-01	1.00E+00	2.86E-01	1.00E+00	3.09E-02	1.00E+00	8.20E-01	1.00E+00	2.79E-01	1.00E+00	4.40E-01	1.00E+00	4.50E-01	1.00E+00	positive regulation of I-kappaB kinase/NF-ka	P
GO:0043154	10	5.77E-01	1.00E+00	2.40E-01	1.00E+00	7.87E-01	1.00E+00	3.16E-02	1.00E+00	2.34E-01	1.00E+00	7.42E-01	1.00E+00	8.31E-01	1.00E+00	8.25E-01	1.00E+00	negative regulation of caspase activity	P
GO:0043161	28	1.61E-02	9.83E-01	3.74E-03	3.82E-01	4.88E-03	1.88E-01	2.89E-03	1.42E-01	6.24E-02	1.00E+00	4.42E-02	1.00E+00	8.41E-01	1.00E+00	4.40E-02	1.00E+00	proteasomal ubiquitin-dependent protein ca	P
GO:0043167	4079	1.33E-06	2.00E-03	1.05E-07	2.66E-03	2.23E-04	1.61E-02	1.36E-05	1.77E-03	7.03E-05	1.56E-03	1.64E-04	1.36E-02	3.13E-05	2.00E-03	4.22E-04	2.10E-02	ion binding	F
GO:0043168	62	8.10E-01	1.00E+00	1.00E+00	1.00E+00	8.00E-01	1.00E+00	1.00E+00	1.00E+00	6.08E-01	1.00E+00	1.00E+00	1.00E+00	7.74E-01	1.00E+00	1.00E+00	1.00E+00	anion binding	F
GO:0043169	3713	2.29E-06	2.00E-03	4.06E-07	2.66E-03	3.88E-04	1.61E-02	2.46E-05	1.92E-03	2.82E-04	8.00E-03	4.24E-04	2.00E-02	1.22E-05	2.00E-03	5.23E-04	2.10E-02	cation binding	F
GO:0043170	4593	1.45E-32	0.00E+00	0.00E+00	0.00E+00	4.44E-25	0.00E+00	1.44E-39	0.00E+00	2.82E-19	0.00E+00	1.04E-39	0.00E+00	4.31E-06	2.00E-03	1.10E-20	0.00E+00	macromolecule metabolism	P
GO:0043176	39	5.74E-01	1.00E+00	9.67E-01	1.00E+00	9.59E-01	1.00E+00	9.76E-01	1.00E+00	8.47E-01	1.00E+00	9.65E-01	1.00E+00	7.29E-02	1.00E+00	2.51E-01	1.00E+00	amine binding	F
GO:0043193	12	1.53E-01	1.00E+00	2.24E-01	1.00E+00	3.70E-01	1.00E+00	9.42E-02	1.00E+00	3.04E-01	1.00E+00	8.42E-01	1.00E+00	1.10E-01	1.00E+00	4.96E-01	1.00E+00	positive regulation of gene-specific transcrip	P
GO:0043197	15	6.81E-01	1.00E+00	9.78E-01	1.00E+00	1.00E+00	1.00E+00	9.64E-01	1.00E+00	5.34E-01	1.00E+00	9.98E-01	1.00E+00	3.19E-01	1.00E+00	8.30E-01	1.00E+00	dendritic spine	C
GO:0043198	13	4.73E-01	1.00E+00	7.12E-01	1.00E+00	8.81E-01	1.00E+00	7.03E-01	1.00E+00	5.77E-01	1.00E+00	6.45E-01	1.00E+00	2.57E-01	1.00E+00	6.92E-01	1.00E+00	dendritic shaft	C
GO:0043226	7761	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.06E-39	0.00E+00	0.00E+00	0.00E+00	3.82E-09	0.00E+00	1.47E-32	0.00E+00	organelle	C
GO:0043227	6906	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.60E-39	0.00E+00	0.00E+00	0.00E+00	1.20E-08	6.33E-04	1.34E-34	0.00E+00	membrane-bound organelle	C
GO:0043228	1766	2.84E-14	6.62E-04	6.86E-19	0.00E+00	1.04E-13	0.00E+00	2.93E-16	0.00E+00	3.31E-07	0.00E+00	1.43E-09	7.71E-04	3.66E-03	6.72E-02	1.22E-04	4.00E-03	non-membrane-bound organelle	C
GO:0043229	7758	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.50E-40	0.00E+00	0.00E+00	0.00E+00	3.56E-09	0.00E+00	1.06E-32	0.00E+00	intracellular organelle	C
GO:0043231	6902	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.19E-39	0.00E+00	0.00E+00	0.00E+00	1.02E-08	6.33E-04	1.45E-34	0.00E+00	intracellular membrane-bound organelle	C
GO:0043232	1766	2.84E-14	6.62E-04	6.86E-19	0.00E+00	1.04E-13	0.00E+00	2.93E-16	0.00E+00	3.31E-07	0.00E+00	1.43E-09	7.71E-04	3.66E-03	6.72E-02	1.22E-04	4.00E-03	intracellular non-membrane-bound organelle	C
GO:0043233	924	5.43E-16	0.00E+00	1.51E-34	0.00E+00	2.01E-14	0.00E+00	8.23E-27	0.00E+00	1.51E-08	0.00E+00	9.20E-22	0.00E+00	7.18E-03	2.01E-01	8.22E-10	0.00E+00	organelle lumen	C
GO:0043234	2236	2.53E-17	0.00E+00	3.27E-35	0.00E+00	3.21E-14	0.00E+00	2.61E-33	0.00E+00	2.03E-08	0.00E+00	1.01E-18	0.00E+00	4.45E-03	7.75E-02	5.36E-06	3.91E-03	protein complex	C
GO:0043235	80	7.66E-02	1.00E+00	8.53E-01	1.00E+00	3.06E-01	1.00E+00	7.01E-01	1.00E+00	6.63E-01	1.00E+00	9.75E-01	1.00E+00	5.20E-03	9.40E-02	3.37E-01	1.00E+00	receptor complex	C
GO:0043269	37	4.95E-01	1.00E+00	9.96E-01	1.00E+00	8.65E-01	1.00E+00	6.31E-01	1.00E+00	8.50E-01	1.00E+00	1.00E+00	1.00E+00	3.51E-02	7.53E-01	5.82E-01	1.00E+00	regulation of ion transport	P
GO:0043270	11	1.73E-01	1.00E+00	4.31E-01	1.00E+00	2.78E-01	1.00E+00	5.03E-01	1.00E+00	2.20E-01	1.00E+00	9.35E-01	1.00E+00	5.57E-02	1.00E+00	9.16E-02	1.00E+00	positive regulation of ion transport	P
GO:0043279	13	6.21E-01	1.00E+00	9.99E-01	1.00E+00	9.69E-01	1.00E+00	9.91E-01	1.00E+00	5.29E-01	1.00E+00	1.00E+00	1.00E+00	1.91E-01	1.00E+00	8.70E-01	1.00E+00	response to alkaloid	P
GO:0043280	37	4.59E-03	2.28E-01	7.21E-02	1.00E+00	1.40E-02	8.10E-01	1.07E-01	1.00E+00	3.43E-02	1.00E+00	7.68E-02	1.00E+00	1.71E-02	4.71E-01	1.24E-01	1.00E+00	positive regulation of caspase activity	P
GO:0043281	50	8.99E-03	9.83E-01	2.77E-02	1.00E+00	4.15E-02	1.00E+00	1.07E-02	3.78E-01	1.98E-02	7.19E-01	9.21E-02	1.00E+00	4.50E-02	8.34E-01	1.77E-01	1.00E+00	regulation of caspase activity	P
GO:0043283	2902	2.61E-37	0.00E+00	0.00E+00	0.00E+00	2.68E-29	0.00E+00	0.00E+00	0.00E+00	9.35E-26	0.00E+00	3.75E-40	0.00E+00	9.57E-07	8.79E-04	1.56E-21	0.00E+00	biopolymer metabolism	P
GO:0043284	42	9.85E-02	1.00E+00	7.56E-01	1.00E+00	2.85E-01	1.00E+00	9.89E-01	1.00E+00	5.69E-02	1.00E+00	3.91E-01	1.00E+00	1.66E-01	1.00E+00	4.72E-01	1.00E+00	biopolymer biosynthesis	P
GO:0043285	283	2.36E-08	9.73E-04	5.24E-12	0.00E+00	4.48E-07	9.88E-04	1.33E-09	0.00E+00	9.32E-07	7.65E-04	7.65E-07	2.00E-03	3.24E-02	7.53E-01	2.41E-05	3.91E-03	biopolymer catabolism	P
GO:0043292	86	5.92E-01	1.00E+00	9.97E-01	1.00E+00	3.12E-01	1.00E+00	9.98E-01	1.00E+00	6.42E-01	1.00E+00	9.90E-01	1.00E+00	4.91E-01	1.00E+00	9.48E-01	1.00E+00	contractile fiber	C
GO:0043296	108	6.39E-01	1.00E+00	2.81E-01	1.00E+00	6.59E-01	1.00E+00	2.21E-01	1.00E+00	9.82E-01	1.00E+00	9.08E-01	1.00E+00	3.93E-02	7.83E-01	8.88E-02	1.00E+00	apical junction complex	C
GO:0043299	13	1.58E-02	9.83E-01	1.01E-01	1.00E+00	8.31E-02	1.00E+00	3.88E-02	1.00E+00	1.93E-01	1.00E+00	7.72E-01	1.00E+00	4.64E-02	8.34E-01	7.62E-02	1.00E+00	leukocyte degranulation	P
GO:0043330	10	7.46E-01	1.00E+00	6.92E-01	1.00E+00	3.30E-01	1.00E+00	4.28E-01	1.00E+00	8.65E-01	1.00E+00	7.34E-01	1.00E+00	7.61E-01	1.00E+00	9.98E-01	1.00E+00	response to exogenous dsRNA	P
GO:0043331	13	9.05E-01	1.00E+00	5.44E-01	1.00E+00	5.07E-01	1.00E+00	3.96E-01	1.00E+00	9.23E-01	1.00E+00	3.76E-01	1.00E+00	9.06E-01	1.00E+00	9.94E-01	1.00E+00	response to dsRNA	P
GO:0043367	17	1.03E-01	1.00E+00	8.48E-01	1.00E+00	2.85E-01	1.00E+00	6.85E-01	1.00E+00	1.30E-01	1.00E+00	9.87E-01	1.00E+00	3.20E-01	1.00E+00	7.51E-01	1.00E+00	CD4-positive, alpha beta T cell differentiatio	P
GO:0043393	11	4.31E-02	1.00E+00	1.78E-01	1.00E+00	9.61E-02	1.00E+00	2.86E-01	1.00E+00	2.86E-02	1.00E+00	5.10E-01	1.00E+00	1.37E-01	1.00E+00	8.08E-02	1.00E+00	regulation of protein binding	P
GO:0043405	92	7.89E-01	1.00E+00	6.91E-01	1.00E+00	9.04E-01	1.00E+00	9.60E-01	1.00E+00	7.51E-01	1.00E+00	6.29E-01	1.00E+00	3.23E-01	1.00E+00	3.22E-01	1.00E+00	regulation of MAPK activity	P
GO:0043406	66	8.99E-01	1.00E+00	7.61E-01	1.00E+00	9.74E-01	1.00E+00	9.86E-01	1.00E+00	6.53E-01	1.00E+00	5.96E-01	1.00E+00	6.82E-01	1.00E+00	2.23E-01	1.00E+00	positive regulation of MAPK activity	P
GO:0043407	21	7.60E-01	1.00E+00	4.33E-01	1.00E+00	9.81E-01	1.00E+00	5.95E-01	1.00E+00	9.11E-01	1.00E+00	7.13E-01	1.00E+00	1.35E-01	1.00E+00	5.74E-01	1.00E+00	negative regulation of MAPK activity	P
GO:0043408	28	4.67E-01	1.00E+00	6.85E-01	1.00E+00	8.20E-01	1.00E+00	2.47E-01	1.00E+00	8.69E-01	1.00E+00	9.82E-01	1.00E+00	3.10E-01	1.00E+00	6.69E-01	1.00E+00	regulation of MAPKKK cascade	P
GO:0043410	18	5.73E-01	1.00E+00	8.16E-01	1.00E+00	6.84E-01	1.00E+00	4.45E-01	1.00E+00	9.28E-01	1.00E+00	9.76E-01	1.00E+00	8.13E-01	1.00E+00	5.59E-01	1.00E+00	positive regulation of MAPKKK cascade	P
GO:0043412	1816	3.00E-13	6.62E-04	5.23E-26	0.00E+00	5.59E-10	0.00E+00	2.94E-15	0.00E+00	7.49E-10	0.00E+00	2.24E-16	0.00E+00	1.00E-03	2.40E-02	4.92E-15	0.00E+00	biopolymer modification	P
GO:0043413	89	5.49E-01	1.00E+00	4.32E-02	1.00E+00	5.47E-01	1.00E+00	1.54E-01	1.00E+00	9.38E-01	1.00E+00	1.45E-01	1.00E+00	1.44E-01	1.00E+00	3.86E-03	2.16E-01	biopolymer glycosylation	P
GO:0043414	69	1.65E-02	9.83E-01	7.52E-03	5.59E-01	1.96E-02	8.10E-01	5.24E-02	1.00E+00	8.75E-03	3.69E-01	5.53E-03	2.02E-01	1.99E-01	1.00E+00	3.64E-02	1.00E+00	biopolymer methylation	P
GO:0043433	21	6.02E-01	1.00E+00	4.25E-01	1.00E+00	2.91E-01	1.00E+00	2.57E-01	1.00E+00	9.14E-01	1.00E+00	3.29E-01	1.00E+00	6.24E-01	1.00E+00	7.37E-01	1.00E+00	negative regulation of transcription factor ac	P
GO:0043434	20	2.95E-01	1.00E+00	9.23E-01	1.00E+00	1.59E-01	1.00E+00	9.93E-01	1.00E+00	4.38E-01	1.00E+00	8.50E-01	1.00E+00	5.48E-01	1.00E+00	3.29E-01	1.00E+00	response to peptide hormone stimulus	P
GO:0043449	28	6.78E-01	1.00E+00	7.33E-01	1.00E+00	7.80E-01	1.00E+00	9.21E-01	1.00E+00	5.68E-01	1.00E+00	7.10E-01	1.00E+00	4.01E-01	1.00E+00	5.90E-01	1.00E+00	alkene metabolism	P
GO:0043450	19	8.92E-01	1.00E+00	6.33E-01	1.00E+00	9.20E-01	1.00E+00	6.78E-01	1.00E+00	7.15E-01	1.00E+00	7.67E-01	1.00E+00	6.79E-01	1.00E+00	4.62E-01	1.00E+00	alkene biosynthesis	P
GO:0043473	40	9.86E-01	1.00E+00	2.86E-01	1.00E+00	9.99E-01	1.00E+00	3.87E-01	1.00E+00	9.27E-01	1.00E+00	5.51E-01	1.00E+00	9.68E-01	1.00E+00	1.05E-01	1.00E+00	pigmentation	P
GO:0043487	17	7.83E-01	1.00E+00	6.70E-01	1.00E+00	7.78E-01	1.00E+00	9.11E-01	1.00E+00	6.71E-01	1.00E+00	9.00E-01	1.00E+00	9.41E-01	1.00E+00	2.21E-01	1.00E+00	regulation of RNA stability	P
GO:0043488	15	7.00E-01	1.00E+00	7.62E-01	1.00E+00	7.01E-01	1.00E+00	9.61E-01	1.00E+00	5.99E-01	1.00E+00	8.18E-01	1.00E+00	9.01E-01	1.00E+00	4.88E-01	1.00E+00	regulation of mRNA stability	P
GO:0043491	12	9.64E-01	1.00E+00	3.76E-01	1.00E+00	9.95E-01	1.00E+00	2.60E-01	1.00E+00	6.86E-01	1.00E+00	8.10E-01	1.00E+00	9.88E-01	1.00E+00	1.13E-01	1.00E+00	protein kinase B signaling cascade	P
GO:0043492	132	2.94E-01	1.00E+00	2.52E-01	1.00E+00	9.67E-01	1.00E+00	8.69E-01	1.00E+00	2.24E-01	1.00E+00	9.54E-02	1.00E+00	1.31E-01	1.00E+00	2.80E-01	1.00E+00	ATPase activity, coupled to movement of su	F
GO:0043498	12	6.82E-01	1.00E+00	3.94E-01	1.00E+00	4.31E-01	1.00E+00	5.29E-01	1.00E+00	9.98E-01	1.00E+00	6.57E-01	1.00E+00	7.14E-01	1.00E+00	2.53E-01	1.00E+00	cell surface binding	F
GO:0043506	21	9.31E-01	1.00E+00	5.32E-01	1.00E+00	9.99E-01	1.00E+00	5.36E-01	1.00E+00	4.36E-01	1.00E+00	4.63E-01	1.00E+00	7.15E-01	1.00E+00	4.87E-01	1.00E+00	regulation of JNK activity	P
GO:0043507	16	8.31E-01	1.00E+00	7.39E-01	1.00E+00	9.93E-01	1.00E+00	7.90E-01	1.00E+00	4.29E-01	1.00E+00	6.94E-01	1.00E+00	5.28E-01	1.00E+00	5.41E-01	1.00E+00	positive regulation of JNK activity	P

GO:0043523	60	4.57E-01	1.00E+00	5.87E-01	1.00E+00	5.72E-01	1.00E+00	6.74E-01	1.00E+00	2.44E-01	1.00E+00	3.86E-01	1.00E+00	9.60E-01	1.00E+00	8.02E-01	1.00E+00	regulation of neuron apoptosis	P
GO:0043524	34	4.47E-01	1.00E+00	2.06E-01	1.00E+00	3.45E-01	1.00E+00	2.26E-01	1.00E+00	4.29E-01	1.00E+00	1.78E-01	1.00E+00	9.29E-01	1.00E+00	4.92E-01	1.00E+00	negative regulation of neuron apoptosis	P
GO:0043525	16	3.98E-01	1.00E+00	6.87E-01	1.00E+00	7.55E-01	1.00E+00	8.47E-01	1.00E+00	2.49E-01	1.00E+00	3.12E-01	1.00E+00	9.50E-01	1.00E+00	9.95E-01	1.00E+00	positive regulation of neuron apoptosis	P
GO:0043534	10	7.97E-01	1.00E+00	6.62E-01	1.00E+00	8.61E-01	1.00E+00	4.59E-01	1.00E+00	9.70E-01	1.00E+00	9.49E-01	1.00E+00	6.78E-01	1.00E+00	9.98E-01	1.00E+00	blood vessel endothelial cell migration	P
GO:0043542	17	6.38E-01	1.00E+00	5.96E-01	1.00E+00	9.41E-01	1.00E+00	4.36E-01	1.00E+00	6.88E-01	1.00E+00	8.16E-01	1.00E+00	6.31E-01	1.00E+00	9.72E-01	1.00E+00	endothelial cell migration	P
GO:0043543	26	4.73E-02	1.00E+00	1.23E-01	1.00E+00	3.55E-02	1.00E+00	1.56E-01	1.00E+00	2.34E-01	1.00E+00	1.12E-01	1.00E+00	5.26E-01	1.00E+00	1.84E-01	1.00E+00	protein amino acid acylation	P
GO:0043549	192	5.67E-01	1.00E+00	6.07E-01	1.00E+00	6.94E-01	1.00E+00	6.78E-01	1.00E+00	3.62E-01	1.00E+00	7.65E-01	1.00E+00	4.46E-01	1.00E+00	3.08E-01	1.00E+00	regulation of kinase activity	P
GO:0043550	10	6.95E-01	1.00E+00	6.28E-02	1.00E+00	9.02E-01	1.00E+00	3.50E-01	1.00E+00	4.07E-01	1.00E+00	2.68E-01	1.00E+00	6.84E-01	1.00E+00	1.59E-02	9.40E-01	regulation of lipid kinase activity	P
GO:0043565	571	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	1.00E+00	1.00E+00	sequence-specific DNA binding	F
GO:0043566	77	1.00E-01	1.00E+00	5.30E-02	1.00E+00	1.38E-01	1.00E+00	5.24E-02	1.00E+00	1.40E-01	1.00E+00	5.16E-02	1.00E+00	3.71E-01	1.00E+00	5.22E-01	1.00E+00	structure-specific DNA binding	F
GO:0043574	10	2.77E-01	1.00E+00	1.96E-01	1.00E+00	2.51E-01	1.00E+00	2.65E-01	1.00E+00	2.56E-01	1.00E+00	3.73E-01	1.00E+00	6.18E-01	1.00E+00	1.29E-01	1.00E+00	peroxisomal transport	P
GO:0043583	71	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ear development	P
GO:0043588	14	8.82E-01	1.00E+00	8.98E-01	1.00E+00	8.55E-01	1.00E+00	9.62E-01	1.00E+00	6.55E-01	1.00E+00	9.60E-01	1.00E+00	9.22E-01	1.00E+00	4.91E-01	1.00E+00	skin development	P
GO:0043596	11	8.09E-02	1.00E+00	1.96E-01	1.00E+00	5.82E-02	1.00E+00	6.56E-01	1.00E+00	1.92E-01	1.00E+00	1.03E-01	1.00E+00	7.63E-02	1.00E+00	2.37E-01	1.00E+00	replication fork (sensu Eukaryota)	C
GO:0043616	10	7.23E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.93E-01	1.00E+00	9.79E-01	1.00E+00	2.13E-01	1.00E+00	4.55E-01	1.00E+00	keratinocyte proliferation	P
GO:0043621	11	4.00E-01	1.00E+00	9.46E-01	1.00E+00	5.89E-01	1.00E+00	9.18E-01	1.00E+00	5.10E-01	1.00E+00	6.37E-01	1.00E+00	2.65E-01	1.00E+00	9.92E-01	1.00E+00	protein self-association	F
GO:0043627	38	9.47E-01	1.00E+00	9.65E-01	1.00E+00	7.27E-01	1.00E+00	9.99E-01	1.00E+00	9.66E-01	1.00E+00	8.94E-01	1.00E+00	8.26E-01	1.00E+00	7.40E-01	1.00E+00	response to estrogen stimulus	P
GO:0043631	10	3.15E-01	1.00E+00	7.57E-03	5.59E-01	1.50E-01	1.00E+00	4.10E-03	1.42E-01	9.55E-01	1.00E+00	6.89E-02	1.00E+00	1.97E-01	1.00E+00	9.37E-01	1.00E+00	RNA polyadenylation	P
GO:0043632	155	4.98E-06	2.00E-03	7.32E-11	2.66E-03	5.26E-05	3.00E-03	6.34E-08	0.00E+00	2.47E-06	7.65E-04	1.72E-07	1.75E-03	2.81E-01	1.00E+00	1.02E-04	4.00E-03	modification-dependent macromolecule cata	P
GO:0043648	11	2.27E-01	1.00E+00	5.76E-01	1.00E+00	3.12E-01	1.00E+00	9.26E-01	1.00E+00	6.79E-02	1.00E+00	4.95E-01	1.00E+00	4.18E-01	1.00E+00	2.43E-01	1.00E+00	dicarboxylic acid metabolism	P
GO:0043681	10	1.21E-01	1.00E+00	5.40E-03	5.59E-01	5.00E-01	1.00E+00	8.86E-03	3.78E-01	1.80E-01	1.00E+00	2.58E-01	1.00E+00	3.83E-01	1.00E+00	3.76E-01	1.00E+00	protein import into mitochondrion	P
GO:0044237	7393	2.29E-26	0.00E+00	0.00E+00	0.00E+00	3.77E-19	0.00E+00	3.88E-42	0.00E+00	2.02E-17	0.00E+00	1.91E-38	0.00E+00	1.49E-04	6.45E-03	1.13E-15	0.00E+00	cellular metabolism	P
GO:0044238	7393	1.01E-22	0.00E+00	0.00E+00	0.00E+00	7.29E-19	0.00E+00	5.10E-39	0.00E+00	1.55E-15	0.00E+00	3.45E-37	0.00E+00	4.17E-03	7.75E-02	1.88E-13	0.00E+00	primary metabolism	P
GO:0044242	42	8.81E-02	1.00E+00	4.86E-01	1.00E+00	4.03E-02	1.00E+00	8.14E-01	1.00E+00	7.22E-01	1.00E+00	8.04E-01	1.00E+00	1.36E-01	1.00E+00	2.06E-01	1.00E+00	cellular lipid catabolism	P
GO:0044247	14	7.25E-01	1.00E+00	6.64E-01	1.00E+00	8.25E-01	1.00E+00	7.97E-01	1.00E+00	9.03E-01	1.00E+00	7.21E-01	1.00E+00	4.38E-01	1.00E+00	3.85E-01	1.00E+00	cellular polysaccharide catabolism	P
GO:0044248	538	1.17E-07	9.73E-04	1.11E-08	2.66E-03	2.26E-05	3.00E-03	6.44E-06	1.77E-03	1.11E-03	4.40E-02	7.20E-06	2.00E-03	1.85E-04	6.45E-03	1.00E-04	4.00E-03	cellular catabolism	P
GO:0044249	1272	1.81E-03	1.02E-01	1.12E-07	2.66E-03	2.68E-02	1.00E+00	8.67E-06	1.77E-03	6.75E-03	1.65E-01	7.45E-05	5.36E-03	5.19E-01	1.00E+00	1.94E-03	6.30E-02	cellular biosynthesis	P
GO:0044255	623	2.22E-04	1.90E-02	1.18E-03	7.50E-02	1.95E-03	1.18E-01	2.94E-02	1.00E+00	5.99E-02	1.00E+00	1.48E-02	1.00E+00	1.87E-03	5.54E-02	5.32E-04	2.10E-02	cellular lipid metabolism	P
GO:0044257	178	1.98E-05	5.00E-03	4.88E-10	2.66E-03	1.12E-04	1.61E-02	5.88E-07	1.00E-03	3.46E-05	1.56E-03	6.11E-07	2.00E-03	3.08E-01	1.00E+00	4.57E-05	3.91E-03	cellular protein catabolism	P
GO:0044260	3188	3.51E-11	6.62E-04	2.41E-26	0.00E+00	2.28E-08	0.00E+00	5.13E-15	0.00E+00	3.74E-07	7.65E-04	2.21E-15	0.00E+00	4.34E-03	7.75E-02	2.16E-13	0.00E+00	cellular macromolecule metabolism	P
GO:0044262	362	2.09E-02	1.00E+00	1.44E-01	1.00E+00	2.35E-01	1.00E+00	5.67E-01	1.00E+00	7.77E-02	1.00E+00	6.06E-02	1.00E+00	3.44E-02	7.53E-01	2.20E-01	1.00E+00	cellular carbohydrate metabolism	P
GO:0044264	75	2.71E-01	1.00E+00	9.22E-01	1.00E+00	4.90E-01	1.00E+00	9.85E-01	1.00E+00	1.22E-01	1.00E+00	7.39E-01	1.00E+00	3.98E-01	1.00E+00	6.66E-01	1.00E+00	cellular polysaccharide metabolism	P
GO:0044265	303	7.06E-07	2.00E-03	1.45E-08	2.66E-03	3.56E-05	3.00E-03	4.13E-06	1.00E-03	1.07E-04	6.00E-03	7.97E-06	2.00E-03	1.21E-02	4.39E-01	1.71E-04	6.00E-03	cellular macromolecule catabolism	P
GO:0044267	3135	3.37E-11	6.62E-04	4.22E-27	0.00E+00	1.52E-08	0.00E+00	1.23E-15	0.00E+00	5.29E-07	7.65E-04	1.01E-15	0.00E+00	4.60E-03	7.75E-02	1.62E-13	0.00E+00	cellular protein metabolism	P
GO:0044270	65	3.64E-01	1.00E+00	6.41E-02	1.00E+00	4.04E-01	1.00E+00	1.69E-01	1.00E+00	4.73E-01	1.00E+00	1.18E-01	1.00E+00	1.42E-01	1.00E+00	1.02E-01	1.00E+00	nitrogen compound catabolism	P
GO:0044271	123	1.09E-01	1.00E+00	3.83E-01	1.00E+00	4.11E-01	1.00E+00	6.43E-01	1.00E+00	3.40E-01	1.00E+00	3.61E-01	1.00E+00	1.85E-01	1.00E+00	2.78E-01	1.00E+00	nitrogen compound biosynthesis	P
GO:0044272	38	1.55E-01	1.00E+00	1.40E-01	1.00E+00	7.37E-01	1.00E+00	4.13E-01	1.00E+00	1.30E-01	1.00E+00	2.67E-01	1.00E+00	3.58E-01	1.00E+00	7.43E-02	1.00E+00	sulfur compound biosynthesis	P
GO:0044275	92	3.23E-02	1.00E+00	2.47E-01	1.00E+00	1.32E-01	1.00E+00	4.04E-01	1.00E+00	2.81E-01	1.00E+00	1.70E-01	1.00E+00	4.00E-02	8.34E-01	4.15E-01	1.00E+00	cellular carbohydrate catabolism	P
GO:0044403	45	1.19E-01	1.00E+00	6.29E-01	1.00E+00	2.53E-01	1.00E+00	8.90E-01	1.00E+00	3.32E-01	1.00E+00	8.47E-01	1.00E+00	9.05E-02	1.00E+00	1.15E-01	1.00E+00	symbiosis, encompassing mutualism throug	P
GO:0044419	56	1.25E-01	1.00E+00	6.74E-01	1.00E+00	1.43E-01	1.00E+00	7.86E-01	1.00E+00	3.85E-01	1.00E+00	9.59E-01	1.00E+00	2.07E-01	1.00E+00	1.13E-01	1.00E+00	interspecies interaction between organisms	P
GO:0044420	95	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.56E-01	1.00E+00	9.87E-01	1.00E+00	extracellular matrix part	C
GO:0044421	1936	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.37E-01	1.00E+00	9.61E-01	1.00E+00	extracellular region part	C
GO:0044422	3324	6.45E-44	0.00E+00	0.00E+00	0.00E+00	5.82E-30	0.00E+00	0.00E+00	0.00E+00	1.19E-25	0.00E+00	8.30E-38	0.00E+00	9.76E-11	0.00E+00	2.19E-24	0.00E+00	organelle part	C
GO:0044423	15	3.85E-01	1.00E+00	5.78E-01	1.00E+00	3.84E-01	1.00E+00	7.42E-01	1.00E+00	3.17E-01	1.00E+00	3.18E-01	1.00E+00	4.75E-01	1.00E+00	8.10E-01	1.00E+00	virion part	C
GO:0044424	9235	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.35E-12	0.00E+00	2.21E-35	0.00E+00	intracellular part	C
GO:0044425	5583	2.38E-01	1.00E+00	7.10E-01	1.00E+00	9.99E-01	1.00E+00	9.79E-01	1.00E+00	7.32E-01	1.00E+00	9.95E-01	1.00E+00	4.26E-07	6.33E-04	4.57E-06	3.91E-03	membrane part	C
GO:0044427	337	1.32E-07	9.73E-04	6.09E-11	2.66E-03	1.37E-08	0.00E+00	1.22E-10	0.00E+00	9.06E-06	1.56E-03	4.54E-05	2.00E-03	2.25E-01	1.00E+00	6.10E-03	2.58E-01	chromosomal part	C
GO:0044428	1032	1.95E-22	0.00E+00	0.00E+00	0.00E+00	4.21E-20	0.00E+00	3.07E-42	0.00E+00	3.12E-13	0.00E+00	4.62E-30	0.00E+00	1.98E-03	5.54E-02	1.51E-10	0.00E+00	nuclear part	C
GO:0044429	517	2.51E-12	6.62E-04	6.26E-21	0.00E+00	5.27E-09	0.00E+00	1.61E-11	0.00E+00	1.80E-07	0.00E+00	6.27E-15	0.00E+00	1.28E-03	3.80E-02	6.49E-09	0.00E+00	mitochondrial part	C
GO:0044430	649	1.73E-08	9.73E-04	4.55E-05	2.80E-02	4.04E-06	1.69E-03	2.25E-03	4.50E-02	1.28E-05	1.56E-03	2.88E-03	1.43E-01	4.82E-05	2.00E-03	3.00E-03	2.16E-01	cytoskeletal part	C
GO:0044431	372	1.52E-05	5.00E-03	8.93E-07	2.66E-03	9.87E-03	4.74E-01	8.66E-06	1.77E-03	1.55E-03	4.80E-02	1.89E-03	1.43E-01	8.29E-04	2.40E-02	5.14E-04	2.10E-02	Golgi apparatus part	C
GO:0044432	529	1.44E-04	1.90E-02	2.95E-06	2.86E-03	6.48E-02	1.00E+00	3.15E-04	1.30E-02	6.31E-04	4.40E-02	2.94E-03	1.43E-01	1.15E-03	2.40E-02	2.78E-04	1.70E-02	endoplasmic reticulum part	C
GO:0044433	107	5.95E-03	3.64E-01	3.66E-02	1.00E+00	3.04E-02	1.00E+00	8.11E-02	1.00E+00	6.99E-02	1.00E+00	8.63E-02	1.00E+00	2.71E-02	6.06E-01	1.17E-01	1.00E+00	cytoplasmic vesicle part	C
GO:0044437	71	6.98E-01	1.00E+00	1.07E-02	7.51E-01	7.06E-01	1.00E+00	1.00E-01	1.00E+00	9.08E-01	1.00E+00	9.95E-02	1.00E+00	5.92E-01	1.00E+00	1.11E-02	6.43E-01	vacuolar part	C
GO:0044438	43	2.03E-03	1.02E-01	4.17E-03	3.82E-01	8.77E-03	4.69E-01	9.79E-02	1.00E+00	4.88E-03	1.35E-01	8.65E-03	3.55E-01	8.75E-02	1.00E+00	6.45E-02	1.00E+00	microbody part	C
GO:0044439	43	2.03E-03	1.02E-01	4.17E-03	3.82E-01	8.77E-03	4.69E-01	9.79E-02	1.00E+00	4.88E-03	1.35E-01	8.65E-03	3.55E-01	8.75E-02	1.00E+00	6.45E-02	1.00E+00	peroxisomal part	C
GO:0044440	90	5.03E-02	1.00E+00	1.32E-03	7.50E-02	2.70E-01	1.00E+00	2.12E-03	4.50E-02	3.59E-01	1.00E+00	1.28E-01	1.00E+00	8.32E-02	1.00E+00	7.97E-03	4.48E-01	endosomal part	C
GO:0044441	12	8.38E-02	1.00E+00	3.07E-01	1.00E+00	9.40E-02	1.00E+00	2.63E-01	1.00E+00	6.59E-01	1.00E+00	3.55E-01	1.00E+00	2.27E-01	1.00E+00	4.05E-01	1.00E+00	cilium part	C
GO:0044444	3640	2.89E-32	0.00E+00	0.00E+00	0.00E+00	1.17E-18	0.00E+00	4.01E-30	0.00E+00	7.45E-17	0.00E+00	1.54E-26	0.00E+00	3.91E-11	0.00E+00	1.02E-23	0.00E+00	cytoplasmic part	C
GO:0044445	68	2.31E-01	1.00E+00	9.72E-02	1.00E+00	4.38E-01	1.00E+00	4.38E-02	1.00E+00	3.15E-01	1.00E+00	2.58E-01	1.00E+00	2.77E-01	1.00E+00	5.12E-01	1.00E+00	cytosolic part	C
GO:0044446	3324	6.45E-44	0.00E+00	0.00E+00	0.00E+00	5.82E-30	0.00E+00	0.00E+00	0.00E+00	1.19E-25	0.00E+00	8.30E-38	0.00E+00	9.76E-11	0.00E+00	2.19E-24	0.00E+00	intracellular organelle part	C
GO:0044448	58	2.61E-01	1.00E+00	3.76E-02	1.00E+00	3.25E-01	1.00E+00	5.36E-02	1.00E+00	8.45E-01	1.00E+00	3.63E-01	1.00E+00	1.78E-01	1.00E+00	8.67E-02	1.00E+00	cell cortex part	C
GO:0044449	78	6.01E-01	1.00E+00	9.95E-01	1.00E+00	3.79E-01	1.00E+00	9.94E-01	1.00E+00	5.84E-01	1.00E+00	9.85E-01	1.00E+00	5.00E-01	1.00E+00	9.55E-01	1.00E+00	contractile fiber part	C
GO:0044450	25	5.24E-03	3.48E-01	5.23E-03	5.59E-01	1.45E-02	8.10E-01	4.93E-03	1.42E-01	2.73E-03	1.35E-01	9.73E-02	1.00E+00	1.19E-01	1.00E+00	7.94E-02	1.00E+00	microtubule organizing center part	C
GO:0044451	473	3.26E-07	9.73E-04	1.54E-16	0.00E+00	3.68E-06	1.69E-03	1.67E-14	0.00E+00	5.31E-05	1.56E-03	7.83E-10	7.71E-04	5.19E-02	1.00E+00	4.54E-05	3.91E-03	nucleoplasm part	C
GO:0044452	39	1.25E-01	1.00E+00	4.39E-02	1.00E+00	6.34E-02	1.00E+00	9.36E-03	3.78E-01	2.85E-01	1.00E+00	8.58E-02	1.00E+00	9.69E-01	1.00E+00	4.33E-01	1.00E+00	nucleolar part	C
GO:0044453	90	2.02E-07	9.73E-04	2.61E-19	0.00E+00	1.54E-07	9.88E-04	1.80E-12	0.00E+00	2.65E-04	8.00E-03	2.06E-13	0.00E+00	9.71E-03	2.17E-01	2.19E-06	3.91E-03	nuclear membrane part	C
GO:0044454	88	1.28E-06	2.00E-03	3.34E-09	2.66E-03	8.81E-07	9.88E-04	1.77E-07	9.57E-04	1.58E-05	1.56E-03	5.91E-07	2.00E-03	1.14E-02	4.39E-01	4.90E-03	2.58E-01	nuclear chromosome part	C
GO:0044455	86	9.98E-05	1.90E-02	1.62E-09	2.66E-03	2.82E-04	1.61E-02	2.14E-06	1.00E-03	6.46E-03	1.65E-01	2.19E-05	2.00E-03	8.99E-02	1.00E+00	1.46E-03	4.40E-02	mitochondrial membrane part	C
GO:0044456	141	9.51E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	4.17E-02	8.34E-01	8.98E-01	1.00E+00	synapse part	C
GO:0044459	1345	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	7.15E-03	2.01E-01	5.65E-01	1.00E+00	plasma membrane part	C
GO:0044460	11	7.34E-01	1.00E+00	7.29E-01	1.00E+00	8.47E-01	1.00E+00	4.16E-01	1.00E+00	3.69E-01	1.00E+00	8.32E-01	1.00E+00	8.18E-01	1.00E+00	9.33E-01	1.00E+00	flagellar part	C
GO:0044462	22	5.93E-01	1.00E+00	9.96E-01	1.00E+00	9.29E-01	1.00E+00	7.87E-01	1.00E+00	5.64E-01	1.00E+00	1.00E+00	1.00E+00	1.23E-01	1.00E+00	9.64E-01	1.00E+00	external encapsulating structure part	C
GO:0044463	94	7.00E-01	1.00E+00	8.21E-01	1.00E+00	7.56E-01	1.00E+00	7.45E-01	1.00E+00	4.45E-01	1.00E+00	8.01E-01	1.00E+00	8.73E-01	1.00E+00	9.42E-01	1.00E+00	cell projection part	C
GO:0044464	13388	1.33E-43	0.00E+00	0.00E+00	0.00E+00	1.20E-21	0.00E+00	0.00E+00	0.00E+00	1.92E-25	0.00E+00	1.81E-29	0.00E+00	1.05E-12	0.00E+00	7.22E-29	0.00E+00	cell part	C

GO:0045005	15	2.47E-02	1.00E+00	1.93E-03	1.62E-01	9.51E-02	1.00E+00	2.22E-02	7.69E-01	6.95E-02	1.00E+00	2.34E-03	1.43E-01	2.93E-02	6.06E-01	3.43E-02	1.00E+00	maintenance of fidelity during DNA-depende	P
GO:0045017	11	1.41E-02	9.83E-01	5.67E-01	1.00E+00	3.93E-02	1.00E+00	7.85E-01	1.00E+00	1.99E-01	1.00E+00	8.25E-01	1.00E+00	9.62E-02	1.00E+00	2.84E-01	1.00E+00	glycerolipid biosynthesis	P
GO:0045028	108	9.93E-01	1.00E+00	9.99E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	8.03E-01	1.00E+00	1.00E+00	1.00E+00	8.75E-01	1.00E+00	2.48E-01	1.00E+00	purinergic nucleotide receptor activity, G-pro	F
GO:0045045	226	2.71E-02	1.00E+00	1.25E-01	1.00E+00	8.14E-02	1.00E+00	3.16E-02	1.00E+00	1.21E-01	1.00E+00	5.03E-01	1.00E+00	1.03E-01	1.00E+00	2.51E-01	1.00E+00	secretory pathway	P
GO:0045047	22	2.50E-02	1.00E+00	5.46E-04	7.30E-02	3.91E-02	1.00E+00	1.25E-03	4.40E-02	1.10E-02	4.14E-01	2.23E-03	1.43E-01	4.40E-01	1.00E+00	3.61E-01	1.00E+00	protein targeting to ER	P
GO:0045055	84	4.99E-01	1.00E+00	9.96E-01	1.00E+00	5.70E-01	1.00E+00	8.52E-01	1.00E+00	8.11E-01	1.00E+00	1.00E+00	1.00E+00	2.69E-01	1.00E+00	7.19E-01	1.00E+00	regulated secretory pathway	P
GO:0045058	19	9.67E-01	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.89E-01	1.00E+00	4.49E-01	1.00E+00	T cell selection	P
GO:0045061	15	9.63E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.92E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	5.31E-01	1.00E+00	7.90E-01	1.00E+00	thymic T cell selection	P
GO:0045072	12	2.56E-01	1.00E+00	1.00E+00	1.00E+00	3.87E-01	1.00E+00	1.00E+00	1.00E+00	3.64E-01	1.00E+00	1.00E+00	1.00E+00	3.02E-01	1.00E+00	1.00E+00	1.00E+00	regulation of interferon-gamma biosynthesis	P
GO:0045076	15	3.09E-01	1.00E+00	6.09E-01	1.00E+00	6.64E-01	1.00E+00	9.86E-01	1.00E+00	6.31E-01	1.00E+00	3.92E-01	1.00E+00	5.85E-02	1.00E+00	2.28E-01	1.00E+00	regulation of interleukin-2 biosynthesis	P
GO:0045078	10	3.34E-01	1.00E+00	1.00E+00	1.00E+00	3.91E-01	1.00E+00	1.00E+00	1.00E+00	4.11E-01	1.00E+00	1.00E+00	1.00E+00	3.93E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of interferon-gamma bios	P
GO:0045087	107	2.88E-01	1.00E+00	9.81E-01	1.00E+00	1.65E-01	1.00E+00	9.88E-01	1.00E+00	7.05E-01	1.00E+00	8.42E-01	1.00E+00	7.78E-02	1.00E+00	8.62E-01	1.00E+00	innate immune response	P
GO:0045088	12	2.91E-01	1.00E+00	3.01E-01	1.00E+00	8.13E-01	1.00E+00	4.91E-01	1.00E+00	5.03E-01	1.00E+00	3.79E-01	1.00E+00	5.17E-02	1.00E+00	9.84E-02	1.00E+00	regulation of innate immune response	P
GO:0045089	11	6.48E-01	1.00E+00	4.00E-01	1.00E+00	9.68E-01	1.00E+00	4.92E-01	1.00E+00	6.12E-01	1.00E+00	3.81E-01	1.00E+00	1.16E-01	1.00E+00	2.07E-01	1.00E+00	positive regulation of innate immune respon	P
GO:0045095	18	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	keratin filament	C
GO:0045103	18	5.68E-01	1.00E+00	6.71E-01	1.00E+00	7.19E-01	1.00E+00	6.80E-01	1.00E+00	9.33E-02	1.00E+00	4.41E-01	1.00E+00	9.92E-01	1.00E+00	9.09E-01	1.00E+00	intermediate filament-based process	P
GO:0045104	15	6.87E-01	1.00E+00	9.86E-01	1.00E+00	8.66E-01	1.00E+00	9.25E-01	1.00E+00	1.40E-01	1.00E+00	9.24E-01	1.00E+00	9.90E-01	1.00E+00	9.80E-01	1.00E+00	intermediate filament cytoskeleton organiza	P
GO:0045109	11	9.85E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	7.23E-01	1.00E+00	4.05E-01	1.00E+00	8.05E-01	1.00E+00	9.63E-01	1.00E+00	9.93E-01	1.00E+00	intermediate filament organization	P
GO:0045111	93	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.33E-01	1.00E+00	9.97E-01	1.00E+00	9.11E-01	1.00E+00	9.80E-01	1.00E+00	intermediate filament cytoskeleton	C
GO:0045120	17	4.22E-02	1.00E+00	6.49E-06	3.00E-03	6.03E-02	1.00E+00	6.02E-04	2.70E-02	6.19E-02	1.00E+00	2.48E-04	1.36E-02	1.12E-01	1.00E+00	3.01E-02	1.00E+00	pronucleus	C
GO:0045121	59	2.82E-01	1.00E+00	3.12E-01	1.00E+00	2.75E-01	1.00E+00	1.85E-01	1.00E+00	3.72E-01	1.00E+00	6.12E-01	1.00E+00	3.50E-01	1.00E+00	5.46E-01	1.00E+00	lipid raft	C
GO:0045125	21	1.53E-01	1.00E+00	2.18E-01	1.00E+00	7.13E-01	1.00E+00	2.01E-01	1.00E+00	1.25E-01	1.00E+00	6.14E-01	1.00E+00	2.05E-01	1.00E+00	6.18E-02	1.00E+00	bioactive lipid receptor activity	F
GO:0045132	10	4.73E-01	1.00E+00	2.48E-03	1.87E-01	2.10E-01	1.00E+00	5.62E-02	1.00E+00	1.00E+00	1.00E+00	1.91E-03	1.43E-01	6.78E-01	1.00E+00	3.59E-02	1.00E+00	meiotic chromosome segregation	P
GO:0045137	66	8.14E-01	1.00E+00	3.21E-01	1.00E+00	5.57E-01	1.00E+00	4.48E-01	1.00E+00	7.88E-01	1.00E+00	4.67E-01	1.00E+00	9.32E-01	1.00E+00	3.77E-01	1.00E+00	development of primary sexual characteristi	P
GO:0045165	128	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.43E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cell fate commitment	P
GO:0045168	15	9.98E-01	1.00E+00	9.65E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	9.25E-01	1.00E+00	8.60E-01	1.00E+00	9.56E-01	1.00E+00	9.90E-01	1.00E+00	cell-cell signaling during cell fate commitme	P
GO:0045177	134	6.35E-01	1.00E+00	9.88E-01	1.00E+00	9.45E-01	1.00E+00	9.61E-01	1.00E+00	5.43E-01	1.00E+00	9.96E-01	1.00E+00	3.98E-01	1.00E+00	8.02E-01	1.00E+00	apical part of cell	C
GO:0045178	31	8.02E-01	1.00E+00	8.69E-01	1.00E+00	5.64E-01	1.00E+00	9.85E-01	1.00E+00	9.79E-01	1.00E+00	4.92E-01	1.00E+00	6.38E-01	1.00E+00	9.78E-01	1.00E+00	basal part of cell	C
GO:0045182	136	3.50E-05	6.00E-03	3.93E-08	2.66E-03	3.80E-05	3.00E-03	5.17E-05	5.41E-03	6.58E-05	1.56E-03	2.58E-07	1.75E-03	4.61E-01	1.00E+00	3.36E-02	1.00E+00	translation regulator activity	F
GO:0045184	856	2.09E-16	0.00E+00	3.45E-25	0.00E+00	1.44E-10	0.00E+00	1.67E-17	0.00E+00	3.41E-11	0.00E+00	3.86E-14	0.00E+00	1.75E-05	2.00E-03	5.73E-10	0.00E+00	establishment of protein localization	P
GO:0045185	20	2.08E-01	1.00E+00	2.71E-01	1.00E+00	6.18E-01	1.00E+00	1.54E-01	1.00E+00	1.91E-01	1.00E+00	2.78E-01	1.00E+00	1.69E-01	1.00E+00	8.58E-01	1.00E+00	maintenance of protein localization	P
GO:0045190	25	1.38E-02	9.83E-01	4.47E-02	1.00E+00	7.95E-02	1.00E+00	4.05E-02	1.00E+00	1.23E-01	1.00E+00	5.06E-01	1.00E+00	1.85E-02	4.71E-01	8.56E-03	4.48E-01	isotype switching	P
GO:0045191	13	7.38E-02	1.00E+00	3.41E-01	1.00E+00	2.26E-01	1.00E+00	3.49E-01	1.00E+00	1.59E-01	1.00E+00	7.42E-01	1.00E+00	9.78E-02	1.00E+00	1.05E-01	1.00E+00	regulation of isotype switching	P
GO:0045202	269	8.72E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	1.00E+00	1.00E+00	6.72E-02	1.00E+00	3.74E-01	1.00E+00	synapse	C
GO:0045211	124	9.06E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	2.82E-02	6.06E-01	8.87E-01	1.00E+00	postsynaptic membrane	C
GO:0045214	12	4.91E-01	1.00E+00	3.44E-01	1.00E+00	3.45E-01	1.00E+00	1.91E-01	1.00E+00	1.00E+00	1.00E+00	5.02E-01	1.00E+00	3.67E-01	1.00E+00	6.90E-01	1.00E+00	sarcomere organization	P
GO:0045216	11	1.07E-01	1.00E+00	2.84E-01	1.00E+00	1.51E-01	1.00E+00	3.03E-01	1.00E+00	2.75E-01	1.00E+00	4.74E-01	1.00E+00	2.60E-01	1.00E+00	3.27E-01	1.00E+00	intercellular junction assembly and mainten	P
GO:0045259	16	4.23E-01	1.00E+00	5.85E-02	1.00E+00	9.48E-01	1.00E+00	4.83E-01	1.00E+00	1.36E-01	1.00E+00	4.99E-02	1.00E+00	6.43E-01	1.00E+00	2.36E-01	1.00E+00	proton-transporting ATP synthase complex	C
GO:0045263	10	3.92E-01	1.00E+00	1.59E-01	1.00E+00	9.60E-01	1.00E+00	5.34E-01	1.00E+00	1.63E-01	1.00E+00	5.84E-02	1.00E+00	2.67E-01	1.00E+00	5.83E-01	1.00E+00	proton-transporting ATP synthase complex,	C
GO:0045271	14	2.07E-02	1.00E+00	1.51E-03	7.50E-02	2.48E-02	1.00E+00	6.22E-04	2.70E-02	1.84E-01	1.00E+00	2.20E-02	1.00E+00	5.97E-02	1.00E+00	4.78E-02	1.00E+00	respiratory chain complex I	C
GO:0045296	12	4.48E-01	1.00E+00	2.78E-01	1.00E+00	8.62E-01	1.00E+00	6.45E-01	1.00E+00	1.59E-01	1.00E+00	2.58E-01	1.00E+00	1.56E-01	1.00E+00	8.09E-02	1.00E+00	cadherin binding	F
GO:0045309	10	2.20E-01	1.00E+00	2.59E-01	1.00E+00	4.34E-01	1.00E+00	3.72E-02	1.00E+00	7.48E-01	1.00E+00	4.72E-01	1.00E+00	5.70E-02	1.00E+00	9.52E-01	1.00E+00	protein phosphorylated amino acid binding	F
GO:0045321	257	5.36E-02	1.00E+00	2.37E-01	1.00E+00	3.67E-01	1.00E+00	7.53E-02	1.00E+00	5.33E-01	1.00E+00	9.93E-01	1.00E+00	1.94E-02	4.71E-01	1.09E-01	1.00E+00	leukocyte activation	P
GO:0045333	34	1.78E-04	1.90E-02	1.51E-02	1.00E+00	6.41E-03	2.83E-01	9.69E-03	3.78E-01	1.31E-02	4.81E-01	8.67E-02	1.00E+00	3.77E-03	6.72E-02	1.80E-02	9.40E-01	cellular respiration	P
GO:0045351	10	5.63E-01	1.00E+00	6.14E-01	1.00E+00	3.18E-01	1.00E+00	6.37E-01	1.00E+00	2.86E-01	1.00E+00	1.80E-01	1.00E+00	9.95E-01	1.00E+00	9.76E-01	1.00E+00	interferon type I biosynthesis	P
GO:0045408	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	9.26E-01	1.00E+00	9.99E-01	1.00E+00	regulation of interleukin-6 biosynthesis	P
GO:0045426	10	7.10E-03	3.64E-01	6.50E-03	5.59E-01	1.20E-02	4.74E-01	2.74E-02	1.00E+00	7.26E-03	3.18E-01	1.64E-01	1.00E+00	2.69E-02	6.06E-01	2.27E-02	1.00E+00	quinone cofactor biosynthesis	P
GO:0045428	14	8.60E-01	1.00E+00	7.56E-01	1.00E+00	5.73E-01	1.00E+00	6.05E-01	1.00E+00	9.68E-01	1.00E+00	8.49E-01	1.00E+00	4.94E-01	1.00E+00	6.59E-01	1.00E+00	regulation of nitric oxide biosynthesis	P
GO:0045429	11	8.67E-01	1.00E+00	8.37E-01	1.00E+00	8.51E-01	1.00E+00	7.73E-01	1.00E+00	9.55E-01	1.00E+00	9.53E-01	1.00E+00	3.49E-01	1.00E+00	6.14E-01	1.00E+00	positive regulation of nitric oxide biosynthes	P
GO:0045444	32	9.35E-02	1.00E+00	9.55E-02	1.00E+00	2.84E-01	1.00E+00	1.24E-01	1.00E+00	3.39E-01	1.00E+00	1.96E-01	1.00E+00	1.22E-01	1.00E+00	1.42E-01	1.00E+00	fat cell differentiation	P
GO:0045445	45	9.99E-01	1.00E+00	9.99E-01	1.00E+00	8.57E-01	1.00E+00	7.15E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	myoblast differentiation	P
GO:0045446	11	9.41E-01	1.00E+00	8.38E-01	1.00E+00	9.81E-01	1.00E+00	9.01E-01	1.00E+00	1.00E+00	1.00E+00	8.00E-01	1.00E+00	4.11E-01	1.00E+00	5.86E-01	1.00E+00	endothelial cell differentiation	P
GO:0045449	2397	4.87E-01	1.00E+00	1.51E-06	2.66E-03	1.14E-01	1.00E+00	1.28E-09	0.00E+00	2.77E-01	1.00E+00	1.44E-04	1.36E-02	9.87E-01	1.00E+00	6.80E-01	1.00E+00	regulation of transcription	P
GO:0045453	17	8.75E-01	1.00E+00	9.03E-01	1.00E+00	8.45E-01	1.00E+00	6.26E-01	1.00E+00	9.38E-01	1.00E+00	8.98E-01	1.00E+00	8.78E-01	1.00E+00	9.51E-01	1.00E+00	bone resorption	P
GO:0045454	57	4.57E-02	1.00E+00	4.34E-01	1.00E+00	2.07E-01	1.00E+00	3.79E-01	1.00E+00	4.84E-02	1.00E+00	7.96E-01	1.00E+00	4.92E-01	1.00E+00	1.95E-01	1.00E+00	cell redox homeostasis	P
GO:0045471	20	7.07E-01	1.00E+00	9.95E-01	1.00E+00	7.50E-01	1.00E+00	1.00E+00	1.00E+00	7.54E-01	1.00E+00	1.00E+00	1.00E+00	4.12E-01	1.00E+00	5.80E-01	1.00E+00	response to ethanol	P
GO:0045494	13	8.47E-01	1.00E+00	8.00E-01	1.00E+00	7.44E-01	1.00E+00	6.43E-01	1.00E+00	7.78E-01	1.00E+00	6.76E-01	1.00E+00	9.08E-01	1.00E+00	9.13E-01	1.00E+00	photoreceptor maintenance	P
GO:0045576	13	2.14E-01	1.00E+00	2.42E-01	1.00E+00	3.34E-01	1.00E+00	9.78E-02	1.00E+00	7.30E-01	1.00E+00	6.88E-01	1.00E+00	2.29E-01	1.00E+00	3.52E-01	1.00E+00	mast cell activation	P
GO:0045577	13	1.50E-01	1.00E+00	7.51E-02	1.00E+00	5.29E-01	1.00E+00	1.65E-01	1.00E+00	6.13E-01	1.00E+00	4.03E-01	1.00E+00	2.52E-02	5.60E-01	7.17E-02	1.00E+00	regulation of B cell differentiation	P
GO:0045580	21	4.52E-01	1.00E+00	6.51E-01	1.00E+00	8.86E-01	1.00E+00	3.91E-01	1.00E+00	9.84E-01	1.00E+00	9.19E-01	1.00E+00	1.84E-01	1.00E+00	5.52E-01	1.00E+00	regulation of T cell differentiation	P
GO:0045582	16	2.39E-01	1.00E+00	5.36E-01	1.00E+00	6.49E-01	1.00E+00	3.27E-01	1.00E+00	9.51E-01	1.00E+00	7.21E-01	1.00E+00	1.80E-01	1.00E+00	4.23E-01	1.00E+00	positive regulation of T cell differentiation	P
GO:0045595	209	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	8.52E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	regulation of cell differentiation	P
GO:0045596	115	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	6.42E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of cell differentiation	P
GO:0045597	83	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.28E-01	1.00E+00	positive regulation of cell differentiation	P
GO:0045619	30	3.86E-01	1.00E+00	5.51E-01	1.00E+00	7.39E-01	1.00E+00	3.59E-01	1.00E+00	9.56E-01	1.00E+00	9.36E-01	1.00E+00	1.49E-01	1.00E+00	4.75E-01	1.00E+00	regulation of lymphocyte differentiation	P
GO:0045621	20	6.46E-02	1.00E+00	4.96E-01	1.00E+00	2.76E-01	1.00E+00	3.93E-01	1.00E+00	7.35E-01	1.00E+00	7.20E-01	1.00E+00	1.22E-01	1.00E+00	2.80E-01	1.00E+00	positive regulation of lymphocyte differentiat	P
GO:0045637	53	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.92E-01	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	regulation of myeloid cell differentiation	P
GO:0045638	25	9.99E-01	1.00E+00	9.59E-01	1.00E+00	9.62E-01	1.00E+00	9.20E-01	1.00E+00	9.99E-01	1.00E+00	9.04E-01	1.00E+00	1.00E+00	1.00E+00	9.15E-01	1.00E+00	negative regulation of myeloid cell differentia	P
GO:0045639	22	9.64E-01	1.00E+00	9.94E-01	1.00E+00	9.68E-01	1.00E+00	9.98E-01	1.00E+00	9.16E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	9.51E-01	1.00E+00	positive regulation of myeloid cell differentia	P
GO:0045646	14	4.72E-01	1.00E+00	6.14E-01	1.00E+00	8.52E-01	1.00E+00	6.83E-01	1.00E+00	2.56E-01	1.00E+00	5.15E-01	1.00E+00	5.78E-01	1.00E+00	4.63E-01	1.00E+00	regulation of erythrocyte differentiation	P
GO:0045661	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of myoblast differentiation	P
GO:0045664	42	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	regulation of neuron differentiation	P
GO:0045665	29	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	negative regulation of neuron differentiation	P
GO:0045666	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	7.88E-01	1.00E+00	positive regulation of neuron differentiation	P
GO:0045667	27	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.04E-01	1.00E+00	regulation of osteoblast differentiation	P

GO:0045669	19	1.00E+00	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.80E-01	1.00E+00	7.74E-01	1.00E+00	positive regulation of osteoblast differentiati	P
GO:0045670	16	9.70E-01	1.00E+00	9.37E-01	1.00E+00	7.68E-01	1.00E+00	8.07E-01	1.00E+00	9.40E-01	1.00E+00	8.45E-01	1.00E+00	1.00E+00	1.00E+00	7.66E-01	1.00E+00	regulation of osteoclast differentiation	P
GO:0045685	12	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	regulation of glial cell differentiation	P
GO:0045727	56	6.12E-01	1.00E+00	9.87E-01	1.00E+00	8.10E-01	1.00E+00	9.92E-01	1.00E+00	8.70E-01	1.00E+00	9.08E-01	1.00E+00	1.53E-01	1.00E+00	6.85E-01	1.00E+00	positive regulation of protein biosynthesis	P
GO:0045735	72	7.61E-01	1.00E+00	8.11E-01	1.00E+00	6.71E-01	1.00E+00	9.50E-01	1.00E+00	7.15E-01	1.00E+00	5.51E-01	1.00E+00	7.23E-01	1.00E+00	6.29E-01	1.00E+00	nutrient reservoir activity	F
GO:0045736	10	1.64E-01	1.00E+00	5.06E-02	1.00E+00	2.50E-01	1.00E+00	1.41E-03	4.40E-02	3.84E-01	1.00E+00	5.53E-01	1.00E+00	2.01E-01	1.00E+00	4.30E-01	1.00E+00	negative regulation of cyclin-dependent prot	P
GO:0045740	10	2.79E-01	1.00E+00	2.26E-01	1.00E+00	4.38E-01	1.00E+00	8.12E-01	1.00E+00	7.20E-01	1.00E+00	2.68E-01	1.00E+00	9.99E-02	1.00E+00	1.30E-01	1.00E+00	positive regulation of DNA replication	P
GO:0045761	20	9.46E-01	1.00E+00	9.90E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.56E-01	1.00E+00	9.89E-01	1.00E+00	9.79E-01	1.00E+00	9.51E-01	1.00E+00	regulation of adenylate cyclase activity	P
GO:0045762	16	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.93E-01	1.00E+00	positive regulation of adenylate cyclase acti	P
GO:0045763	15	9.56E-01	1.00E+00	9.70E-01	1.00E+00	9.94E-01	1.00E+00	6.79E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	3.64E-01	1.00E+00	9.80E-01	1.00E+00	negative regulation of amino acid metabolis	P
GO:0045764	46	9.32E-01	1.00E+00	8.65E-01	1.00E+00	9.46E-01	1.00E+00	8.38E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	3.81E-01	1.00E+00	4.53E-01	1.00E+00	positive regulation of amino acid metabolism	P
GO:0045765	40	8.66E-01	1.00E+00	1.00E+00	1.00E+00	7.19E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	5.02E-01	1.00E+00	1.00E+00	1.00E+00	regulation of angiogenesis	P
GO:0045766	12	9.99E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.92E-01	1.00E+00	9.96E-01	1.00E+00	positive regulation of angiogenesis	P
GO:0045767	12	3.89E-01	1.00E+00	3.19E-01	1.00E+00	2.16E-01	1.00E+00	2.84E-01	1.00E+00	8.15E-01	1.00E+00	6.42E-01	1.00E+00	7.03E-01	1.00E+00	2.37E-01	1.00E+00	regulation of anti-apoptosis	P
GO:0045778	16	9.71E-01	1.00E+00	7.98E-01	1.00E+00	9.84E-01	1.00E+00	9.52E-01	1.00E+00	9.09E-01	1.00E+00	6.34E-01	1.00E+00	6.78E-01	1.00E+00	6.30E-01	1.00E+00	positive regulation of ossification	P
GO:0045785	12	5.17E-01	1.00E+00	8.40E-01	1.00E+00	8.21E-01	1.00E+00	9.99E-01	1.00E+00	9.22E-01	1.00E+00	9.62E-01	1.00E+00	1.22E-01	1.00E+00	5.79E-02	1.00E+00	positive regulation of cell adhesion	P
GO:0045786	153	1.57E-02	9.83E-01	1.27E-01	1.00E+00	2.50E-02	1.00E+00	1.18E-02	3.78E-01	5.20E-02	1.00E+00	4.36E-01	1.00E+00	2.17E-01	1.00E+00	7.56E-01	1.00E+00	negative regulation of progression through c	P
GO:0045787	32	8.68E-01	1.00E+00	5.31E-01	1.00E+00	9.22E-01	1.00E+00	4.67E-01	1.00E+00	3.70E-01	1.00E+00	4.06E-01	1.00E+00	9.87E-01	1.00E+00	8.01E-01	1.00E+00	positive regulation of progression through ce	P
GO:0045792	54	9.28E-02	1.00E+00	4.06E-01	1.00E+00	6.77E-02	1.00E+00	9.20E-02	1.00E+00	6.48E-01	1.00E+00	8.88E-01	1.00E+00	5.98E-02	1.00E+00	3.84E-01	1.00E+00	negative regulation of cell size	P
GO:0045793	11	8.96E-01	1.00E+00	5.47E-01	1.00E+00	7.71E-01	1.00E+00	7.25E-01	1.00E+00	7.83E-01	1.00E+00	2.97E-01	1.00E+00	6.33E-01	1.00E+00	8.55E-01	1.00E+00	positive regulation of cell size	P
GO:0045807	27	9.44E-01	1.00E+00	9.90E-01	1.00E+00	9.78E-01	1.00E+00	9.57E-01	1.00E+00	8.88E-01	1.00E+00	9.70E-01	1.00E+00	6.26E-01	1.00E+00	9.88E-01	1.00E+00	positive regulation of endocytosis	P
GO:0045814	17	2.91E-02	1.00E+00	4.20E-04	4.30E-02	4.94E-02	1.00E+00	5.52E-02	1.00E+00	1.03E-01	1.00E+00	1.62E-02	1.00E+00	1.68E-01	1.00E+00	6.16E-03	2.58E-01	negative regulation of gene expression, epic	P
GO:0045830	10	1.47E-01	1.00E+00	3.74E-01	1.00E+00	1.65E-01	1.00E+00	3.86E-01	1.00E+00	3.15E-01	1.00E+00	6.46E-01	1.00E+00	1.57E-01	1.00E+00	1.03E-01	1.00E+00	positive regulation of isotype switching	P
GO:0045834	13	2.62E-01	1.00E+00	7.08E-01	1.00E+00	7.83E-01	1.00E+00	7.53E-01	1.00E+00	4.32E-01	1.00E+00	1.00E+00	1.00E+00	1.61E-01	1.00E+00	7.41E-02	1.00E+00	positive regulation of lipid metabolism	P
GO:0045840	15	9.63E-01	1.00E+00	8.74E-01	1.00E+00	9.55E-01	1.00E+00	8.73E-01	1.00E+00	7.89E-01	1.00E+00	6.11E-01	1.00E+00	9.95E-01	1.00E+00	9.22E-01	1.00E+00	positive regulation of mitosis	P
GO:0045859	184	5.54E-01	1.00E+00	7.45E-01	1.00E+00	6.45E-01	1.00E+00	7.07E-01	1.00E+00	3.79E-01	1.00E+00	8.30E-01	1.00E+00	4.46E-01	1.00E+00	5.87E-01	1.00E+00	regulation of protein kinase activity	P
GO:0045860	126	8.61E-01	1.00E+00	9.03E-01	1.00E+00	8.98E-01	1.00E+00	9.78E-01	1.00E+00	3.31E-01	1.00E+00	7.46E-01	1.00E+00	9.22E-01	1.00E+00	5.20E-01	1.00E+00	positive regulation of protein kinase activity	P
GO:0045884	15	8.17E-01	1.00E+00	8.78E-01	1.00E+00	8.86E-01	1.00E+00	8.05E-01	1.00E+00	8.00E-01	1.00E+00	9.86E-01	1.00E+00	3.51E-01	1.00E+00	7.49E-01	1.00E+00	regulation of survival gene product activity	P
GO:0045892	244	4.97E-01	1.00E+00	1.20E-01	1.00E+00	6.89E-01	1.00E+00	6.32E-02	1.00E+00	6.02E-01	1.00E+00	3.21E-01	1.00E+00	3.98E-01	1.00E+00	3.80E-01	1.00E+00	negative regulation of transcription, DNA-de	P
GO:0045893	353	6.13E-01	1.00E+00	8.76E-01	1.00E+00	5.22E-01	1.00E+00	6.15E-01	1.00E+00	7.79E-01	1.00E+00	9.92E-01	1.00E+00	6.84E-01	1.00E+00	4.74E-01	1.00E+00	positive regulation of transcription, DNA-dep	P
GO:0045926	63	4.92E-02	1.00E+00	3.79E-01	1.00E+00	4.97E-02	1.00E+00	1.27E-01	1.00E+00	3.62E-01	1.00E+00	7.94E-01	1.00E+00	9.77E-02	1.00E+00	3.49E-01	1.00E+00	negative regulation of growth	P
GO:0045927	36	9.58E-01	1.00E+00	8.71E-01	1.00E+00	9.63E-01	1.00E+00	9.93E-01	1.00E+00	8.27E-01	1.00E+00	9.80E-01	1.00E+00	8.67E-01	1.00E+00	2.80E-01	1.00E+00	positive regulation of growth	P
GO:0045930	14	3.24E-01	1.00E+00	9.74E-01	1.00E+00	4.22E-01	1.00E+00	6.55E-01	1.00E+00	1.99E-01	1.00E+00	9.99E-01	1.00E+00	4.61E-01	1.00E+00	9.01E-01	1.00E+00	negative regulation of progression through r	P
GO:0045934	337	1.04E-01	1.00E+00	7.73E-03	5.59E-01	2.49E-01	1.00E+00	7.65E-03	3.78E-01	1.40E-01	1.00E+00	4.66E-02	1.00E+00	1.42E-01	1.00E+00	1.48E-01	1.00E+00	negative regulation of nucleobase, nucleosi	P
GO:0045935	441	5.21E-01	1.00E+00	9.43E-01	1.00E+00	3.29E-01	1.00E+00	7.48E-01	1.00E+00	9.48E-01	1.00E+00	1.00E+00	1.00E+00	5.26E-01	1.00E+00	4.67E-01	1.00E+00	positive regulation of nucleobase, nucleosid	P
GO:0045936	17	4.81E-01	1.00E+00	3.72E-01	1.00E+00	5.52E-01	1.00E+00	1.73E-02	7.69E-01	6.54E-01	1.00E+00	7.96E-01	1.00E+00	2.92E-01	1.00E+00	8.61E-01	1.00E+00	negative regulation of phosphate metabolism	P
GO:0045937	38	5.95E-01	1.00E+00	8.25E-01	1.00E+00	6.03E-01	1.00E+00	7.37E-01	1.00E+00	9.62E-01	1.00E+00	9.76E-01	1.00E+00	2.43E-01	1.00E+00	3.92E-01	1.00E+00	positive regulation of phosphate metabolism	P
GO:0045941	420	5.98E-01	1.00E+00	9.29E-01	1.00E+00	3.27E-01	1.00E+00	6.96E-01	1.00E+00	9.15E-01	1.00E+00	9.99E-01	1.00E+00	6.96E-01	1.00E+00	4.50E-01	1.00E+00	positive regulation of transcription	P
GO:0045944	289	9.78E-01	1.00E+00	9.99E-01	1.00E+00	9.34E-01	1.00E+00	9.84E-01	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.53E-01	1.00E+00	8.78E-01	1.00E+00	positive regulation of transcription from RNA	P
GO:0045954	13	6.61E-01	1.00E+00	9.41E-01	1.00E+00	8.12E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	5.47E-01	1.00E+00	1.18E-01	1.00E+00	7.37E-01	1.00E+00	positive regulation of natural killer cell media	P
GO:0046006	10	2.77E-01	1.00E+00	2.37E-02	1.00E+00	1.25E-01	1.00E+00	6.42E-02	1.00E+00	4.46E-01	1.00E+00	3.57E-01	1.00E+00	3.35E-01	1.00E+00	3.10E-02	1.00E+00	regulation of activated T cell proliferation	P
GO:0046034	43	4.87E-01	1.00E+00	4.13E-01	1.00E+00	9.76E-01	1.00E+00	6.21E-01	1.00E+00	2.49E-01	1.00E+00	5.06E-01	1.00E+00	5.29E-01	1.00E+00	3.89E-01	1.00E+00	ATP metabolism	P
GO:0046036	12	9.92E-02	1.00E+00	7.31E-02	1.00E+00	4.69E-02	1.00E+00	1.04E-01	1.00E+00	6.29E-02	1.00E+00	6.78E-02	1.00E+00	7.71E-01	1.00E+00	2.86E-01	1.00E+00	CTP metabolism	P
GO:0046039	12	1.03E-01	1.00E+00	6.66E-02	1.00E+00	8.81E-02	1.00E+00	7.37E-02	1.00E+00	6.99E-02	1.00E+00	8.10E-02	1.00E+00	4.91E-01	1.00E+00	2.76E-01	1.00E+00	GTP metabolism	P
GO:0046051	11	1.04E-01	1.00E+00	1.02E-01	1.00E+00	5.89E-02	1.00E+00	1.63E-01	1.00E+00	5.18E-02	1.00E+00	9.12E-02	1.00E+00	7.68E-01	1.00E+00	2.83E-01	1.00E+00	UTP metabolism	P
GO:0046058	26	9.00E-01	1.00E+00	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.70E-01	1.00E+00	9.07E-01	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	9.00E-01	1.00E+00	cAMP metabolism	P
GO:0046068	17	9.08E-01	1.00E+00	9.94E-01	1.00E+00	9.95E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.45E-01	1.00E+00	7.29E-01	1.00E+00	cGMP metabolism	P
GO:0046148	32	1.18E-01	1.00E+00	1.86E-01	1.00E+00	1.68E-01	1.00E+00	1.55E-01	1.00E+00	5.30E-02	1.00E+00	3.60E-01	1.00E+00	2.81E-01	1.00E+00	2.27E-01	1.00E+00	pigment biosynthesis	P
GO:0046164	77	1.03E-02	9.83E-01	1.52E-01	1.00E+00	4.68E-02	1.00E+00	3.02E-01	1.00E+00	1.50E-01	1.00E+00	5.69E-02	1.00E+00	1.93E-02	4.71E-01	6.59E-01	1.00E+00	alcohol catabolism	P
GO:0046165	32	5.35E-02	1.00E+00	3.23E-01	1.00E+00	4.19E-01	1.00E+00	2.59E-01	1.00E+00	9.51E-02	1.00E+00	6.95E-01	1.00E+00	5.67E-02	1.00E+00	2.79E-01	1.00E+00	alcohol biosynthesis	P
GO:0046209	23	5.23E-01	1.00E+00	9.05E-01	1.00E+00	5.54E-01	1.00E+00	7.87E-01	1.00E+00	9.18E-01	1.00E+00	9.48E-01	1.00E+00	1.24E-01	1.00E+00	5.96E-01	1.00E+00	nitric oxide metabolism	P
GO:0046323	14	7.28E-01	1.00E+00	6.54E-01	1.00E+00	9.90E-01	1.00E+00	6.02E-01	1.00E+00	5.60E-01	1.00E+00	6.87E-01	1.00E+00	3.36E-01	1.00E+00	3.47E-01	1.00E+00	glucose import	P
GO:0046324	13	7.38E-01	1.00E+00	6.35E-01	1.00E+00	9.92E-01	1.00E+00	5.76E-01	1.00E+00	5.40E-01	1.00E+00	6.88E-01	1.00E+00	3.66E-01	1.00E+00	3.21E-01	1.00E+00	regulation of glucose import	P
GO:0046328	25	9.17E-01	1.00E+00	9.95E-01	1.00E+00	9.64E-01	1.00E+00	9.68E-01	1.00E+00	9.99E-01	1.00E+00	9.49E-01	1.00E+00	5.05E-01	1.00E+00	1.00E+00	1.00E+00	regulation of JNK cascade	P
GO:0046330	15	8.32E-01	1.00E+00	9.91E-01	1.00E+00	9.49E-01	1.00E+00	9.68E-01	1.00E+00	9.98E-01	1.00E+00	8.62E-01	1.00E+00	4.50E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of JNK cascade	P
GO:0046332	17	9.98E-01	1.00E+00	9.83E-01	1.00E+00	9.60E-01	1.00E+00	9.91E-01	1.00E+00	9.62E-01	1.00E+00	9.74E-01	1.00E+00	9.96E-01	1.00E+00	8.31E-01	1.00E+00	SMAD binding	F
GO:0046348	11	1.00E+00	1.00E+00	8.65E-01	1.00E+00	9.80E-01	1.00E+00	8.34E-01	1.00E+00	9.90E-01	1.00E+00	8.82E-01	1.00E+00	1.00E+00	1.00E+00	6.65E-01	1.00E+00	amino sugar catabolism	P
GO:0046356	24	3.67E-02	1.00E+00	3.29E-02	1.00E+00	3.15E-02	1.00E+00	1.85E-02	7.69E-01	2.44E-01	1.00E+00	1.91E-01	1.00E+00	9.38E-02	1.00E+00	2.75E-02	1.00E+00	acetyl-CoA catabolism	P
GO:0046364	31	4.75E-02	1.00E+00	3.45E-01	1.00E+00	4.34E-01	1.00E+00	3.09E-01	1.00E+00	9.54E-02	1.00E+00	7.32E-01	1.00E+00	4.82E-02	1.00E+00	2.67E-01	1.00E+00	monosaccharide biosynthesis	P
GO:0046365	68	1.40E-02	9.83E-01	1.64E-01	1.00E+00	5.59E-02	1.00E+00	3.92E-01	1.00E+00	1.16E-01	1.00E+00	5.44E-02	1.00E+00	2.89E-02	6.06E-01	5.10E-01	1.00E+00	monosaccharide catabolism	P
GO:0046394	93	4.17E-01	1.00E+00	5.72E-01	1.00E+00	9.28E-01	1.00E+00	9.01E-01	1.00E+00	2.84E-01	1.00E+00	5.43E-01	1.00E+00	1.39E-01	1.00E+00	8.64E-02	1.00E+00	carboxylic acid biosynthesis	P
GO:0046425	21	6.73E-01	1.00E+00	7.45E-01	1.00E+00	6.23E-01	1.00E+00	8.20E-01	1.00E+00	9.97E-01	1.00E+00	9.27E-01	1.00E+00	2.38E-01	1.00E+00	2.73E-01	1.00E+00	regulation of JAK-STAT cascade	P
GO:0046427	12	4.83E-01	1.00E+00	7.30E-01	1.00E+00	5.56E-01	1.00E+00	8.68E-01	1.00E+00	9.74E-01	1.00E+00	9.96E-01	1.00E+00	1.77E-01	1.00E+00	9.87E-02	1.00E+00	positive regulation of JAK-STAT cascade	P
GO:0046456	26	8.76E-01	1.00E+00	8.65E-01	1.00E+00	9.75E-01	1.00E+00	6.38E-01	1.00E+00	5.89E-01	1.00E+00	9.86E-01	1.00E+00	6.98E-01	1.00E+00	5.28E-01	1.00E+00	icosanoid biosynthesis	P
GO:0046460	10	2.53E-02	1.00E+00	6.97E-01	1.00E+00	5.45E-02	1.00E+00	8.29E-01	1.00E+00	2.61E-01	1.00E+00	8.31E-01	1.00E+00	1.22E-01	1.00E+00	4.62E-01	1.00E+00	neutral lipid biosynthesis	P
GO:0046463	10	2.53E-02	1.00E+00	6.97E-01	1.00E+00	5.45E-02	1.00E+00	8.29E-01	1.00E+00	2.61E-01	1.00E+00	8.31E-01	1.00E+00	1.22E-01	1.00E+00	4.62E-01	1.00E+00	acylglycerol biosynthesis	P
GO:0046466	21	8.67E-02	1.00E+00	2.21E-01	1.00E+00	5.75E-03	1.88E-01	3.29E-01	1.00E+00	7.77E-01	1.00E+00	4.01E-01	1.00E+00	5.46E-01	1.00E+00	1.99E-01	1.00E+00	membrane lipid catabolism	P
GO:0046467	94	5.27E-02	1.00E+00	4.57E-02	1.00E+00	8.99E-03	4.69E-01	7.56E-03	3.78E-01	2.73E-01	1.00E+00	2.17E-01	1.00E+00	5.70E-01	1.00E+00	7.25E-01	1.00E+00	membrane lipid biosynthesis	P
GO:0046470	13	1.08E-02	9.83E-01	3.25E-02	1.00E+00	7.39E-03	2.83E-01	1.44E-01	1.00E+00	8.81E-02	1.00E+00	7.74E-02	1.00E+00	8.86E-02	1.00E+00	1.47E-01	1.00E+00	phosphatidylcholine metabolism	P
GO:0046474	38	3.69E-02	1.00E+00	4.39E-03	3.82E-01	3.85E-03	1.88E-01	1.26E-02	3.78E-01	2.19E-01	1.00E+00	2.45E-02	1.00E+00	6.01E-01	1.00E+00	5.13E-01	1.00E+00	glycerophospholipid biosynthesis	P
GO:0046483	91	3.78E-04	5.20E-02	1.86E-04	2.80E-02	2.88E-02	1.00E+00	2.09E-02	7.69E-01	1.03E-02	4.14E-01	2.43E-03	1.43E-01	1.73E-03	5.54E-02	1.42E-03	4.40E-02	heterocycle metabolism	P
GO:0046486	36	2.35E-01	1.00E+00	7.67E-01	1.00E+00	7.91E-01	1.00E+00	9.17E-01	1.00E+00	9.21E-01	1.00E+00	9.88E-01	1.00E+00	2.36E-02	5.60E-01	3.19E-01	1.00E+00	glycerolipid metabolism	P
GO:0046488	14	1.50E-02	9.83E-01	2.72E-02	1.00E+00	2.23E-02	1.00E+00	6.49E-02	1.00E+00	3.15E-01	1.00E+00	2.73E-02	1.00E+00	1.99E-02	4.71E-01	5.45E-02	1.00E+00	phosphatidylinositol metabolism	P
GO:0046489	26	5.39E-02	1.00E+00	2.74E-03	1.87E-01	1.01E-02	4.74E-01	8.86E-03	3.78E-01	1.87E-01	1.00E+00	3.41E-02	1.00E+00	5.97E-01	1.00E+00	2.41E-01	1.00E+00	phosphoinositide biosynthesis	P
GO:0046504	11	1.41E-02	9.83E-01	5.67E-01	1.00E+00	3.93E-02	1.00E+00	7.85E-01	1.00E+00	1.99E-01	1.00E+00	8.25E-01	1.00E+00	9.62E-02	1.00E+00	2.84E-01	1.00E+00	glycerol ether biosynthesis	P

GO:0046519	32	2.92E-02	1.00E+00	1.68E-04	2.80E-02	6.85E-02	1.00E+00	1.43E-03	4.40E-02	2.62E-01	1.00E+00	4.20E-02	1.00E+00	1.73E-01	1.00E+00	5.68E-02	1.00E+00	sphingoid metabolism	P
GO:0046520	10	4.36E-01	1.00E+00	1.20E-02	7.51E-01	6.07E-01	1.00E+00	5.95E-02	1.00E+00	3.91E-01	1.00E+00	2.95E-01	1.00E+00	3.89E-01	1.00E+00	1.95E-01	1.00E+00	sphingoid biosynthesis	P
GO:0046527	11	2.43E-01	1.00E+00	7.56E-01	1.00E+00	3.18E-01	1.00E+00	4.37E-01	1.00E+00	1.40E-01	1.00E+00	8.37E-01	1.00E+00	3.48E-01	1.00E+00	7.34E-01	1.00E+00	glucosyltransferase activity	F
GO:0046530	23	5.74E-01	1.00E+00	3.44E-01	1.00E+00	2.48E-01	1.00E+00	1.78E-01	1.00E+00	8.53E-01	1.00E+00	5.30E-01	1.00E+00	5.29E-01	1.00E+00	3.37E-01	1.00E+00	photoreceptor cell differentiation	P
GO:0046545	43	4.96E-01	1.00E+00	2.90E-01	1.00E+00	1.90E-01	1.00E+00	6.61E-01	1.00E+00	8.28E-01	1.00E+00	3.66E-01	1.00E+00	5.62E-01	1.00E+00	9.39E-02	1.00E+00	development of primary female sexual chara	P
GO:0046546	26	9.28E-01	1.00E+00	5.03E-01	1.00E+00	9.88E-01	1.00E+00	3.86E-01	1.00E+00	7.84E-01	1.00E+00	6.92E-01	1.00E+00	9.95E-01	1.00E+00	9.85E-01	1.00E+00	development of primary male sexual charac	P
GO:0046578	12	6.43E-01	1.00E+00	7.18E-01	1.00E+00	9.16E-01	1.00E+00	7.04E-01	1.00E+00	7.74E-01	1.00E+00	7.64E-01	1.00E+00	2.56E-01	1.00E+00	5.60E-01	1.00E+00	regulation of Ras protein signal transductior	P
GO:0046620	14	6.19E-01	1.00E+00	9.68E-01	1.00E+00	8.73E-01	1.00E+00	9.53E-01	1.00E+00	5.62E-01	1.00E+00	9.99E-01	1.00E+00	7.83E-01	1.00E+00	7.30E-01	1.00E+00	regulation of organ size	P
GO:0046631	42	4.15E-01	1.00E+00	9.36E-01	1.00E+00	8.83E-01	1.00E+00	7.50E-01	1.00E+00	5.28E-01	1.00E+00	1.00E+00	1.00E+00	1.31E-01	1.00E+00	6.83E-01	1.00E+00	alpha-beta T cell activation	P
GO:0046632	31	2.09E-01	1.00E+00	8.21E-01	1.00E+00	7.07E-01	1.00E+00	5.63E-01	1.00E+00	3.13E-01	1.00E+00	9.97E-01	1.00E+00	7.67E-02	1.00E+00	4.09E-01	1.00E+00	alpha-beta T cell differentiation	P
GO:0046633	13	6.75E-01	1.00E+00	6.90E-01	1.00E+00	8.78E-01	1.00E+00	7.58E-01	1.00E+00	9.65E-01	1.00E+00	9.74E-01	1.00E+00	2.04E-01	1.00E+00	5.06E-01	1.00E+00	alpha-beta T cell proliferation	P
GO:0046634	13	7.41E-01	1.00E+00	5.41E-01	1.00E+00	9.65E-01	1.00E+00	3.54E-01	1.00E+00	9.99E-01	1.00E+00	9.54E-01	1.00E+00	1.11E-01	1.00E+00	4.95E-01	1.00E+00	regulation of alpha-beta T cell activation	P
GO:0046635	10	4.02E-01	1.00E+00	2.27E-01	1.00E+00	8.02E-01	1.00E+00	1.93E-01	1.00E+00	9.76E-01	1.00E+00	8.23E-01	1.00E+00	5.05E-02	1.00E+00	2.88E-01	1.00E+00	positive regulation of alpha-beta T cell activa	P
GO:0046640	10	5.81E-01	1.00E+00	5.09E-01	1.00E+00	8.15E-01	1.00E+00	5.54E-01	1.00E+00	9.83E-01	1.00E+00	9.18E-01	1.00E+00	1.34E-01	1.00E+00	4.03E-01	1.00E+00	regulation of alpha-beta T cell proliferation	P
GO:0046649	232	3.39E-02	1.00E+00	2.33E-01	1.00E+00	3.09E-01	1.00E+00	7.55E-02	1.00E+00	3.71E-01	1.00E+00	9.85E-01	1.00E+00	2.46E-02	5.60E-01	1.88E-01	1.00E+00	lymphocyte activation	P
GO:0046651	98	1.11E-01	1.00E+00	8.94E-01	1.00E+00	4.03E-01	1.00E+00	2.81E-01	1.00E+00	2.76E-01	1.00E+00	9.97E-01	1.00E+00	7.35E-02	1.00E+00	7.50E-01	1.00E+00	lymphocyte proliferation	P
GO:0046658	13	9.21E-01	1.00E+00	9.79E-01	1.00E+00	7.95E-01	1.00E+00	9.34E-01	1.00E+00	9.58E-01	1.00E+00	1.00E+00	1.00E+00	7.34E-01	1.00E+00	9.99E-01	1.00E+00	anchored to plasma membrane	C
GO:0046660	46	6.21E-01	1.00E+00	4.04E-01	1.00E+00	2.41E-01	1.00E+00	7.56E-01	1.00E+00	8.87E-01	1.00E+00	4.70E-01	1.00E+00	6.71E-01	1.00E+00	1.36E-01	1.00E+00	female sex differentiation	P
GO:0046661	40	9.64E-01	1.00E+00	5.73E-01	1.00E+00	9.61E-01	1.00E+00	5.52E-01	1.00E+00	8.14E-01	1.00E+00	7.59E-01	1.00E+00	9.99E-01	1.00E+00	8.81E-01	1.00E+00	male sex differentiation	P
GO:0046677	31	2.31E-02	1.00E+00	1.04E-01	1.00E+00	5.16E-01	1.00E+00	5.44E-01	1.00E+00	1.21E-01	1.00E+00	5.96E-02	1.00E+00	9.87E-03	2.17E-01	1.13E-01	1.00E+00	response to antibiotic	P
GO:0046777	63	1.58E-01	1.00E+00	9.20E-02	1.00E+00	1.46E-01	1.00E+00	1.96E-01	1.00E+00	2.54E-01	1.00E+00	1.63E-01	1.00E+00	3.32E-01	1.00E+00	6.86E-02	1.00E+00	protein amino acid autophosphorylation	P
GO:0046785	15	3.12E-01	1.00E+00	9.08E-01	1.00E+00	4.54E-01	1.00E+00	8.60E-01	1.00E+00	7.50E-01	1.00E+00	9.29E-01	1.00E+00	1.64E-01	1.00E+00	9.36E-01	1.00E+00	microtubule polymerization	P
GO:0046822	31	1.41E-02	9.83E-01	1.40E-02	1.00E+00	1.93E-01	1.00E+00	5.45E-02	1.00E+00	1.05E-01	1.00E+00	1.32E-01	1.00E+00	1.41E-02	4.39E-01	1.61E-02	9.40E-01	regulation of nucleocytoplasmic transport	P
GO:0046823	10	5.62E-02	1.00E+00	2.72E-01	1.00E+00	1.14E-01	1.00E+00	5.68E-01	1.00E+00	1.20E-01	1.00E+00	1.55E-01	1.00E+00	6.04E-03	2.01E-01	2.20E-01	1.00E+00	negative regulation of nucleocytoplasmic tra	P
GO:0046824	14	2.59E-01	1.00E+00	2.78E-01	1.00E+00	9.69E-01	1.00E+00	5.04E-01	1.00E+00	5.43E-01	1.00E+00	9.21E-01	1.00E+00	7.60E-02	1.00E+00	1.03E-01	1.00E+00	positive regulation of nucleocytoplasmic trar	P
GO:0046834	16	2.04E-02	1.00E+00	7.68E-03	5.59E-01	4.15E-02	1.00E+00	2.61E-02	7.69E-01	4.05E-02	1.00E+00	9.98E-03	4.01E-01	7.80E-02	1.00E+00	3.02E-03	2.16E-01	lipid phosphorylation	P
GO:0046839	14	7.25E-01	1.00E+00	1.45E-01	1.00E+00	5.32E-01	1.00E+00	7.99E-02	1.00E+00	6.08E-01	1.00E+00	7.09E-01	1.00E+00	8.91E-01	1.00E+00	7.70E-02	1.00E+00	phospholipid dephosphorylation	P
GO:0046847	13	8.09E-02	1.00E+00	4.81E-02	1.00E+00	1.74E-01	1.00E+00	3.38E-01	1.00E+00	1.42E-01	1.00E+00	1.41E-01	1.00E+00	2.03E-01	1.00E+00	1.30E-02	9.40E-01	filopodium formation	P
GO:0046849	157	1.00E+00	1.00E+00	9.79E-01	1.00E+00	9.98E-01	1.00E+00	9.32E-01	1.00E+00	9.99E-01	1.00E+00	9.69E-01	1.00E+00	9.98E-01	1.00E+00	8.05E-01	1.00E+00	bone remodeling	P
GO:0046850	44	9.62E-01	1.00E+00	9.97E-01	1.00E+00	9.95E-01	1.00E+00	9.95E-01	1.00E+00	7.03E-01	1.00E+00	9.98E-01	1.00E+00	8.80E-01	1.00E+00	8.34E-01	1.00E+00	regulation of bone remodeling	P
GO:0046851	17	3.81E-01	1.00E+00	8.91E-01	1.00E+00	5.76E-01	1.00E+00	6.42E-01	1.00E+00	2.53E-01	1.00E+00	9.99E-01	1.00E+00	3.56E-01	1.00E+00	6.51E-01	1.00E+00	negative regulation of bone remodeling	P
GO:0046852	18	9.76E-01	1.00E+00	8.71E-01	1.00E+00	9.80E-01	1.00E+00	9.65E-01	1.00E+00	8.16E-01	1.00E+00	7.32E-01	1.00E+00	8.04E-01	1.00E+00	6.96E-01	1.00E+00	positive regulation of bone remodeling	P
GO:0046854	15	1.29E-02	9.83E-01	3.34E-03	2.13E-01	2.35E-02	1.00E+00	1.13E-02	3.78E-01	3.54E-02	1.00E+00	5.36E-03	2.02E-01	7.21E-02	1.00E+00	1.35E-03	4.40E-02	phosphoinositide phosphorylation	P
GO:0046872	3998	8.11E-07	2.00E-03	3.07E-08	2.66E-03	1.64E-04	1.61E-02	6.72E-06	1.77E-03	7.05E-05	1.56E-03	7.00E-05	5.36E-03	2.73E-05	2.00E-03	3.54E-04	2.10E-02	metal ion binding	F
GO:0046873	50	3.32E-01	1.00E+00	1.37E-01	1.00E+00	5.88E-01	1.00E+00	8.38E-02	1.00E+00	1.06E-01	1.00E+00	6.88E-01	1.00E+00	6.66E-01	1.00E+00	1.44E-01	1.00E+00	metal ion transporter activity	F
GO:0046879	69	8.89E-01	1.00E+00	8.39E-01	1.00E+00	9.13E-01	1.00E+00	7.70E-01	1.00E+00	5.36E-01	1.00E+00	8.58E-01	1.00E+00	9.80E-01	1.00E+00	5.41E-01	1.00E+00	hormone secretion	P
GO:0046883	28	8.55E-01	1.00E+00	2.84E-01	1.00E+00	8.01E-01	1.00E+00	3.75E-01	1.00E+00	5.74E-01	1.00E+00	3.11E-01	1.00E+00	9.99E-01	1.00E+00	1.19E-01	1.00E+00	regulation of hormone secretion	P
GO:0046888	14	8.31E-01	1.00E+00	2.82E-01	1.00E+00	8.81E-01	1.00E+00	2.05E-01	1.00E+00	4.92E-01	1.00E+00	3.63E-01	1.00E+00	1.00E+00	1.00E+00	2.39E-01	1.00E+00	negative regulation of hormone secretion	P
GO:0046890	14	4.44E-01	1.00E+00	7.40E-01	1.00E+00	3.91E-01	1.00E+00	7.25E-01	1.00E+00	6.16E-01	1.00E+00	8.68E-01	1.00E+00	5.89E-01	1.00E+00	4.51E-01	1.00E+00	regulation of lipid biosynthesis	P
GO:0046903	341	2.68E-02	1.00E+00	1.66E-01	1.00E+00	1.92E-01	1.00E+00	8.11E-02	1.00E+00	6.96E-02	1.00E+00	4.85E-01	1.00E+00	9.60E-02	1.00E+00	2.04E-01	1.00E+00	secretion	P
GO:0046906	194	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	6.04E-01	1.00E+00	7.12E-01	1.00E+00	tetrapyrrole binding	F
GO:0046907	774	1.76E-15	0.00E+00	3.64E-22	0.00E+00	7.61E-11	0.00E+00	1.60E-17	0.00E+00	7.43E-11	0.00E+00	1.77E-13	0.00E+00	5.90E-05	2.00E-03	4.28E-07	1.94E-03	intracellular transport	P
GO:0046914	2665	4.28E-07	2.00E-03	9.53E-17	0.00E+00	4.36E-07	9.88E-04	7.30E-14	0.00E+00	1.41E-06	7.65E-04	8.93E-12	0.00E+00	3.15E-02	7.53E-01	7.21E-04	3.30E-02	transition metal ion binding	F
GO:0046915	30	3.45E-01	1.00E+00	1.29E-01	1.00E+00	3.94E-01	1.00E+00	5.17E-02	1.00E+00	9.43E-02	1.00E+00	6.34E-01	1.00E+00	8.99E-01	1.00E+00	3.05E-01	1.00E+00	transition metal ion transporter activity	F
GO:0046916	43	1.07E-01	1.00E+00	4.46E-01	1.00E+00	6.39E-02	1.00E+00	1.89E-01	1.00E+00	8.17E-02	1.00E+00	5.00E-01	1.00E+00	6.06E-01	1.00E+00	9.79E-01	1.00E+00	transition metal ion homeostasis	P
GO:0046928	30	9.18E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	8.02E-01	1.00E+00	1.00E+00	1.00E+00	4.10E-01	1.00E+00	8.99E-01	1.00E+00	regulation of neurotransmitter secretion	P
GO:0046930	57	4.80E-10	9.73E-04	2.15E-18	0.00E+00	1.50E-10	0.00E+00	2.84E-15	0.00E+00	5.95E-05	1.56E-03	4.47E-12	0.00E+00	2.19E-02	5.60E-01	1.20E-05	3.91E-03	pore complex	C
GO:0046933	37	6.80E-01	1.00E+00	2.64E-01	1.00E+00	9.98E-01	1.00E+00	7.04E-01	1.00E+00	2.65E-01	1.00E+00	2.57E-01	1.00E+00	8.57E-01	1.00E+00	2.28E-01	1.00E+00	hydrogen-transporting ATP synthase activity	F
GO:0046942	132	7.03E-01	1.00E+00	9.03E-01	1.00E+00	8.17E-01	1.00E+00	9.48E-01	1.00E+00	9.17E-01	1.00E+00	9.45E-01	1.00E+00	4.93E-01	1.00E+00	3.45E-01	1.00E+00	carboxylic acid transport	P
GO:0046943	122	8.76E-01	1.00E+00	9.98E-01	1.00E+00	7.83E-01	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	6.98E-01	1.00E+00	8.05E-01	1.00E+00	carboxylic acid transporter activity	F
GO:0046961	39	7.04E-01	1.00E+00	3.24E-01	1.00E+00	9.98E-01	1.00E+00	7.46E-01	1.00E+00	2.62E-01	1.00E+00	3.32E-01	1.00E+00	8.96E-01	1.00E+00	2.62E-01	1.00E+00	hydrogen-transporting ATPase activity, rotat	F
GO:0046966	20	7.87E-02	1.00E+00	8.30E-02	1.00E+00	3.95E-02	1.00E+00	1.95E-02	7.69E-01	2.30E-01	1.00E+00	5.27E-01	1.00E+00	3.21E-01	1.00E+00	4.11E-01	1.00E+00	thyroid hormone receptor binding	F
GO:0046982	139	8.34E-02	1.00E+00	4.78E-01	1.00E+00	5.62E-01	1.00E+00	3.94E-01	1.00E+00	1.25E-01	1.00E+00	5.54E-01	1.00E+00	7.46E-02	1.00E+00	7.38E-01	1.00E+00	protein heterodimerization activity	F
GO:0046983	370	7.58E-05	7.00E-03	8.22E-02	1.00E+00	1.50E-02	8.10E-01	2.09E-01	1.00E+00	3.53E-03	1.35E-01	1.60E-01	1.00E+00	4.63E-04	1.89E-02	2.24E-01	1.00E+00	protein dimerization activity	F
GO:0047485	32	6.43E-02	1.00E+00	1.34E-01	1.00E+00	3.20E-02	1.00E+00	1.05E-01	1.00E+00	1.62E-01	1.00E+00	3.11E-01	1.00E+00	3.73E-01	1.00E+00	3.32E-01	1.00E+00	protein N-terminus binding	F
GO:0048002	33	9.92E-01	1.00E+00	1.32E-01	1.00E+00	9.45E-01	1.00E+00	6.78E-02	1.00E+00	7.66E-01	1.00E+00	1.43E-01	1.00E+00	1.00E+00	1.00E+00	9.59E-01	1.00E+00	antigen processing and presentation of pept	P
GO:0048008	10	8.85E-01	1.00E+00	4.84E-01	1.00E+00	8.57E-01	1.00E+00	2.23E-01	1.00E+00	5.49E-01	1.00E+00	6.89E-01	1.00E+00	6.10E-01	1.00E+00	7.41E-01	1.00E+00	platelet-derived growth factor receptor signa	P
GO:0048009	16	9.07E-01	1.00E+00	9.96E-01	1.00E+00	9.72E-01	1.00E+00	9.98E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	4.50E-01	1.00E+00	4.85E-01	1.00E+00	insulin-like growth factor receptor signaling p	P
GO:0048010	15	9.16E-01	1.00E+00	9.94E-01	1.00E+00	9.78E-01	1.00E+00	9.97E-01	1.00E+00	8.16E-01	1.00E+00	9.26E-01	1.00E+00	5.99E-01	1.00E+00	9.51E-01	1.00E+00	vascular endothelial growth factor receptor s	P
GO:0048011	12	2.80E-01	1.00E+00	2.74E-02	1.00E+00	9.01E-01	1.00E+00	7.60E-02	1.00E+00	1.63E-01	1.00E+00	6.45E-02	1.00E+00	2.50E-01	1.00E+00	2.98E-02	1.00E+00	nerve growth factor receptor signaling pathv	P
GO:0048015	61	5.49E-01	1.00E+00	2.71E-01	1.00E+00	5.68E-01	1.00E+00	3.54E-01	1.00E+00	3.39E-01	1.00E+00	2.74E-01	1.00E+00	7.41E-01	1.00E+00	2.74E-01	1.00E+00	phosphoinositide-mediated signaling	P
GO:0048029	22	2.14E-01	1.00E+00	8.06E-01	1.00E+00	1.00E+00	1.00E+00	5.49E-01	1.00E+00	9.73E-01	1.00E+00	9.63E-01	1.00E+00	4.21E-03	7.75E-02	5.62E-01	1.00E+00	monosaccharide binding	F
GO:0048037	287	4.38E-03	2.28E-01	1.38E-02	1.00E+00	5.10E-02	1.00E+00	3.51E-01	1.00E+00	8.13E-03	3.18E-01	6.26E-03	3.17E-01	1.27E-02	4.39E-01	9.15E-02	1.00E+00	cofactor binding	F
GO:0048041	15	2.42E-01	1.00E+00	3.41E-01	1.00E+00	1.20E-01	1.00E+00	1.52E-01	1.00E+00	7.47E-01	1.00E+00	5.74E-01	1.00E+00	2.59E-01	1.00E+00	5.64E-01	1.00E+00	focal adhesion formation	P
GO:0048048	10	3.04E-01	1.00E+00	1.44E-01	1.00E+00	3.71E-01	1.00E+00	1.99E-01	1.00E+00	1.93E-01	1.00E+00	1.46E-01	1.00E+00	7.98E-01	1.00E+00	1.13E-01	1.00E+00	embryonic eye morphogenesis	P
GO:0048066	17	9.59E-01	1.00E+00	2.24E-01	1.00E+00	9.99E-01	1.00E+00	3.14E-01	1.00E+00	9.51E-01	1.00E+00	5.89E-01	1.00E+00	8.53E-01	1.00E+00	9.93E-02	1.00E+00	pigmentation during development	P
GO:0048144	19	3.58E-01	1.00E+00	1.89E-01	1.00E+00	5.49E-01	1.00E+00	9.78E-02	1.00E+00	5.26E-01	1.00E+00	1.95E-01	1.00E+00	6.53E-01	1.00E+00	6.75E-01	1.00E+00	fibroblast proliferation	P
GO:0048145	19	3.58E-01	1.00E+00	1.89E-01	1.00E+00	5.49E-01	1.00E+00	9.78E-02	1.00E+00	5.26E-01	1.00E+00	1.95E-01	1.00E+00	6.53E-01	1.00E+00	6.75E-01	1.00E+00	regulation of fibroblast proliferation	P
GO:0048146	14	8.21E-01	1.00E+00	3.24E-01	1.00E+00	7.96E-01	1.00E+00	2.25E-01	1.00E+00	8.07E-01	1.00E+00	2.42E-01	1.00E+00	4.48E-01	1.00E+00	8.19E-01	1.00E+00	positive regulation of fibroblast proliferation	P
GO:0048167	37	2.46E-01	1.00E+00	9.65E-01	1.00E+00	3.79E-01	1.00E+00	8.81E-01	1.00E+00	3.13E-01	1.00E+00	9.99E-01	1.00E+00	2.84E-01	1.00E+00	7.91E-01	1.00E+00	regulation of synaptic plasticity	P
GO:0048168	22	4.12E-01	1.00E+00	9.87E-01	1.00E+00	3.21E-01	1.00E+00	8.94E-01	1.00E+00	3.60E-01	1.00E+00	9.99E-01	1.00E+00	7.58E-01	1.00E+00	9.72E-01	1.00E+00	regulation of neuronal synaptic plasticity	P
GO:0048169	15	5.64E-01	1.00E+00	8.19E-01	1.00E+00	9.69E-01	1.00E+00	5.77E-01	1.00E+00	2.40E-01	1.00E+00	9.44E-01	1.00E+00	5.14E-01	1.00E+00	9.24E-01	1.00E+00	regulation of long-term neuronal synaptic pla	P
GO:0048193	63	8.17E-04	9.30E-02	1.06E-04	2.80E-02	5.03E-03	1.88E-01	6.52E-04	2.70E-02	3.67E-02	1.00E+00	1.89E-03	1.43E-01	8.27E-02	1.00E+00	7.08E-02	1.00E+00	Golgi vesicle transport	P
GO:0048232	213	6.74E-03	3.64E-01	2.62E-03	1.87E-01	1.04E-02	4.74E-01	1.86E-03	4.40E-02	4.44E-02	1.00E+00	2.34E-02	1.00E+00	2.89E-01	1.00E+00	2.58E-01	1.00E+00	male gamete generation	P
GO:0048265	16	9.82E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.04E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	4.42E-01	1.00E+00	9.94E-01	1.00E+00	response to pain	P

GO:0048278	19	4.28E-01	1.00E+00	2.04E-01	1.00E+00	5.37E-01	1.00E+00	3.35E-01	1.00E+00	5.41E-01	1.00E+00	4.21E-01	1.00E+00	2.29E-01	1.00E+00	6.36E-02	1.00E+00	vesicle docking	P
GO:0048286	16	8.44E-01	1.00E+00	7.10E-01	1.00E+00	8.12E-01	1.00E+00	9.55E-01	1.00E+00	8.85E-01	1.00E+00	7.62E-01	1.00E+00	7.31E-01	1.00E+00	2.74E-01	1.00E+00	alveolus development	P
GO:0048305	11	9.48E-02	1.00E+00	5.63E-01	1.00E+00	2.31E-01	1.00E+00	7.10E-01	1.00E+00	5.80E-01	1.00E+00	5.26E-01	1.00E+00	5.71E-02	1.00E+00	2.87E-01	1.00E+00	immunoglobulin secretion	P
GO:0048306	17	5.44E-01	1.00E+00	6.30E-01	1.00E+00	4.06E-01	1.00E+00	8.02E-01	1.00E+00	3.78E-01	1.00E+00	7.14E-01	1.00E+00	6.89E-01	1.00E+00	2.04E-01	1.00E+00	calcium-dependent protein binding	F
GO:0048332	35	7.06E-01	1.00E+00	9.74E-02	1.00E+00	7.64E-01	1.00E+00	3.25E-01	1.00E+00	6.23E-01	1.00E+00	2.05E-01	1.00E+00	6.04E-01	1.00E+00	2.87E-02	1.00E+00	mesoderm morphogenesis	P
GO:0048339	11	1.20E-01	1.00E+00	4.22E-02	1.00E+00	4.13E-01	1.00E+00	7.75E-02	1.00E+00	2.33E-01	1.00E+00	1.60E-01	1.00E+00	6.37E-01	1.00E+00	7.48E-02	1.00E+00	paraxial mesoderm development	P
GO:0048384	10	9.89E-01	1.00E+00	9.95E-01	1.00E+00	8.76E-01	1.00E+00	9.97E-01	1.00E+00	9.89E-01	1.00E+00	9.43E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	retinoic acid receptor signaling pathway	P
GO:0048468	623	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.45E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	cell development	P
GO:0048469	87	9.09E-01	1.00E+00	9.99E-01	1.00E+00	7.25E-01	1.00E+00	9.83E-01	1.00E+00	9.77E-01	1.00E+00	9.99E-01	1.00E+00	6.46E-01	1.00E+00	9.97E-01	1.00E+00	cell maturation	P
GO:0048471	82	6.42E-01	1.00E+00	2.01E-01	1.00E+00	5.63E-01	1.00E+00	5.61E-01	1.00E+00	4.89E-01	1.00E+00	2.45E-01	1.00E+00	9.50E-01	1.00E+00	9.98E-02	1.00E+00	perinuclear region	C
GO:0048475	61	8.77E-07	2.00E-03	2.14E-07	2.66E-03	1.47E-03	7.90E-02	4.34E-07	1.00E-03	3.60E-05	1.56E-03	1.24E-04	1.36E-02	8.63E-04	2.40E-02	1.94E-03	6.30E-02	coated membrane	C
GO:0048477	28	4.32E-01	1.00E+00	1.42E-01	1.00E+00	4.55E-01	1.00E+00	2.92E-01	1.00E+00	4.35E-01	1.00E+00	3.26E-01	1.00E+00	5.72E-01	1.00E+00	5.92E-02	1.00E+00	oogenesis	P
GO:0048483	15	9.90E-01	1.00E+00	1.00E+00	1.00E+00	8.84E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.99E-01	1.00E+00	autonomic nervous system development	P
GO:0048489	27	2.93E-01	1.00E+00	8.22E-01	1.00E+00	2.70E-01	1.00E+00	5.79E-01	1.00E+00	5.36E-01	1.00E+00	9.99E-01	1.00E+00	2.78E-01	1.00E+00	6.71E-01	1.00E+00	synaptic vesicle transport	P
GO:0048500	15	9.08E-02	1.00E+00	5.44E-04	7.30E-02	1.84E-01	1.00E+00	1.69E-03	4.40E-02	8.41E-02	1.00E+00	1.32E-03	5.10E-02	3.95E-01	1.00E+00	2.33E-01	1.00E+00	signal recognition particle	C
GO:0048511	83	8.26E-01	1.00E+00	8.01E-01	1.00E+00	8.54E-01	1.00E+00	9.81E-01	1.00E+00	9.86E-01	1.00E+00	7.97E-01	1.00E+00	4.04E-01	1.00E+00	2.45E-01	1.00E+00	rhythmic process	P
GO:0048513	1403	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	organ development	P
GO:0048514	205	9.99E-01	1.00E+00	9.93E-01	1.00E+00	1.00E+00	1.00E+00	7.17E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.63E-01	1.00E+00	9.90E-01	1.00E+00	blood vessel morphogenesis	P
GO:0048515	43	2.31E-01	1.00E+00	8.22E-03	5.59E-01	6.84E-02	1.00E+00	4.11E-02	1.00E+00	7.99E-01	1.00E+00	1.59E-02	1.00E+00	7.43E-01	1.00E+00	2.16E-01	1.00E+00	spermatid differentiation	P
GO:0048518	1341	7.21E-01	1.00E+00	9.60E-01	1.00E+00	8.90E-01	1.00E+00	5.68E-01	1.00E+00	9.14E-01	1.00E+00	1.00E+00	1.00E+00	3.26E-01	1.00E+00	4.74E-01	1.00E+00	positive regulation of biological process	P
GO:0048519	1208	2.65E-01	1.00E+00	4.84E-01	1.00E+00	6.57E-01	1.00E+00	7.13E-02	1.00E+00	5.93E-01	1.00E+00	9.53E-01	1.00E+00	7.35E-02	1.00E+00	7.51E-01	1.00E+00	negative regulation of biological process	P
GO:0048522	1093	6.61E-01	1.00E+00	9.44E-01	1.00E+00	8.64E-01	1.00E+00	5.05E-01	1.00E+00	9.07E-01	1.00E+00	9.99E-01	1.00E+00	3.08E-01	1.00E+00	7.38E-01	1.00E+00	positive regulation of cellular process	P
GO:0048523	1095	3.20E-01	1.00E+00	4.54E-01	1.00E+00	5.56E-01	1.00E+00	6.27E-02	1.00E+00	6.31E-01	1.00E+00	8.97E-01	1.00E+00	1.36E-01	1.00E+00	8.63E-01	1.00E+00	negative regulation of cellular process	P
GO:0048534	289	8.94E-01	1.00E+00	7.22E-01	1.00E+00	8.98E-01	1.00E+00	2.76E-01	1.00E+00	7.68E-01	1.00E+00	9.85E-01	1.00E+00	9.79E-01	1.00E+00	9.69E-01	1.00E+00	hemopoietic or lymphoid organ developmen	P
GO:0048535	19	8.19E-01	1.00E+00	1.00E+00	1.00E+00	8.37E-01	1.00E+00	9.71E-01	1.00E+00	7.56E-01	1.00E+00	1.00E+00	1.00E+00	8.68E-01	1.00E+00	9.73E-01	1.00E+00	lymph node development	P
GO:0048536	16	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	9.99E-01	1.00E+00	9.13E-01	1.00E+00	9.84E-01	1.00E+00	spleen development	P
GO:0048538	18	4.49E-01	1.00E+00	7.28E-01	1.00E+00	7.36E-01	1.00E+00	7.93E-01	1.00E+00	3.59E-01	1.00E+00	7.34E-01	1.00E+00	4.34E-01	1.00E+00	3.61E-01	1.00E+00	thymus development	P
GO:0048545	65	9.93E-01	1.00E+00	9.83E-01	1.00E+00	8.36E-01	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	7.46E-01	1.00E+00	9.91E-01	1.00E+00	9.29E-01	1.00E+00	response to steroid hormone stimulus	P
GO:0048546	18	9.35E-01	1.00E+00	8.93E-01	1.00E+00	9.92E-01	1.00E+00	9.36E-01	1.00E+00	5.80E-01	1.00E+00	9.86E-01	1.00E+00	8.63E-01	1.00E+00	3.30E-01	1.00E+00	digestive tract morphogenesis	P
GO:0048547	16	8.65E-01	1.00E+00	7.91E-01	1.00E+00	9.70E-01	1.00E+00	8.54E-01	1.00E+00	5.34E-01	1.00E+00	9.62E-01	1.00E+00	7.73E-01	1.00E+00	2.41E-01	1.00E+00	gut morphogenesis	P
GO:0048557	10	5.40E-01	1.00E+00	6.07E-01	1.00E+00	7.93E-01	1.00E+00	5.56E-01	1.00E+00	1.71E-01	1.00E+00	8.42E-01	1.00E+00	9.19E-01	1.00E+00	3.31E-01	1.00E+00	embryonic digestive tract morphogenesis	P
GO:0048562	24	5.98E-01	1.00E+00	3.70E-01	1.00E+00	7.70E-01	1.00E+00	3.63E-01	1.00E+00	2.07E-01	1.00E+00	4.91E-01	1.00E+00	9.43E-01	1.00E+00	2.12E-01	1.00E+00	embryonic organ morphogenesis	P
GO:0048565	26	9.71E-01	1.00E+00	8.65E-01	1.00E+00	1.00E+00	1.00E+00	6.28E-01	1.00E+00	9.52E-01	1.00E+00	1.00E+00	1.00E+00	4.13E-01	1.00E+00	5.07E-01	1.00E+00	gut development	P
GO:0048566	17	9.07E-01	1.00E+00	9.08E-01	1.00E+00	9.94E-01	1.00E+00	9.59E-01	1.00E+00	6.48E-01	1.00E+00	9.98E-01	1.00E+00	7.16E-01	1.00E+00	2.26E-01	1.00E+00	embryonic gut development	P
GO:0048567	10	7.71E-01	1.00E+00	7.01E-01	1.00E+00	9.93E-01	1.00E+00	9.24E-01	1.00E+00	4.06E-01	1.00E+00	9.36E-01	1.00E+00	3.94E-01	1.00E+00	1.32E-01	1.00E+00	ectodermal gut morphogenesis	P
GO:0048568	46	5.56E-01	1.00E+00	6.13E-01	1.00E+00	6.53E-01	1.00E+00	6.89E-01	1.00E+00	3.62E-01	1.00E+00	7.34E-01	1.00E+00	6.86E-01	1.00E+00	1.78E-01	1.00E+00	embryonic organ development	P
GO:0048583	16	8.71E-01	1.00E+00	9.06E-01	1.00E+00	9.96E-01	1.00E+00	6.13E-01	1.00E+00	9.99E-01	1.00E+00	9.88E-01	1.00E+00	3.32E-01	1.00E+00	7.34E-01	1.00E+00	regulation of response to stimulus	P
GO:0048584	11	9.10E-01	1.00E+00	9.27E-01	1.00E+00	9.90E-01	1.00E+00	9.64E-01	1.00E+00	9.62E-01	1.00E+00	9.57E-01	1.00E+00	5.59E-01	1.00E+00	8.79E-01	1.00E+00	positive regulation of response to stimulus	P
GO:0048589	51	2.94E-01	1.00E+00	3.07E-01	1.00E+00	6.51E-01	1.00E+00	4.28E-01	1.00E+00	5.32E-01	1.00E+00	6.08E-01	1.00E+00	1.39E-01	1.00E+00	5.26E-02	1.00E+00	developmental growth	P
GO:0048592	43	3.96E-01	1.00E+00	3.35E-01	1.00E+00	1.31E-01	1.00E+00	2.20E-01	1.00E+00	5.26E-01	1.00E+00	3.60E-01	1.00E+00	8.54E-01	1.00E+00	5.55E-01	1.00E+00	eye morphogenesis	P
GO:0048593	18	6.70E-02	1.00E+00	2.18E-01	1.00E+00	5.01E-02	1.00E+00	2.11E-01	1.00E+00	1.34E-01	1.00E+00	2.98E-01	1.00E+00	2.38E-01	1.00E+00	1.70E-01	1.00E+00	eye morphogenesis (sensu Vertebrata)	P
GO:0048598	239	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic morphogenesis	P
GO:0048599	12	2.48E-01	1.00E+00	1.38E-01	1.00E+00	1.30E-01	1.00E+00	2.43E-01	1.00E+00	5.81E-01	1.00E+00	2.86E-01	1.00E+00	3.29E-01	1.00E+00	7.35E-02	1.00E+00	oocyte development	P
GO:0048609	111	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.87E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.87E-01	1.00E+00	5.74E-01	1.00E+00	reproductive organismal physiological proce	P
GO:0048627	26	8.03E-01	1.00E+00	8.45E-01	1.00E+00	5.16E-01	1.00E+00	4.68E-01	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	4.87E-01	1.00E+00	9.62E-01	1.00E+00	myoblast development	P
GO:0048628	25	7.35E-01	1.00E+00	7.97E-01	1.00E+00	4.77E-01	1.00E+00	4.28E-01	1.00E+00	1.00E+00	1.00E+00	8.94E-01	1.00E+00	4.30E-01	1.00E+00	9.41E-01	1.00E+00	myoblast maturation	P
GO:0048637	78	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.40E-01	1.00E+00	9.22E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.73E-01	1.00E+00	1.00E+00	1.00E+00	skeletal muscle development	P
GO:0048644	19	8.57E-01	1.00E+00	1.00E+00	1.00E+00	3.71E-01	1.00E+00	9.88E-01	1.00E+00	9.17E-01	1.00E+00	1.00E+00	1.00E+00	8.25E-01	1.00E+00	1.00E+00	1.00E+00	muscle morphogenesis	P
GO:0048646	80	9.37E-01	1.00E+00	5.38E-01	1.00E+00	9.30E-01	1.00E+00	4.32E-01	1.00E+00	8.48E-01	1.00E+00	8.49E-01	1.00E+00	7.85E-01	1.00E+00	2.76E-01	1.00E+00	anatomical structure formation	P
GO:0048659	30	8.81E-01	1.00E+00	9.00E-01	1.00E+00	9.70E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	5.19E-01	1.00E+00	3.78E-01	1.00E+00	6.96E-01	1.00E+00	smooth muscle cell proliferation	P
GO:0048660	28	8.72E-01	1.00E+00	9.38E-01	1.00E+00	9.47E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	5.11E-01	1.00E+00	3.79E-01	1.00E+00	8.58E-01	1.00E+00	regulation of smooth muscle cell proliferatio	P
GO:0048661	19	9.26E-01	1.00E+00	8.25E-01	1.00E+00	9.25E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	3.34E-01	1.00E+00	6.50E-01	1.00E+00	8.18E-01	1.00E+00	positive regulation of smooth muscle cell pr	P
GO:0048663	33	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	neuron fate commitment	P
GO:0048665	13	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.57E-01	1.00E+00	neuron fate specification	P
GO:0048666	259	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.61E-01	1.00E+00	1.00E+00	1.00E+00	neuron development	P
GO:0048667	189	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.18E-01	1.00E+00	9.97E-01	1.00E+00	neuron morphogenesis during differentiatior	P
GO:0048675	24	8.06E-01	1.00E+00	8.19E-01	1.00E+00	9.35E-01	1.00E+00	7.49E-01	1.00E+00	8.83E-01	1.00E+00	8.88E-01	1.00E+00	3.73E-01	1.00E+00	7.31E-01	1.00E+00	axon extension	P
GO:0048699	390	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	generation of neurons	P
GO:0048701	13	9.83E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.45E-01	1.00E+00	9.95E-01	1.00E+00	7.21E-01	1.00E+00	4.91E-01	1.00E+00	embryonic cranial skeleton morphogenesis	P
GO:0048704	50	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic skeletal morphogenesis	P
GO:0048705	63	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	skeletal morphogenesis	P
GO:0048706	66	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	embryonic skeletal development	P
GO:0048709	20	8.72E-01	1.00E+00	8.98E-01	1.00E+00	4.74E-01	1.00E+00	9.05E-01	1.00E+00	8.49E-01	1.00E+00	8.30E-01	1.00E+00	9.98E-01	1.00E+00	9.07E-01	1.00E+00	oligodendrocyte differentiation	P
GO:0048729	108	9.95E-01	1.00E+00	9.77E-01	1.00E+00	9.03E-01	1.00E+00	9.99E-01	1.00E+00	9.13E-01	1.00E+00	9.76E-01	1.00E+00	9.91E-01	1.00E+00	4.22E-01	1.00E+00	tissue morphogenesis	P
GO:0048730	73	9.97E-01	1.00E+00	1.00E+00	1.00E+00	8.62E-01	1.00E+00	1.00E+00	1.00E+00	9.10E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	7.96E-01	1.00E+00	epidermis morphogenesis	P
GO:0048731	798	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	system development	P
GO:0048732	85	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	6.08E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	gland development	P
GO:0048736	91	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	appendage development	P
GO:0048738	14	7.07E-01	1.00E+00	6.01E-01	1.00E+00	5.80E-01	1.00E+00	5.20E-01	1.00E+00	7.03E-01	1.00E+00	6.78E-01	1.00E+00	9.25E-01	1.00E+00	6.39E-01	1.00E+00	cardiac muscle development	P
GO:0048741	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	9.08E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	skeletal muscle fiber development	P
GO:0048747	76	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.21E-01	1.00E+00	9.08E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.68E-01	1.00E+00	1.00E+00	1.00E+00	muscle fiber development	P
GO:0048754	66	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.92E-01	1.00E+00	branching morphogenesis of a tube	P
GO:0048762	42	9.89E-01	1.00E+00	6.63E-01	1.00E+00	9.88E-01	1.00E+00	2.15E-01	1.00E+00	9.86E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	1.00E+00	1.00E+00	mesenchymal cell differentiation	P
GO:0048770	75	2.03E-03	1.02E-01	3.88E-05	2.80E-02	2.79E-02	1.00E+00	7.61E-03	3.78E-01	2.56E-02	1.00E+00	1.62E-04	1.36E-02	8.75E-02	1.00E+00	3.07E-03	2.16E-01	pigment granule	C
GO:0048771	176	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.75E-01	1.00E+00	9.79E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	9.95E-01	1.00E+00	8.54E-01	1.00E+00	tissue remodeling	P

GO:0048806	18	1.00E+00	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.81E-01	1.00E+00	9.96E-01	1.00E+00	1.00E+00	1.00E+00	7.14E-01	1.00E+00	genitalia development	P
GO:0048812	188	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.44E-01	1.00E+00	9.98E-01	1.00E+00	neurite morphogenesis	P
GO:0048813	15	1.81E-01	1.00E+00	6.75E-01	1.00E+00	1.77E-01	1.00E+00	6.98E-01	1.00E+00	3.12E-01	1.00E+00	8.80E-01	1.00E+00	2.30E-01	1.00E+00	2.14E-01	1.00E+00	dendrite morphogenesis	P
GO:0048820	15	2.44E-01	1.00E+00	1.37E-01	1.00E+00	1.92E-01	1.00E+00	1.57E-01	1.00E+00	4.59E-01	1.00E+00	5.51E-01	1.00E+00	2.40E-01	1.00E+00	1.77E-01	1.00E+00	hair follicle maturation	P
GO:0048821	15	5.21E-01	1.00E+00	5.72E-01	1.00E+00	4.87E-01	1.00E+00	6.42E-01	1.00E+00	3.82E-01	1.00E+00	6.96E-01	1.00E+00	5.87E-01	1.00E+00	5.99E-01	1.00E+00	erythrocyte development	P
GO:0048839	59	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	inner ear development	P
GO:0048854	13	2.74E-01	1.00E+00	1.23E-01	1.00E+00	1.66E-01	1.00E+00	1.45E-01	1.00E+00	4.16E-01	1.00E+00	2.14E-02	1.00E+00	4.80E-01	1.00E+00	3.70E-01	1.00E+00	brain morphogenesis	P
GO:0048856	2071	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.29E-01	1.00E+00	9.99E-01	1.00E+00	anatomical structure development	P
GO:0048858	188	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.44E-01	1.00E+00	9.98E-01	1.00E+00	cell projection morphogenesis	P
GO:0050136	30	2.95E-02	1.00E+00	1.87E-03	1.62E-01	7.40E-02	1.00E+00	2.35E-03	6.52E-02	4.13E-01	1.00E+00	2.43E-02	1.00E+00	6.35E-02	1.00E+00	6.78E-02	1.00E+00	NADH dehydrogenase (quinone) activity	F
GO:0050381	36	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.91E-01	1.00E+00	1.00E+00	1.00E+00	3.56E-01	1.00E+00	7.84E-01	1.00E+00	unspecific monooxygenase activity	F
GO:0050432	11	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.66E-01	1.00E+00	1.00E+00	1.00E+00	catecholamine secretion	P
GO:0050435	10	3.84E-02	1.00E+00	1.16E-01	1.00E+00	8.09E-02	1.00E+00	5.42E-02	1.00E+00	4.18E-01	1.00E+00	2.87E-01	1.00E+00	2.32E-01	1.00E+00	1.04E-01	1.00E+00	beta-amyloid metabolism	P
GO:0050650	11	8.20E-01	1.00E+00	8.31E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	2.73E-01	1.00E+00	9.99E-01	1.00E+00	8.88E-01	1.00E+00	2.52E-01	1.00E+00	chondroitin sulfate proteoglycan biosynthesi	P
GO:0050654	11	8.20E-01	1.00E+00	8.31E-01	1.00E+00	1.00E+00	1.00E+00	9.83E-01	1.00E+00	2.73E-01	1.00E+00	9.99E-01	1.00E+00	8.88E-01	1.00E+00	2.52E-01	1.00E+00	chondroitin sulfate proteoglycan metabolism	P
GO:0050657	58	1.57E-05	5.00E-03	7.46E-08	2.66E-03	9.86E-06	1.69E-03	2.02E-07	9.57E-04	1.39E-03	4.80E-02	6.13E-06	2.00E-03	1.51E-01	1.00E+00	2.67E-01	1.00E+00	nucleic acid transport	P
GO:0050658	58	1.57E-05	5.00E-03	7.46E-08	2.66E-03	9.86E-06	1.69E-03	2.02E-07	9.57E-04	1.39E-03	4.80E-02	6.13E-06	2.00E-03	1.51E-01	1.00E+00	2.67E-01	1.00E+00	RNA transport	P
GO:0050660	83	3.33E-03	1.86E-01	1.61E-01	1.00E+00	8.08E-02	1.00E+00	3.67E-01	1.00E+00	2.70E-02	1.00E+00	2.33E-01	1.00E+00	2.78E-03	5.54E-02	5.54E-02	1.00E+00	FAD binding	F
GO:0050661	30	1.27E-02	9.83E-01	8.26E-01	1.00E+00	5.47E-01	1.00E+00	9.76E-01	1.00E+00	1.18E-01	1.00E+00	9.51E-01	1.00E+00	2.98E-03	5.54E-02	1.95E-01	1.00E+00	NADP binding	F
GO:0050662	210	1.38E-02	9.83E-01	6.35E-02	1.00E+00	1.40E-01	1.00E+00	4.73E-01	1.00E+00	5.04E-02	1.00E+00	4.40E-02	1.00E+00	1.22E-02	4.39E-01	1.78E-01	1.00E+00	coenzyme binding	F
GO:0050663	21	8.75E-01	1.00E+00	9.35E-01	1.00E+00	8.31E-01	1.00E+00	9.84E-01	1.00E+00	9.23E-01	1.00E+00	8.88E-01	1.00E+00	8.68E-01	1.00E+00	6.59E-01	1.00E+00	cytokine secretion	P
GO:0050670	68	1.66E-01	1.00E+00	9.38E-01	1.00E+00	7.62E-01	1.00E+00	4.22E-01	1.00E+00	1.34E-01	1.00E+00	9.98E-01	1.00E+00	5.22E-02	1.00E+00	7.62E-01	1.00E+00	regulation of lymphocyte proliferation	P
GO:0050671	46	6.80E-01	1.00E+00	6.87E-01	1.00E+00	9.45E-01	1.00E+00	3.25E-01	1.00E+00	6.22E-01	1.00E+00	9.76E-01	1.00E+00	1.90E-01	1.00E+00	3.10E-01	1.00E+00	positive regulation of lymphocyte proliferatic	P
GO:0050672	25	2.42E-01	1.00E+00	9.86E-01	1.00E+00	6.99E-01	1.00E+00	6.21E-01	1.00E+00	2.69E-01	1.00E+00	1.00E+00	1.00E+00	1.23E-01	1.00E+00	9.94E-01	1.00E+00	negative regulation of lymphocyte proliferati	P
GO:0050673	52	9.73E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	1.00E+00	1.00E+00	8.96E-01	1.00E+00	1.00E+00	1.00E+00	6.68E-01	1.00E+00	9.95E-01	1.00E+00	epithelial cell proliferation	P
GO:0050678	43	9.92E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.32E-01	1.00E+00	1.00E+00	1.00E+00	7.51E-01	1.00E+00	9.99E-01	1.00E+00	regulation of epithelial cell proliferation	P
GO:0050679	22	9.64E-01	1.00E+00	1.00E+00	1.00E+00	9.89E-01	1.00E+00	9.97E-01	1.00E+00	8.64E-01	1.00E+00	1.00E+00	1.00E+00	9.41E-01	1.00E+00	9.90E-01	1.00E+00	positive regulation of epithelial cell proliferat	P
GO:0050680	18	8.66E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.85E-01	1.00E+00	9.12E-01	1.00E+00	1.00E+00	1.00E+00	3.28E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of epithelial cell prolifera	P
GO:0050707	18	8.21E-01	1.00E+00	9.12E-01	1.00E+00	7.79E-01	1.00E+00	9.88E-01	1.00E+00	9.16E-01	1.00E+00	8.48E-01	1.00E+00	7.70E-01	1.00E+00	5.67E-01	1.00E+00	regulation of cytokine secretion	P
GO:0050708	32	6.88E-01	1.00E+00	7.63E-01	1.00E+00	9.18E-01	1.00E+00	9.92E-01	1.00E+00	6.14E-01	1.00E+00	7.11E-01	1.00E+00	4.11E-01	1.00E+00	2.03E-01	1.00E+00	regulation of protein secretion	P
GO:0050709	10	5.21E-01	1.00E+00	7.85E-01	1.00E+00	6.68E-01	1.00E+00	7.92E-01	1.00E+00	2.26E-01	1.00E+00	5.56E-01	1.00E+00	9.56E-01	1.00E+00	8.42E-01	1.00E+00	negative regulation of protein secretion	P
GO:0050714	16	9.45E-01	1.00E+00	9.26E-01	1.00E+00	9.74E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.56E-01	1.00E+00	5.34E-01	1.00E+00	1.82E-01	1.00E+00	positive regulation of protein secretion	P
GO:0050715	12	9.63E-01	1.00E+00	9.70E-01	1.00E+00	9.87E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.17E-01	1.00E+00	6.73E-01	1.00E+00	5.18E-01	1.00E+00	positive regulation of cytokine secretion	P
GO:0050727	38	9.58E-01	1.00E+00	8.25E-01	1.00E+00	1.00E+00	1.00E+00	8.19E-01	1.00E+00	9.60E-01	1.00E+00	8.60E-01	1.00E+00	4.13E-01	1.00E+00	4.66E-01	1.00E+00	regulation of inflammatory response	P
GO:0050728	15	7.88E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	9.82E-01	1.00E+00	9.98E-01	1.00E+00	2.51E-01	1.00E+00	6.07E-01	1.00E+00	negative regulation of inflammatory respons	P
GO:0050729	17	8.57E-01	1.00E+00	6.23E-01	1.00E+00	8.35E-01	1.00E+00	7.26E-01	1.00E+00	8.24E-01	1.00E+00	9.74E-01	1.00E+00	6.02E-01	1.00E+00	2.23E-01	1.00E+00	positive regulation of inflammatory response	P
GO:0050730	47	9.94E-01	1.00E+00	9.64E-01	1.00E+00	1.00E+00	1.00E+00	8.23E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	3.62E-01	1.00E+00	6.27E-01	1.00E+00	regulation of peptidyl-tyrosine phosphorylati	P
GO:0050731	29	8.47E-01	1.00E+00	7.03E-01	1.00E+00	9.20E-01	1.00E+00	5.76E-01	1.00E+00	1.00E+00	1.00E+00	9.69E-01	1.00E+00	2.46E-01	1.00E+00	2.71E-01	1.00E+00	positive regulation of peptidyl-tyrosine phos	P
GO:0050750	12	9.95E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	9.76E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	6.31E-01	1.00E+00	1.00E+00	1.00E+00	low-density lipoprotein receptor binding	F
GO:0050764	21	6.40E-01	1.00E+00	9.76E-01	1.00E+00	8.40E-01	1.00E+00	9.61E-01	1.00E+00	5.95E-01	1.00E+00	9.84E-01	1.00E+00	3.66E-01	1.00E+00	9.44E-01	1.00E+00	regulation of phagocytosis	P
GO:0050766	19	9.63E-01	1.00E+00	9.97E-01	1.00E+00	9.84E-01	1.00E+00	9.87E-01	1.00E+00	9.20E-01	1.00E+00	9.97E-01	1.00E+00	5.82E-01	1.00E+00	9.86E-01	1.00E+00	positive regulation of phagocytosis	P
GO:0050767	61	2.32E-01	1.00E+00	8.45E-01	1.00E+00	3.28E-01	1.00E+00	9.54E-01	1.00E+00	7.89E-01	1.00E+00	8.39E-01	1.00E+00	1.33E-01	1.00E+00	4.57E-01	1.00E+00	regulation of neurogenesis	P
GO:0050768	26	1.29E-01	1.00E+00	2.55E-01	1.00E+00	2.74E-01	1.00E+00	2.26E-01	1.00E+00	6.35E-01	1.00E+00	5.66E-01	1.00E+00	1.19E-01	1.00E+00	2.90E-01	1.00E+00	negative regulation of neurogenesis	P
GO:0050769	23	5.13E-01	1.00E+00	7.56E-01	1.00E+00	4.66E-01	1.00E+00	9.49E-01	1.00E+00	7.36E-01	1.00E+00	7.05E-01	1.00E+00	4.10E-01	1.00E+00	3.06E-01	1.00E+00	positive regulation of neurogenesis	P
GO:0050770	34	3.74E-01	1.00E+00	9.60E-01	1.00E+00	7.60E-01	1.00E+00	9.75E-01	1.00E+00	8.64E-01	1.00E+00	9.13E-01	1.00E+00	9.20E-02	1.00E+00	6.54E-01	1.00E+00	regulation of axonogenesis	P
GO:0050771	13	1.01E-01	1.00E+00	2.53E-01	1.00E+00	3.42E-01	1.00E+00	1.59E-01	1.00E+00	8.98E-01	1.00E+00	4.11E-01	1.00E+00	1.16E-01	1.00E+00	2.41E-01	1.00E+00	negative regulation of axonogenesis	P
GO:0050772	14	8.67E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	8.92E-01	1.00E+00	1.00E+00	1.00E+00	4.76E-01	1.00E+00	7.90E-01	1.00E+00	positive regulation of axonogenesis	P
GO:0050776	124	3.78E-01	1.00E+00	9.35E-01	1.00E+00	6.78E-01	1.00E+00	9.41E-01	1.00E+00	9.55E-01	1.00E+00	9.70E-01	1.00E+00	1.95E-02	4.71E-01	3.90E-01	1.00E+00	regulation of immune response	P
GO:0050777	12	5.14E-02	1.00E+00	7.66E-01	1.00E+00	6.55E-01	1.00E+00	6.66E-01	1.00E+00	9.58E-02	1.00E+00	9.90E-01	1.00E+00	5.18E-02	1.00E+00	5.61E-01	1.00E+00	negative regulation of immune response	P
GO:0050778	104	7.04E-01	1.00E+00	9.11E-01	1.00E+00	6.62E-01	1.00E+00	8.13E-01	1.00E+00	9.92E-01	1.00E+00	9.59E-01	1.00E+00	1.19E-01	1.00E+00	6.51E-01	1.00E+00	positive regulation of immune response	P
GO:0050789	4440	6.20E-02	1.00E+00	3.64E-06	2.86E-03	1.46E-01	1.00E+00	5.89E-09	0.00E+00	9.59E-02	1.00E+00	5.79E-03	2.02E-01	3.47E-01	1.00E+00	1.15E-01	1.00E+00	regulation of biological process	P
GO:0050790	404	7.77E-04	9.30E-02	1.49E-02	1.00E+00	3.00E-02	1.00E+00	9.21E-02	1.00E+00	1.84E-03	5.40E-02	1.52E-01	1.00E+00	8.11E-03	2.17E-01	1.59E-03	4.50E-02	regulation of catalytic activity	P
GO:0050791	3850	3.26E-02	1.00E+00	4.57E-07	2.66E-03	6.30E-02	1.00E+00	1.47E-10	0.00E+00	5.09E-02	1.00E+00	1.54E-03	5.10E-02	3.91E-01	1.00E+00	2.05E-01	1.00E+00	regulation of physiological process	P
GO:0050792	10	9.53E-01	1.00E+00	9.95E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	6.89E-01	1.00E+00	9.04E-01	1.00E+00	8.05E-01	1.00E+00	9.40E-01	1.00E+00	regulation of viral life cycle	P
GO:0050793	284	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.20E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	9.88E-01	1.00E+00	regulation of development	P
GO:0050794	3957	1.09E-01	1.00E+00	2.52E-06	2.86E-03	1.21E-01	1.00E+00	7.97E-10	0.00E+00	1.55E-01	1.00E+00	1.97E-03	1.43E-01	5.79E-01	1.00E+00	3.79E-01	1.00E+00	regulation of cellular process	P
GO:0050796	16	3.95E-01	1.00E+00	1.07E-01	1.00E+00	4.96E-01	1.00E+00	3.52E-01	1.00E+00	2.20E-01	1.00E+00	1.04E-01	1.00E+00	8.76E-01	1.00E+00	3.26E-02	1.00E+00	regulation of insulin secretion	P
GO:0050798	16	5.22E-01	1.00E+00	1.00E-01	1.00E+00	1.71E-01	1.00E+00	1.82E-01	1.00E+00	6.59E-01	1.00E+00	4.15E-01	1.00E+00	5.11E-01	1.00E+00	6.63E-02	1.00E+00	activated T cell proliferation	P
GO:0050801	178	2.72E-01	1.00E+00	9.92E-01	1.00E+00	5.49E-01	1.00E+00	8.01E-01	1.00E+00	2.67E-01	1.00E+00	1.00E+00	1.00E+00	2.17E-01	1.00E+00	9.54E-01	1.00E+00	ion homeostasis	P
GO:0050803	72	7.94E-01	1.00E+00	9.94E-01	1.00E+00	9.12E-01	1.00E+00	9.69E-01	1.00E+00	8.71E-01	1.00E+00	1.00E+00	1.00E+00	3.81E-01	1.00E+00	7.36E-01	1.00E+00	regulation of synapse structure and function	P
GO:0050804	68	9.04E-01	1.00E+00	9.98E-01	1.00E+00	9.02E-01	1.00E+00	9.76E-01	1.00E+00	8.16E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	8.90E-01	1.00E+00	regulation of synaptic transmission	P
GO:0050805	10	6.10E-01	1.00E+00	1.00E+00	1.00E+00	9.13E-01	1.00E+00	1.00E+00	1.00E+00	2.81E-01	1.00E+00	1.00E+00	1.00E+00	5.92E-01	1.00E+00	8.78E-01	1.00E+00	negative regulation of synaptic transmission	P
GO:0050806	14	1.00E+00	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.85E-01	1.00E+00	9.85E-01	1.00E+00	9.37E-01	1.00E+00	1.00E+00	1.00E+00	8.48E-01	1.00E+00	positive regulation of synaptic transmission	P
GO:0050808	31	9.79E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	3.16E-01	1.00E+00	8.66E-01	1.00E+00	synapse organization and biogenesis	P
GO:0050817	122	9.86E-01	1.00E+00	9.48E-01	1.00E+00	8.57E-01	1.00E+00	9.54E-01	1.00E+00	9.76E-01	1.00E+00	9.96E-01	1.00E+00	9.27E-01	1.00E+00	3.30E-01	1.00E+00	coagulation	P
GO:0050818	26	8.63E-01	1.00E+00	3.35E-01	1.00E+00	8.36E-01	1.00E+00	3.62E-01	1.00E+00	6.36E-01	1.00E+00	8.44E-01	1.00E+00	7.18E-01	1.00E+00	8.06E-02	1.00E+00	regulation of coagulation	P
GO:0050819	18	9.41E-01	1.00E+00	8.69E-01	1.00E+00	9.73E-01	1.00E+00	9.96E-01	1.00E+00	8.34E-01	1.00E+00	9.89E-01	1.00E+00	6.02E-01	1.00E+00	2.05E-01	1.00E+00	negative regulation of coagulation	P
GO:0050821	14	1.15E-01	1.00E+00	1.05E-01	1.00E+00	5.52E-02	1.00E+00	7.05E-02	1.00E+00	7.67E-02	1.00E+00	1.88E-01	1.00E+00	8.46E-01	1.00E+00	4.33E-01	1.00E+00	protein stabilization	P
GO:0050824	169	1.00E+00	1.00E+00	9.27E-01	1.00E+00	9.96E-01	1.00E+00	2.90E-01	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	water binding	F
GO:0050825	169	1.00E+00	1.00E+00	9.27E-01	1.00E+00	9.96E-01	1.00E+00	2.90E-01	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	ice binding	F
GO:0050826	169	1.00E+00	1.00E+00	9.27E-01	1.00E+00	9.96E-01	1.00E+00	2.90E-01	1.00E+00	9.95E-01	1.00E+00	9.90E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	response to freezing	P
GO:0050830	12	1.13E-03	9.30E-02	1.07E-01	1.00E+00	5.26E-01	1.00E+00	1.19E-01	1.00E+00	5.49E-01	1.00E+00	4.85E-01	1.00E+00	1.54E-05	2.00E-03	1.20E-01	1.00E+00	defense response to Gram-positive bacteriu	P
GO:0050839	15	5.25E-01	1.00E+00	2.01E-01	1.00E+00	8.79E-01	1.00E+00	5.75E-01	1.00E+00	2.02E-01	1.00E+00	1.61E-01	1.00E+00	2.19E-01	1.00E+00	5.64E-02	1.00E+00	cell adhesion molecule binding	F
GO:0050848	13	7.81E-01	1.00E+00	2.60E-01	1.00E+00	8.13E-01	1.00E+00	2.77E-01	1.00E+00	9.39E-01	1.00E+00	8.69E-01	1.00E+00	2.48E-01	1.00E+00	1.81E-01	1.00E+00	regulation of calcium-mediated signaling	P
GO:0050850	12	8.49E-01	1.00E+00	3.46E-01	1.00E+00	9.14E-01	1.00E+00	4.44E-01	1.00E+00	9.96E-01	1.00E+00	9.13E-01	1.00E+00	1.99E-01	1.00E+00	1.75E-01	1.00E+00	positive regulation of calcium-mediated sign	P

GO:0050851	34	3.50E-02	1.00E+00	3.16E-01	1.00E+00	2.71E-02	1.00E+00	1.18E-01	1.00E+00	4.28E-01	1.00E+00	8.04E-01	1.00E+00	1.22E-01	1.00E+00	2.98E-01	1.00E+00	antigen receptor-mediated signaling pathwa	P
GO:0050852	23	8.75E-02	1.00E+00	4.90E-01	1.00E+00	9.26E-02	1.00E+00	1.71E-01	1.00E+00	2.24E-01	1.00E+00	4.96E-01	1.00E+00	2.82E-01	1.00E+00	8.81E-01	1.00E+00	T cell receptor signaling pathway	P
GO:0050853	13	1.15E-01	1.00E+00	1.38E-01	1.00E+00	1.13E-01	1.00E+00	6.68E-02	1.00E+00	5.95E-01	1.00E+00	7.53E-01	1.00E+00	1.18E-01	1.00E+00	1.04E-01	1.00E+00	B cell receptor signaling pathway	P
GO:0050854	12	5.73E-02	1.00E+00	4.29E-01	1.00E+00	8.19E-02	1.00E+00	1.58E-01	1.00E+00	3.35E-01	1.00E+00	6.02E-01	1.00E+00	2.81E-01	1.00E+00	5.90E-01	1.00E+00	regulation of antigen receptor-mediated sign	P
GO:0050856	10	9.04E-03	9.83E-01	3.43E-01	1.00E+00	5.96E-02	1.00E+00	1.07E-01	1.00E+00	1.56E-01	1.00E+00	4.55E-01	1.00E+00	1.67E-01	1.00E+00	7.14E-01	1.00E+00	regulation of T cell receptor signaling pathw	P
GO:0050863	74	5.59E-02	1.00E+00	6.05E-01	1.00E+00	3.34E-01	1.00E+00	4.75E-01	1.00E+00	4.13E-01	1.00E+00	9.46E-01	1.00E+00	1.98E-02	4.71E-01	2.85E-01	1.00E+00	regulation of T cell activation	P
GO:0050864	48	5.28E-01	1.00E+00	6.27E-01	1.00E+00	8.15E-01	1.00E+00	1.83E-01	1.00E+00	5.49E-01	1.00E+00	9.81E-01	1.00E+00	1.93E-01	1.00E+00	4.20E-01	1.00E+00	regulation of B cell activation	P
GO:0050868	21	4.87E-01	1.00E+00	8.56E-01	1.00E+00	7.39E-01	1.00E+00	6.72E-01	1.00E+00	5.47E-01	1.00E+00	9.02E-01	1.00E+00	2.41E-01	1.00E+00	8.60E-01	1.00E+00	negative regulation of T cell activation	P
GO:0050869	14	9.40E-01	1.00E+00	9.47E-01	1.00E+00	9.62E-01	1.00E+00	7.26E-01	1.00E+00	8.37E-01	1.00E+00	9.67E-01	1.00E+00	9.83E-01	1.00E+00	1.00E+00	1.00E+00	negative regulation of B cell activation	P
GO:0050870	52	5.27E-02	1.00E+00	3.93E-01	1.00E+00	2.82E-01	1.00E+00	4.52E-01	1.00E+00	7.34E-01	1.00E+00	8.29E-01	1.00E+00	3.25E-02	7.53E-01	1.30E-01	1.00E+00	positive regulation of T cell activation	P
GO:0050871	33	4.16E-01	1.00E+00	6.25E-01	1.00E+00	6.02E-01	1.00E+00	2.80E-01	1.00E+00	5.05E-01	1.00E+00	9.40E-01	1.00E+00	1.65E-01	1.00E+00	2.26E-01	1.00E+00	positive regulation of B cell activation	P
GO:0050874	2054	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.58E-01	1.00E+00	9.96E-01	1.00E+00	organismal physiological process	P
GO:0050875	10564	5.27E-40	0.00E+00	0.00E+00	0.00E+00	5.81E-22	0.00E+00	0.00E+00	0.00E+00	6.39E-22	0.00E+00	2.32E-36	0.00E+00	8.99E-11	0.00E+00	3.30E-21	0.00E+00	cellular physiological process	P
GO:0050876	112	1.00E+00	1.00E+00	9.94E-01	1.00E+00	9.86E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.84E-01	1.00E+00	5.38E-01	1.00E+00	reproductive physiological process	P
GO:0050877	529	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	7.06E-01	1.00E+00	8.88E-01	1.00E+00	neurophysiological process	P
GO:0050878	133	9.98E-01	1.00E+00	9.97E-01	1.00E+00	9.61E-01	1.00E+00	9.99E-01	1.00E+00	9.78E-01	1.00E+00	9.99E-01	1.00E+00	9.86E-01	1.00E+00	6.57E-01	1.00E+00	regulation of body fluids	P
GO:0050879	62	8.68E-01	1.00E+00	1.00E+00	1.00E+00	9.88E-01	1.00E+00	1.00E+00	1.00E+00	8.34E-01	1.00E+00	9.98E-01	1.00E+00	5.65E-01	1.00E+00	6.69E-01	1.00E+00	organismal movement	P
GO:0050880	48	9.16E-01	1.00E+00	1.00E+00	1.00E+00	8.07E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	1.00E+00	1.00E+00	8.63E-01	1.00E+00	9.99E-01	1.00E+00	regulation of blood vessel size	P
GO:0050881	42	5.33E-01	1.00E+00	9.79E-01	1.00E+00	7.85E-01	1.00E+00	9.99E-01	1.00E+00	6.50E-01	1.00E+00	9.80E-01	1.00E+00	3.87E-01	1.00E+00	4.49E-01	1.00E+00	musculoskeletal movement	P
GO:0050884	10	9.35E-02	1.00E+00	1.00E+00	1.00E+00	2.36E-01	1.00E+00	9.86E-01	1.00E+00	1.53E-01	1.00E+00	1.00E+00	1.00E+00	2.15E-01	1.00E+00	9.52E-01	1.00E+00	regulation of posture	P
GO:0050885	32	7.87E-01	1.00E+00	9.46E-01	1.00E+00	8.02E-01	1.00E+00	9.89E-01	1.00E+00	8.98E-01	1.00E+00	9.80E-01	1.00E+00	6.63E-01	1.00E+00	3.53E-01	1.00E+00	regulation of balance	P
GO:0050886	17	8.87E-01	1.00E+00	1.00E+00	1.00E+00	9.96E-01	1.00E+00	9.99E-01	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	7.41E-01	1.00E+00	8.77E-01	1.00E+00	endocrine physiological process	P
GO:0050892	13	3.34E-01	1.00E+00	7.36E-01	1.00E+00	2.26E-01	1.00E+00	7.79E-01	1.00E+00	4.48E-01	1.00E+00	7.07E-01	1.00E+00	3.31E-01	1.00E+00	7.04E-01	1.00E+00	intestinal absorption	P
GO:0050896	2087	6.90E-01	1.00E+00	9.29E-01	1.00E+00	9.08E-01	1.00E+00	8.30E-01	1.00E+00	8.82E-01	1.00E+00	9.58E-01	1.00E+00	8.06E-02	1.00E+00	5.42E-01	1.00E+00	response to stimulus	P
GO:0050897	13	2.61E-01	1.00E+00	2.45E-01	1.00E+00	5.31E-01	1.00E+00	1.90E-01	1.00E+00	3.72E-01	1.00E+00	1.85E-01	1.00E+00	6.60E-01	1.00E+00	7.41E-01	1.00E+00	cobalt ion binding	F
GO:0050900	50	9.95E-01	1.00E+00	6.82E-01	1.00E+00	9.34E-01	1.00E+00	7.06E-01	1.00E+00	9.89E-01	1.00E+00	8.97E-01	1.00E+00	9.87E-01	1.00E+00	2.77E-01	1.00E+00	leukocyte migration	P
GO:0050905	19	6.86E-01	1.00E+00	1.00E+00	1.00E+00	9.52E-01	1.00E+00	9.99E-01	1.00E+00	4.72E-01	1.00E+00	9.95E-01	1.00E+00	4.41E-01	1.00E+00	9.63E-01	1.00E+00	neuromuscular physiological process	P
GO:0050906	23	9.22E-01	1.00E+00	9.99E-01	1.00E+00	9.42E-01	1.00E+00	1.00E+00	1.00E+00	9.30E-01	1.00E+00	9.51E-01	1.00E+00	6.21E-01	1.00E+00	8.76E-01	1.00E+00	detection of stimulus during sensory percep	P
GO:0050909	17	7.35E-01	1.00E+00	7.61E-01	1.00E+00	9.29E-01	1.00E+00	7.21E-01	1.00E+00	3.87E-01	1.00E+00	7.01E-01	1.00E+00	6.44E-01	1.00E+00	6.87E-01	1.00E+00	sensory perception of taste	P
GO:0050918	14	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	7.27E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	6.18E-01	1.00E+00	positive chemotaxis	P
GO:0050920	14	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.56E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	6.64E-01	1.00E+00	regulation of chemotaxis	P
GO:0050921	14	9.96E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	6.56E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	6.64E-01	1.00E+00	positive regulation of chemotaxis	P
GO:0050926	12	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.92E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	5.66E-01	1.00E+00	regulation of positive chemotaxis	P
GO:0050927	12	9.92E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.92E-01	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	5.66E-01	1.00E+00	positive regulation of positive chemotaxis	P
GO:0050930	10	9.77E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	5.11E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	5.17E-01	1.00E+00	induction of positive chemotaxis	P
GO:0050931	18	9.66E-01	1.00E+00	9.33E-01	1.00E+00	9.73E-01	1.00E+00	9.73E-01	1.00E+00	9.44E-01	1.00E+00	9.74E-01	1.00E+00	7.85E-01	1.00E+00	3.58E-01	1.00E+00	pigment cell differentiation	P
GO:0050953	118	4.57E-01	1.00E+00	8.85E-01	1.00E+00	6.22E-01	1.00E+00	9.58E-01	1.00E+00	7.15E-01	1.00E+00	7.68E-01	1.00E+00	1.54E-01	1.00E+00	5.38E-01	1.00E+00	sensory perception of light stimulus	P
GO:0050954	79	9.98E-01	1.00E+00	9.90E-01	1.00E+00	9.99E-01	1.00E+00	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	7.63E-01	1.00E+00	6.90E-01	1.00E+00	sensory perception of mechanical stimulus	P
GO:0050974	11	6.90E-01	1.00E+00	9.49E-01	1.00E+00	4.70E-01	1.00E+00	1.00E+00	1.00E+00	9.48E-01	1.00E+00	6.80E-01	1.00E+00	4.30E-01	1.00E+00	7.81E-01	1.00E+00	detection of mechanical stimulus during sen	P
GO:0050982	13	6.03E-01	1.00E+00	9.44E-01	1.00E+00	3.53E-01	1.00E+00	1.00E+00	1.00E+00	9.14E-01	1.00E+00	7.47E-01	1.00E+00	4.57E-01	1.00E+00	8.55E-01	1.00E+00	detection of mechanical stimulus	P
GO:0051015	41	7.04E-03	3.64E-01	4.79E-02	1.00E+00	3.71E-02	1.00E+00	2.60E-01	1.00E+00	4.45E-02	1.00E+00	4.22E-02	1.00E+00	1.84E-02	4.71E-01	1.87E-01	1.00E+00	actin filament binding	F
GO:0051016	17	7.94E-02	1.00E+00	2.47E-01	1.00E+00	1.93E-01	1.00E+00	5.81E-01	1.00E+00	2.54E-01	1.00E+00	2.86E-01	1.00E+00	1.01E-02	2.17E-01	8.52E-02	1.00E+00	barbed-end actin filament capping	P
GO:0051017	18	5.78E-02	1.00E+00	1.33E-01	1.00E+00	1.02E-01	1.00E+00	2.57E-01	1.00E+00	4.08E-01	1.00E+00	3.40E-01	1.00E+00	6.74E-02	1.00E+00	1.70E-01	1.00E+00	actin filament bundle formation	P
GO:0051020	65	1.52E-02	9.83E-01	6.64E-02	1.00E+00	2.30E-01	1.00E+00	1.46E-01	1.00E+00	5.16E-02	1.00E+00	2.29E-01	1.00E+00	8.76E-03	2.17E-01	5.02E-02	1.00E+00	GTPase binding	F
GO:0051028	53	6.47E-05	7.00E-03	3.03E-07	2.66E-03	2.01E-05	3.00E-03	1.29E-06	1.00E-03	3.91E-03	1.35E-01	2.44E-05	2.00E-03	2.85E-01	1.00E+00	4.35E-01	1.00E+00	mRNA transport	P
GO:0051046	89	9.30E-01	1.00E+00	8.25E-01	1.00E+00	9.98E-01	1.00E+00	9.44E-01	1.00E+00	7.49E-01	1.00E+00	7.75E-01	1.00E+00	7.04E-01	1.00E+00	1.90E-01	1.00E+00	regulation of secretion	P
GO:0051047	25	9.76E-01	1.00E+00	9.16E-01	1.00E+00	9.99E-01	1.00E+00	9.94E-01	1.00E+00	1.00E+00	1.00E+00	9.76E-01	1.00E+00	4.53E-01	1.00E+00	1.66E-01	1.00E+00	positive regulation of secretion	P
GO:0051048	27	6.24E-01	1.00E+00	3.10E-01	1.00E+00	7.84E-01	1.00E+00	2.88E-01	1.00E+00	1.95E-01	1.00E+00	2.12E-01	1.00E+00	1.00E+00	1.00E+00	4.39E-01	1.00E+00	negative regulation of secretion	P
GO:0051049	155	7.38E-02	1.00E+00	6.43E-01	1.00E+00	6.62E-01	1.00E+00	5.76E-01	1.00E+00	3.25E-01	1.00E+00	9.56E-01	1.00E+00	2.02E-03	5.54E-02	1.48E-01	1.00E+00	regulation of transport	P
GO:0051050	68	5.17E-01	1.00E+00	9.07E-01	1.00E+00	9.90E-01	1.00E+00	9.47E-01	1.00E+00	4.83E-01	1.00E+00	9.97E-01	1.00E+00	6.13E-02	1.00E+00	1.88E-01	1.00E+00	positive regulation of transport	P
GO:0051051	36	1.06E-01	1.00E+00	6.29E-01	1.00E+00	1.22E-01	1.00E+00	8.69E-01	1.00E+00	1.78E-01	1.00E+00	3.08E-01	1.00E+00	1.18E-01	1.00E+00	6.95E-01	1.00E+00	negative regulation of transport	P
GO:0051052	48	3.94E-03	1.86E-01	1.96E-02	1.00E+00	2.61E-02	1.00E+00	5.08E-02	1.00E+00	2.93E-02	1.00E+00	7.08E-02	1.00E+00	2.08E-02	5.29E-01	3.93E-02	1.00E+00	regulation of DNA metabolism	P
GO:0051053	18	6.09E-04	5.20E-02	2.85E-02	1.00E+00	1.61E-02	8.10E-01	4.21E-02	1.00E+00	2.48E-02	1.00E+00	5.36E-02	1.00E+00	2.59E-02	6.06E-01	1.49E-01	1.00E+00	negative regulation of DNA metabolism	P
GO:0051054	15	1.38E-01	1.00E+00	2.76E-01	1.00E+00	1.86E-01	1.00E+00	4.33E-01	1.00E+00	7.14E-01	1.00E+00	4.25E-01	1.00E+00	5.30E-02	1.00E+00	1.69E-01	1.00E+00	positive regulation of DNA metabolism	P
GO:0051056	169	7.80E-01	1.00E+00	9.83E-01	1.00E+00	9.86E-01	1.00E+00	9.98E-01	1.00E+00	6.89E-01	1.00E+00	9.58E-01	1.00E+00	4.07E-01	1.00E+00	7.76E-01	1.00E+00	regulation of small GTPase mediated signal	P
GO:0051057	12	8.96E-01	1.00E+00	7.53E-01	1.00E+00	9.99E-01	1.00E+00	8.07E-01	1.00E+00	5.55E-01	1.00E+00	9.98E-01	1.00E+00	8.00E-01	1.00E+00	3.50E-01	1.00E+00	positive regulation of small GTPase mediate	P
GO:0051059	22	2.60E-02	1.00E+00	2.23E-01	1.00E+00	1.11E-02	4.74E-01	5.07E-02	1.00E+00	3.32E-01	1.00E+00	2.01E-01	1.00E+00	2.47E-01	1.00E+00	9.83E-01	1.00E+00	NF-kappaB binding	F
GO:0051082	84	3.13E-03	1.39E-01	6.08E-07	2.66E-03	4.64E-02	1.00E+00	3.67E-05	5.41E-03	5.87E-04	4.40E-02	2.09E-04	1.36E-02	3.00E-01	1.00E+00	7.06E-02	1.00E+00	unfolded protein binding	F
GO:0051084	14	9.97E-01	1.00E+00	1.37E-01	1.00E+00	1.00E+00	1.00E+00	2.02E-01	1.00E+00	9.72E-01	1.00E+00	2.45E-01	1.00E+00	1.00E+00	1.00E+00	5.80E-01	1.00E+00	posttranslational protein folding	P
GO:0051085	12	9.98E-01	1.00E+00	8.46E-02	1.00E+00	1.00E+00	1.00E+00	1.67E-01	1.00E+00	9.97E-01	1.00E+00	1.76E-01	1.00E+00	1.00E+00	1.00E+00	5.71E-01	1.00E+00	chaperone cofactor-dependent protein foldir	P
GO:0051087	12	3.98E-01	1.00E+00	1.88E-01	1.00E+00	6.33E-01	1.00E+00	1.34E-01	1.00E+00	2.98E-01	1.00E+00	2.87E-01	1.00E+00	1.00E+00	1.00E+00	3.73E-01	1.00E+00	chaperone binding	F
GO:0051090	51	3.06E-01	1.00E+00	2.87E-01	1.00E+00	7.41E-02	1.00E+00	2.35E-01	1.00E+00	5.95E-01	1.00E+00	2.91E-01	1.00E+00	6.04E-01	1.00E+00	3.86E-01	1.00E+00	regulation of transcription factor activity	P
GO:0051091	29	4.02E-01	1.00E+00	4.98E-01	1.00E+00	3.24E-01	1.00E+00	5.83E-01	1.00E+00	4.38E-01	1.00E+00	5.67E-01	1.00E+00	4.88E-01	1.00E+00	2.28E-01	1.00E+00	positive regulation of transcription factor act	P
GO:0051092	21	1.81E-01	1.00E+00	7.30E-01	1.00E+00	1.74E-01	1.00E+00	6.50E-01	1.00E+00	2.56E-01	1.00E+00	5.27E-01	1.00E+00	1.81E-01	1.00E+00	7.81E-01	1.00E+00	activation of NF-kappaB transcription factor	P
GO:0051093	141	1.00E+00	1.00E+00	9.92E-01	1.00E+00	1.00E+00	1.00E+00	6.45E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	negative regulation of development	P
GO:0051094	117	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.62E-01	1.00E+00	7.01E-01	1.00E+00	positive regulation of development	P
GO:0051098	36	6.30E-02	1.00E+00	9.11E-02	1.00E+00	1.82E-01	1.00E+00	1.31E-01	1.00E+00	3.73E-02	1.00E+00	2.84E-01	1.00E+00	1.92E-01	1.00E+00	1.51E-01	1.00E+00	regulation of binding	P
GO:0051099	11	2.78E-01	1.00E+00	3.57E-01	1.00E+00	4.22E-01	1.00E+00	3.36E-01	1.00E+00	7.97E-02	1.00E+00	3.13E-01	1.00E+00	8.72E-01	1.00E+00	8.32E-01	1.00E+00	positive regulation of binding	P
GO:0051101	19	2.02E-01	1.00E+00	1.45E-01	1.00E+00	2.42E-01	1.00E+00	8.28E-02	1.00E+00	2.08E-01	1.00E+00	3.03E-01	1.00E+00	3.30E-01	1.00E+00	4.28E-01	1.00E+00	regulation of DNA binding	P
GO:0051119	46	1.53E-01	1.00E+00	6.85E-01	1.00E+00	6.47E-01	1.00E+00	9.12E-01	1.00E+00	2.78E-01	1.00E+00	7.50E-01	1.00E+00	3.60E-02	7.53E-01	5.21E-01	1.00E+00	sugar transporter activity	F
GO:0051128	109	3.99E-03	1.86E-01	5.34E-02	1.00E+00	5.28E-02	1.00E+00	4.50E-02	1.00E+00	1.24E-02	4.81E-01	2.67E-01	1.00E+00	2.08E-02	5.29E-01	7.97E-02	1.00E+00	regulation of cell organization and biogenes	P
GO:0051129	46	4.88E-03	3.48E-01	9.51E-02	1.00E+00	1.69E-01	1.00E+00	2.14E-01	1.00E+00	1.25E-02	4.81E-01	1.79E-01	1.00E+00	1.52E-03	4.40E-02	8.41E-02	1.00E+00	negative regulation of cell organization and	P
GO:0051130	22	3.37E-01	1.00E+00	8.77E-01	1.00E+00	2.95E-01	1.00E+00	4.46E-01	1.00E+00	9.24E-01	1.00E+00	8.61E-01	1.00E+00	3.56E-01	1.00E+00	1.00E+00	1.00E+00	positive regulation of cell organization and b	P
GO:0051145	14	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.94E-01	1.00E+00	5.96E-01	1.00E+00	smooth muscle cell differentiation	P
GO:0051146	39	4.88E-01	1.00E+00	7.04E-01	1.00E+00	3.38E-01	1.00E+00	2.99E-01	1.00E+00	7.94E-01	1.00E+00	8.44E-01	1.00E+00	4.35E-01	1.00E+00	9.73E-01	1.00E+00	striated muscle cell differentiation	P

GO:0051168	40	3.13E-05	6.00E-03	4.79E-05	2.80E-02	2.22E-05	3.00E-03	3.75E-05	5.41E-03	3.38E-03	1.35E-01	5.31E-03	2.02E-01	7.87E-02	1.00E+00	5.23E-02	1.00E+00	nuclear export	P
GO:0051169	120	1.19E-04	1.90E-02	3.28E-07	2.66E-03	2.56E-04	1.61E-02	3.43E-06	1.00E-03	6.17E-03	1.65E-01	5.94E-05	5.36E-03	6.18E-02	1.00E+00	3.12E-03	2.16E-01	nuclear transport	P
GO:0051170	83	2.49E-02	1.00E+00	8.45E-05	2.80E-02	5.60E-02	1.00E+00	1.04E-03	3.60E-02	1.13E-01	1.00E+00	5.52E-04	2.00E-02	1.44E-01	1.00E+00	9.74E-03	4.72E-01	nuclear import	P
GO:0051174	123	9.92E-01	1.00E+00	9.55E-01	1.00E+00	9.90E-01	1.00E+00	8.22E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	7.15E-01	1.00E+00	4.99E-01	1.00E+00	regulation of phosphorus metabolism	P
GO:0051179	3364	1.15E-05	5.00E-03	1.55E-04	2.80E-02	2.43E-01	1.00E+00	2.69E-04	1.15E-02	1.67E-02	7.19E-01	2.19E-01	1.00E+00	1.44E-07	6.33E-04	6.76E-05	3.91E-03	localization	P
GO:0051180	10	1.76E-01	1.00E+00	6.42E-01	1.00E+00	1.00E+00	1.00E+00	9.54E-01	1.00E+00	3.11E-01	1.00E+00	4.11E-01	1.00E+00	6.50E-03	2.01E-01	5.41E-01	1.00E+00	vitamin transport	P
GO:0051181	23	7.49E-01	1.00E+00	6.13E-01	1.00E+00	9.90E-01	1.00E+00	6.62E-01	1.00E+00	5.41E-01	1.00E+00	7.19E-01	1.00E+00	3.07E-01	1.00E+00	3.86E-01	1.00E+00	cofactor transport	P
GO:0051183	12	4.25E-02	1.00E+00	1.50E-01	1.00E+00	3.10E-01	1.00E+00	2.86E-01	1.00E+00	5.48E-02	1.00E+00	1.45E-01	1.00E+00	2.87E-02	6.06E-01	3.25E-01	1.00E+00	vitamin transporter activity	F
GO:0051184	25	4.35E-01	1.00E+00	3.28E-01	1.00E+00	6.34E-01	1.00E+00	3.21E-01	1.00E+00	1.98E-01	1.00E+00	4.67E-01	1.00E+00	3.14E-01	1.00E+00	3.10E-01	1.00E+00	cofactor transporter activity	F
GO:0051186	263	6.85E-04	5.20E-02	1.10E-03	7.30E-02	4.33E-02	1.00E+00	1.01E-02	3.78E-01	6.55E-03	1.65E-01	1.54E-02	1.00E+00	6.12E-03	2.01E-01	4.62E-03	2.58E-01	cofactor metabolism	P
GO:0051187	32	2.95E-02	1.00E+00	1.26E-02	7.51E-01	9.70E-03	4.74E-01	1.43E-02	7.69E-01	2.07E-01	1.00E+00	7.69E-02	1.00E+00	1.34E-01	1.00E+00	1.26E-02	9.40E-01	cofactor catabolism	P
GO:0051188	154	3.99E-02	1.00E+00	5.62E-02	1.00E+00	2.53E-01	1.00E+00	8.25E-02	1.00E+00	4.70E-02	1.00E+00	3.55E-01	1.00E+00	5.24E-02	1.00E+00	4.87E-02	1.00E+00	cofactor biosynthesis	P
GO:0051213	60	1.06E-01	1.00E+00	4.16E-02	1.00E+00	3.51E-01	1.00E+00	4.33E-02	1.00E+00	6.89E-02	1.00E+00	5.25E-02	1.00E+00	1.44E-01	1.00E+00	3.82E-01	1.00E+00	dioxygenase activity	F
GO:0051216	70	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	cartilage development	P
GO:0051219	18	3.56E-02	1.00E+00	3.70E-01	1.00E+00	7.72E-02	1.00E+00	1.34E-01	1.00E+00	2.61E-01	1.00E+00	5.07E-01	1.00E+00	6.10E-02	1.00E+00	8.19E-01	1.00E+00	phosphoprotein binding	F
GO:0051222	17	7.65E-01	1.00E+00	4.65E-01	1.00E+00	1.00E+00	1.00E+00	8.93E-01	1.00E+00	9.67E-01	1.00E+00	7.26E-01	1.00E+00	1.72E-01	1.00E+00	1.34E-01	1.00E+00	positive regulation of protein transport	P
GO:0051223	34	6.87E-02	1.00E+00	3.83E-02	1.00E+00	2.99E-01	1.00E+00	1.65E-01	1.00E+00	2.92E-01	1.00E+00	1.10E-01	1.00E+00	3.19E-02	7.53E-01	2.67E-02	1.00E+00	regulation of protein transport	P
GO:0051224	10	5.62E-02	1.00E+00	2.72E-01	1.00E+00	1.14E-01	1.00E+00	5.68E-01	1.00E+00	1.20E-01	1.00E+00	1.55E-01	1.00E+00	6.04E-03	2.01E-01	2.20E-01	1.00E+00	negative regulation of protein transport	P
GO:0051234	3302	7.33E-06	5.00E-03	1.66E-04	2.80E-02	2.01E-01	1.00E+00	4.01E-04	1.30E-02	1.62E-02	7.19E-01	2.37E-01	1.00E+00	1.24E-07	6.33E-04	4.29E-05	3.91E-03	establishment of localization	P
GO:0051235	36	8.13E-02	1.00E+00	1.65E-01	1.00E+00	1.92E-01	1.00E+00	9.50E-02	1.00E+00	2.46E-01	1.00E+00	5.54E-01	1.00E+00	6.39E-02	1.00E+00	6.32E-01	1.00E+00	maintenance of localization	P
GO:0051236	58	1.57E-05	5.00E-03	7.46E-08	2.66E-03	9.86E-06	1.69E-03	2.02E-07	9.57E-04	1.39E-03	4.80E-02	6.13E-06	2.00E-03	1.51E-01	1.00E+00	2.67E-01	1.00E+00	establishment of RNA localization	P
GO:0051238	10	3.64E-02	1.00E+00	2.39E-01	1.00E+00	2.13E-02	1.00E+00	1.41E-01	1.00E+00	3.10E-01	1.00E+00	7.17E-01	1.00E+00	7.41E-02	1.00E+00	1.23E-01	1.00E+00	sequestering of metal ion	P
GO:0051239	316	9.76E-01	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.18E-01	1.00E+00	8.84E-01	1.00E+00	regulation of organismal physiological proce	P
GO:0051240	144	9.15E-01	1.00E+00	9.95E-01	1.00E+00	8.67E-01	1.00E+00	9.84E-01	1.00E+00	1.00E+00	1.00E+00	9.99E-01	1.00E+00	2.55E-01	1.00E+00	7.29E-01	1.00E+00	positive regulation of organismal physiologic	P
GO:0051241	39	2.91E-01	1.00E+00	9.31E-01	1.00E+00	9.38E-01	1.00E+00	6.07E-01	1.00E+00	2.78E-01	1.00E+00	1.00E+00	1.00E+00	1.16E-01	1.00E+00	7.28E-01	1.00E+00	negative regulation of organismal physiolog	P
GO:0051242	973	4.44E-01	1.00E+00	9.51E-01	1.00E+00	7.42E-01	1.00E+00	5.72E-01	1.00E+00	7.38E-01	1.00E+00	1.00E+00	1.00E+00	2.02E-01	1.00E+00	7.41E-01	1.00E+00	positive regulation of cellular physiological p	P
GO:0051243	933	3.11E-02	1.00E+00	5.83E-02	1.00E+00	1.49E-01	1.00E+00	7.89E-03	3.78E-01	1.68E-01	1.00E+00	4.63E-01	1.00E+00	4.21E-02	8.34E-01	5.95E-01	1.00E+00	negative regulation of cellular physiological	P
GO:0051244	3594	1.99E-02	1.00E+00	1.38E-07	2.66E-03	2.41E-02	1.00E+00	4.00E-11	0.00E+00	2.82E-02	1.00E+00	3.39E-04	1.36E-02	4.36E-01	1.00E+00	3.16E-01	1.00E+00	regulation of cellular physiological process	P
GO:0051246	359	3.58E-02	1.00E+00	4.24E-03	3.82E-01	7.00E-02	1.00E+00	8.92E-04	2.70E-02	1.45E-01	1.00E+00	6.46E-02	1.00E+00	1.80E-01	1.00E+00	7.61E-02	1.00E+00	regulation of protein metabolism	P
GO:0051247	112	6.30E-01	1.00E+00	9.08E-01	1.00E+00	8.73E-01	1.00E+00	7.64E-01	1.00E+00	9.49E-01	1.00E+00	9.71E-01	1.00E+00	1.84E-01	1.00E+00	6.32E-01	1.00E+00	positive regulation of protein metabolism	P
GO:0051248	103	2.95E-02	1.00E+00	1.56E-02	1.00E+00	6.72E-02	1.00E+00	7.78E-03	3.78E-01	1.40E-01	1.00E+00	2.14E-01	1.00E+00	2.32E-02	5.60E-01	2.58E-02	1.00E+00	negative regulation of protein metabolism	P
GO:0051249	101	5.91E-02	1.00E+00	7.34E-01	1.00E+00	4.30E-01	1.00E+00	3.26E-01	1.00E+00	3.32E-01	1.00E+00	9.90E-01	1.00E+00	2.01E-02	4.71E-01	3.83E-01	1.00E+00	regulation of lymphocyte activation	P
GO:0051250	32	3.24E-01	1.00E+00	9.85E-01	1.00E+00	7.89E-01	1.00E+00	7.65E-01	1.00E+00	3.31E-01	1.00E+00	9.93E-01	1.00E+00	1.53E-01	1.00E+00	9.67E-01	1.00E+00	negative regulation of lymphocyte activation	P
GO:0051251	71	7.19E-02	1.00E+00	5.10E-01	1.00E+00	2.76E-01	1.00E+00	3.02E-01	1.00E+00	6.02E-01	1.00E+00	9.30E-01	1.00E+00	4.15E-02	8.34E-01	1.79E-01	1.00E+00	positive regulation of lymphocyte activation	P
GO:0051252	24	7.86E-01	1.00E+00	2.96E-01	1.00E+00	8.55E-01	1.00E+00	3.78E-01	1.00E+00	5.90E-01	1.00E+00	5.91E-01	1.00E+00	9.12E-01	1.00E+00	1.59E-01	1.00E+00	regulation of RNA metabolism	P
GO:0051258	76	1.16E-01	1.00E+00	4.62E-01	1.00E+00	3.60E-01	1.00E+00	3.80E-01	1.00E+00	3.89E-01	1.00E+00	7.94E-01	1.00E+00	4.61E-02	8.34E-01	2.97E-01	1.00E+00	protein polymerization	P
GO:0051259	102	1.09E-01	1.00E+00	4.86E-01	1.00E+00	3.59E-01	1.00E+00	7.36E-01	1.00E+00	1.01E-01	1.00E+00	5.38E-01	1.00E+00	3.60E-01	1.00E+00	5.97E-01	1.00E+00	protein oligomerization	P
GO:0051260	72	3.51E-01	1.00E+00	7.82E-01	1.00E+00	8.24E-01	1.00E+00	9.73E-01	1.00E+00	1.37E-01	1.00E+00	5.30E-01	1.00E+00	5.59E-01	1.00E+00	6.78E-01	1.00E+00	protein homooligomerization	P
GO:0051261	39	3.80E-03	1.86E-01	6.38E-02	1.00E+00	1.37E-01	1.00E+00	1.21E-01	1.00E+00	1.87E-02	7.19E-01	1.29E-01	1.00E+00	3.23E-03	6.72E-02	8.99E-02	1.00E+00	protein depolymerization	P
GO:0051262	19	1.03E-02	9.83E-01	5.34E-02	1.00E+00	6.26E-01	1.00E+00	7.18E-01	1.00E+00	5.95E-02	1.00E+00	1.11E-01	1.00E+00	7.69E-03	2.01E-01	2.65E-01	1.00E+00	protein tetramerization	P
GO:0051270	93	7.15E-01	1.00E+00	9.87E-01	1.00E+00	8.24E-01	1.00E+00	9.99E-01	1.00E+00	7.34E-01	1.00E+00	9.88E-01	1.00E+00	3.36E-01	1.00E+00	6.93E-01	1.00E+00	regulation of cell motility	P
GO:0051271	29	8.52E-01	1.00E+00	7.51E-01	1.00E+00	5.13E-01	1.00E+00	4.03E-01	1.00E+00	9.64E-01	1.00E+00	8.01E-01	1.00E+00	6.80E-01	1.00E+00	9.97E-01	1.00E+00	negative regulation of cell motility	P
GO:0051272	39	4.06E-01	1.00E+00	9.69E-01	1.00E+00	7.69E-01	1.00E+00	1.00E+00	1.00E+00	3.97E-01	1.00E+00	9.93E-01	1.00E+00	1.59E-01	1.00E+00	2.12E-01	1.00E+00	positive regulation of cell motility	P
GO:0051276	337	1.07E-11	6.62E-04	1.52E-15	0.00E+00	4.21E-11	0.00E+00	1.86E-13	0.00E+00	6.15E-08	0.00E+00	5.49E-07	2.00E-03	6.93E-02	1.00E+00	1.72E-06	3.91E-03	chromosome organization and biogenesis	P
GO:0051287	60	4.13E-01	1.00E+00	3.13E-01	1.00E+00	4.88E-01	1.00E+00	6.99E-01	1.00E+00	5.82E-01	1.00E+00	1.88E-01	1.00E+00	3.39E-01	1.00E+00	8.32E-01	1.00E+00	NAD binding	F
GO:0051297	16	1.79E-03	1.02E-01	3.28E-04	4.20E-02	8.53E-04	3.05E-02	3.37E-03	1.42E-01	3.10E-02	1.00E+00	1.27E-02	1.00E+00	1.97E-01	1.00E+00	2.69E-02	1.00E+00	centrosome organization and biogenesis	P
GO:0051301	240	4.99E-11	6.62E-04	1.10E-21	0.00E+00	4.40E-10	0.00E+00	5.89E-16	0.00E+00	5.66E-08	0.00E+00	1.44E-12	0.00E+00	1.91E-02	4.71E-01	4.71E-08	0.00E+00	cell division	P
GO:0051318	10	8.47E-01	1.00E+00	1.09E-01	1.00E+00	8.17E-01	1.00E+00	4.94E-02	1.00E+00	5.87E-01	1.00E+00	1.84E-01	1.00E+00	8.25E-01	1.00E+00	2.19E-01	1.00E+00	G1 phase	P
GO:0051320	14	3.17E-01	1.00E+00	2.62E-01	1.00E+00	3.98E-01	1.00E+00	2.13E-01	1.00E+00	1.63E-01	1.00E+00	2.07E-01	1.00E+00	7.87E-01	1.00E+00	5.50E-01	1.00E+00	S phase	P
GO:0051321	84	1.61E-04	1.90E-02	7.24E-07	2.66E-03	3.70E-05	3.00E-03	1.83E-04	1.10E-02	1.73E-02	7.19E-01	1.96E-04	1.36E-02	6.99E-02	1.00E+00	1.26E-03	4.40E-02	meiotic cell cycle	P
GO:0051325	70	7.91E-01	1.00E+00	3.38E-02	1.00E+00	5.76E-01	1.00E+00	4.80E-03	1.42E-01	3.78E-01	1.00E+00	1.02E-01	1.00E+00	9.52E-01	1.00E+00	3.70E-01	1.00E+00	interphase	P
GO:0051327	83	3.23E-04	3.25E-02	4.46E-07	2.66E-03	5.17E-05	3.00E-03	2.15E-04	1.10E-02	3.18E-02	1.00E+00	1.28E-04	1.36E-02	1.26E-01	1.00E+00	8.71E-04	3.30E-02	M phase of meiotic cell cycle	P
GO:0051329	69	7.53E-01	1.00E+00	3.26E-02	1.00E+00	5.57E-01	1.00E+00	4.74E-03	1.42E-01	3.42E-01	1.00E+00	9.53E-02	1.00E+00	9.39E-01	1.00E+00	3.85E-01	1.00E+00	interphase of mitotic cell cycle	P
GO:0051336	165	8.18E-06	5.00E-03	1.06E-03	7.30E-02	9.34E-04	3.30E-02	7.00E-03	3.78E-01	3.56E-03	1.35E-01	5.35E-02	1.00E+00	6.42E-04	2.40E-02	3.89E-04	2.10E-02	regulation of hydrolase activity	P
GO:0051338	199	5.13E-01	1.00E+00	6.10E-01	1.00E+00	6.93E-01	1.00E+00	6.52E-01	1.00E+00	2.74E-01	1.00E+00	8.32E-01	1.00E+00	3.91E-01	1.00E+00	2.16E-01	1.00E+00	regulation of transferase activity	P
GO:0051339	22	7.61E-01	1.00E+00	8.84E-01	1.00E+00	7.15E-01	1.00E+00	9.61E-01	1.00E+00	6.26E-01	1.00E+00	6.52E-01	1.00E+00	9.92E-01	1.00E+00	9.44E-01	1.00E+00	regulation of lyase activity	P
GO:0051345	50	1.10E-02	9.83E-01	6.32E-02	1.00E+00	2.81E-02	1.00E+00	1.04E-01	1.00E+00	8.23E-02	1.00E+00	1.88E-01	1.00E+00	3.08E-02	7.53E-01	4.48E-02	1.00E+00	positive regulation of hydrolase activity	P
GO:0051347	136	8.88E-01	1.00E+00	8.36E-01	1.00E+00	9.45E-01	1.00E+00	9.80E-01	1.00E+00	3.02E-01	1.00E+00	7.38E-01	1.00E+00	9.23E-01	1.00E+00	2.31E-01	1.00E+00	positive regulation of transferase activity	P
GO:0051348	53	2.08E-01	1.00E+00	3.11E-01	1.00E+00	3.34E-01	1.00E+00	4.16E-02	1.00E+00	5.38E-01	1.00E+00	9.55E-01	1.00E+00	9.73E-02	1.00E+00	5.36E-01	1.00E+00	negative regulation of transferase activity	P
GO:0051349	16	9.64E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.77E-01	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.93E-01	1.00E+00	positive regulation of lyase activity	P
GO:0051384	21	8.59E-01	1.00E+00	7.30E-01	1.00E+00	5.99E-01	1.00E+00	9.58E-01	1.00E+00	6.09E-01	1.00E+00	3.24E-01	1.00E+00	9.85E-01	1.00E+00	9.34E-01	1.00E+00	response to glucocorticoid stimulus	P
GO:0051402	67	4.30E-01	1.00E+00	5.83E-01	1.00E+00	5.98E-01	1.00E+00	5.28E-01	1.00E+00	1.92E-01	1.00E+00	5.34E-01	1.00E+00	9.41E-01	1.00E+00	7.58E-01	1.00E+00	neuron apoptosis	P
GO:0051427	45	1.57E-03	9.30E-02	7.08E-03	5.59E-01	3.56E-04	1.61E-02	7.69E-03	3.78E-01	6.38E-02	1.00E+00	2.42E-02	1.00E+00	3.06E-01	1.00E+00	3.48E-01	1.00E+00	hormone receptor binding	F
GO:0051480	39	2.58E-01	1.00E+00	8.51E-01	1.00E+00	3.38E-01	1.00E+00	8.37E-01	1.00E+00	6.31E-01	1.00E+00	9.68E-01	1.00E+00	8.81E-02	1.00E+00	3.79E-01	1.00E+00	cytosolic calcium ion homeostasis	P
GO:0051536	57	1.15E-03	9.30E-02	4.21E-02	1.00E+00	2.98E-02	1.00E+00	1.83E-02	7.69E-01	6.40E-02	1.00E+00	2.57E-01	1.00E+00	8.43E-03	2.17E-01	1.05E-01	1.00E+00	iron-sulfur cluster binding	F
GO:0051537	19	1.62E-02	9.83E-01	2.03E-01	1.00E+00	7.55E-02	1.00E+00	1.45E-01	1.00E+00	5.98E-01	1.00E+00	4.23E-01	1.00E+00	1.29E-02	4.39E-01	1.99E-01	1.00E+00	2 iron, 2 sulfur cluster binding	F
GO:0051539	22	2.94E-03	1.39E-01	6.17E-04	7.30E-02	6.79E-03	2.83E-01	3.51E-04	1.30E-02	7.78E-02	1.00E+00	3.64E-02	1.00E+00	2.69E-02	6.06E-01	2.43E-02	1.00E+00	4 iron, 4 sulfur cluster binding	F
GO:0051540	57	1.15E-03	9.30E-02	4.21E-02	1.00E+00	2.98E-02	1.00E+00	1.83E-02	7.69E-01	6.40E-02	1.00E+00	2.57E-01	1.00E+00	8.43E-03	2.17E-01	1.05E-01	1.00E+00	metal cluster binding	F
GO:0051591	12	1.28E-01	1.00E+00	5.85E-01	1.00E+00	2.61E-01	1.00E+00	4.09E-01	1.00E+00	2.54E-01	1.00E+00	5.78E-01	1.00E+00	3.44E-01	1.00E+00	7.54E-01	1.00E+00	response to cAMP	P
GO:0051592	15	9.61E-01	1.00E+00	9.58E-01	1.00E+00	9.37E-01	1.00E+00	9.99E-01	1.00E+00	9.96E-01	1.00E+00	9.80E-01	1.00E+00	8.31E-01	1.00E+00	1.01E-01	1.00E+00	response to calcium ion	P
GO:0051603	176	1.83E-05	5.00E-03	5.82E-10	2.66E-03	1.19E-04	1.61E-02	9.26E-07	1.00E-03	3.50E-05	1.56E-03	6.17E-07	2.00E-03	2.75E-01	1.00E+00	5.03E-05	3.91E-03	proteolysis during cellular protein catabolism	P
GO:0051604	14	4.53E-01	1.00E+00	7.42E-01	1.00E+00	6.70E-01	1.00E+00	5.40E-01	1.00E+00	2.75E-01	1.00E+00	7.14E-01	1.00E+00	5.45E-01	1.00E+00	8.08E-01	1.00E+00	protein maturation	P
GO:0051605	13	3.54E-01	1.00E+00	6.27E-01	1.00E+00	5.73E-01	1.00E+00	4.20E-01	1.00E+00	2.35E-01	1.00E+00	5.99E-01	1.00E+00	4.14E-01	1.00E+00	7.29E-01	1.00E+00	proteolysis during protein maturation	P
GO:0051606	69	5.70E-01	1.00E+00	9.12E-01	1.00E+00	6.19E-01	1.00E+00	9.05E-01	1.00E+00	8.03E-01	1.00E+00	8.03E-01	1.00E+00	1.63E-01	1.00E+00	6.73E-01	1.00E+00	detection of stimulus	P
GO:0051607	15	5.85E-01	1.00E+00	7.79E-01	1.00E+00	7.87E-01	1.00E+00	5.06E-01	1.00E+00	4.39E-01	1.00E+00	9.69E-01	1.00E+00	2.24E-01	1.00E+00	6.50E-01	1.00E+00	defense response to virus	P

GO:0051640	33	6.93E-02	1.00E+00	4.92E-02	1.00E+00	7.94E-02	1.00E+00	3.20E-02	1.00E+00	1.91E-02	7.19E-01	1.29E-01	1.00E+00	4.11E-01	1.00E+00	8.69E-02	1.00E+00	organelle localization	P
GO:0051641	810	3.91E-16	0.00E+00	2.27E-22	0.00E+00	3.60E-11	0.00E+00	7.39E-18	0.00E+00	2.38E-11	0.00E+00	4.14E-13	0.00E+00	4.07E-05	2.00E-03	3.75E-07	1.94E-03	cellular localization	P
GO:0051647	10	9.18E-02	1.00E+00	2.09E-01	1.00E+00	2.86E-01	1.00E+00	3.16E-01	1.00E+00	3.79E-02	1.00E+00	1.31E-01	1.00E+00	1.63E-01	1.00E+00	3.04E-01	1.00E+00	nucleus localization	P
GO:0051649	789	1.43E-15	0.00E+00	8.50E-23	0.00E+00	5.23E-11	0.00E+00	3.12E-18	0.00E+00	4.25E-11	0.00E+00	1.30E-13	0.00E+00	8.37E-05	2.00E-03	1.79E-07	0.00E+00	establishment of cellular localization	P
GO:0051656	19	4.23E-02	1.00E+00	5.27E-03	5.59E-01	7.07E-02	1.00E+00	1.11E-02	3.78E-01	1.11E-02	4.14E-01	2.58E-02	1.00E+00	5.68E-01	1.00E+00	1.27E-02	9.40E-01	establishment of organelle localization	P
GO:0051668	10	1.72E-02	9.83E-01	4.06E-01	1.00E+00	1.46E-01	1.00E+00	3.52E-01	1.00E+00	1.03E-01	1.00E+00	3.92E-01	1.00E+00	1.17E-01	1.00E+00	6.05E-01	1.00E+00	localization within membrane	P
GO:0051674	433	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.98E-01	1.00E+00	9.99E-01	1.00E+00	1.00E+00	1.00E+00	6.34E-01	1.00E+00	9.10E-01	1.00E+00	localization of cell	P
GO:0051693	18	5.08E-02	1.00E+00	1.73E-01	1.00E+00	1.77E-01	1.00E+00	4.73E-01	1.00E+00	1.56E-01	1.00E+00	2.28E-01	1.00E+00	7.44E-03	2.01E-01	5.52E-02	1.00E+00	actin filament capping	P
GO:0051701	13	3.63E-01	1.00E+00	6.44E-01	1.00E+00	5.98E-01	1.00E+00	9.72E-01	1.00E+00	4.44E-01	1.00E+00	9.70E-01	1.00E+00	8.57E-02	1.00E+00	1.24E-01	1.00E+00	interaction with host	P
GO:0051704	136	9.22E-01	1.00E+00	1.00E+00	1.00E+00	7.26E-01	1.00E+00	9.99E-01	1.00E+00	9.50E-01	1.00E+00	1.00E+00	1.00E+00	7.67E-01	1.00E+00	7.49E-01	1.00E+00	interaction between organisms	P
GO:0051705	33	9.89E-01	1.00E+00	1.00E+00	1.00E+00	9.95E-01	1.00E+00	9.97E-01	1.00E+00	6.60E-01	1.00E+00	1.00E+00	1.00E+00	9.67E-01	1.00E+00	9.99E-01	1.00E+00	behavioral interaction between organisms	P
GO:0051706	48	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.91E-01	1.00E+00	9.98E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.90E-01	1.00E+00	7.24E-01	1.00E+00	physiological interaction between organisms	P
GO:0051707	160	4.24E-01	1.00E+00	9.95E-01	1.00E+00	7.71E-01	1.00E+00	7.17E-01	1.00E+00	7.51E-01	1.00E+00	9.92E-01	1.00E+00	3.06E-02	7.53E-01	1.00E+00	1.00E+00	response to other organism	P
GO:0051716	24	1.21E-01	1.00E+00	2.30E-01	1.00E+00	1.14E-01	1.00E+00	5.18E-02	1.00E+00	2.80E-01	1.00E+00	7.05E-01	1.00E+00	2.52E-01	1.00E+00	3.47E-01	1.00E+00	cellular response to stimulus	P
GO:0051726	291	2.37E-03	1.02E-01	9.73E-04	7.30E-02	2.20E-03	1.18E-01	5.21E-05	5.41E-03	6.10E-03	1.65E-01	1.40E-02	1.00E+00	2.85E-01	1.00E+00	3.56E-01	1.00E+00	regulation of cell cycle	P
GO:0051789	57	2.72E-03	1.39E-01	5.37E-01	1.00E+00	1.12E-02	4.74E-01	2.48E-01	1.00E+00	1.73E-02	7.19E-01	6.04E-01	1.00E+00	3.30E-02	7.53E-01	9.47E-01	1.00E+00	response to protein stimulus	P
GO:0051869	1127	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.68E-01	1.00E+00	9.44E-01	1.00E+00	physiological response to stimulus	P
GO:0051881	11	6.21E-02	1.00E+00	1.42E-01	1.00E+00	1.16E-01	1.00E+00	8.90E-02	1.00E+00	2.86E-01	1.00E+00	1.50E-01	1.00E+00	5.55E-02	1.00E+00	2.45E-01	1.00E+00	regulation of mitochondrial membrane poter	P
GO:0051899	13	1.76E-01	1.00E+00	6.64E-01	1.00E+00	2.16E-01	1.00E+00	6.62E-01	1.00E+00	3.81E-01	1.00E+00	4.92E-01	1.00E+00	1.33E-01	1.00E+00	6.47E-01	1.00E+00	membrane depolarization	P
GO:0051924	27	2.69E-01	1.00E+00	9.30E-01	1.00E+00	6.67E-01	1.00E+00	2.96E-01	1.00E+00	6.56E-01	1.00E+00	1.00E+00	1.00E+00	2.41E-02	5.60E-01	6.15E-01	1.00E+00	regulation of calcium ion transport	P
GO:0051966	12	9.99E-01	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	1.00E+00	9.97E-01	1.00E+00	1.00E+00	1.00E+00	9.82E-01	1.00E+00	9.66E-01	1.00E+00	regulation of synaptic transmission, glutama	P
GO:0051969	70	8.80E-01	1.00E+00	9.97E-01	1.00E+00	9.18E-01	1.00E+00	9.16E-01	1.00E+00	7.98E-01	1.00E+00	1.00E+00	1.00E+00	7.25E-01	1.00E+00	8.74E-01	1.00E+00	regulation of transmission of nerve impulse	P
GO:0051970	11	4.07E-01	1.00E+00	1.00E+00	1.00E+00	9.05E-01	1.00E+00	1.00E+00	1.00E+00	1.92E-01	1.00E+00	1.00E+00	1.00E+00	2.31E-01	1.00E+00	6.75E-01	1.00E+00	negative regulation of transmission of nerve	P
GO:0051971	15	1.00E+00	1.00E+00	9.67E-01	1.00E+00	1.00E+00	1.00E+00	6.69E-01	1.00E+00	9.93E-01	1.00E+00	9.62E-01	1.00E+00	1.00E+00	1.00E+00	8.95E-01	1.00E+00	positive regulation of transmission of nerve	P
GO:0055001	19	5.10E-01	1.00E+00	5.82E-01	1.00E+00	3.65E-01	1.00E+00	2.75E-01	1.00E+00	9.99E-01	1.00E+00	7.72E-01	1.00E+00	3.14E-01	1.00E+00	8.06E-01	1.00E+00	muscle cell development	P
GO:0055002	18	4.64E-01	1.00E+00	5.20E-01	1.00E+00	3.38E-01	1.00E+00	2.43E-01	1.00E+00	9.99E-01	1.00E+00	7.46E-01	1.00E+00	3.11E-01	1.00E+00	7.42E-01	1.00E+00	striated muscle cell development	P
GO:0055007	13	4.38E-01	1.00E+00	8.95E-01	1.00E+00	2.11E-01	1.00E+00	8.51E-01	1.00E+00	4.66E-01	1.00E+00	6.06E-01	1.00E+00	5.63E-01	1.00E+00	9.62E-01	1.00E+00	cardiac muscle cell differentiation	P
GO:0055008	15	6.63E-01	1.00E+00	1.00E+00	1.00E+00	1.98E-01	1.00E+00	9.70E-01	1.00E+00	7.66E-01	1.00E+00	1.00E+00	1.00E+00	6.78E-01	1.00E+00	9.99E-01	1.00E+00	cardiac muscle morphogensis	P
GO:0055010	13	4.83E-01	1.00E+00	1.00E+00	1.00E+00	1.21E-01	1.00E+00	1.00E+00	1.00E+00	6.50E-01	1.00E+00	1.00E+00	1.00E+00	5.31E-01	1.00E+00	1.00E+00	1.00E+00	ventricular cardiac muscle morphogenesis	P