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| |  | | --- | | The mission of the PANTHER knowledgebase is to support biomedical and other research by providing **comprehensive information about the evolution of protein-coding gene families**, particularly protein phylogeny, function and genetic variation impacting that function. [Learn more](http://pantherdb.org/about.jsp) | | | | | | | | | |
| **PANTHER selected as a** [**Global Core Biodata Resource**](https://globalbiodata.org/scientific-activities/global-core-biodata-resources)**.** [**Click**](http://pantherdb.org/news/news20221215.jsp) **for more details.** |  |  |  |  |  |  |  |
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|  | Current Release: [**PANTHER 17.0**](http://pantherdb.org/news/news20220223.jsp)  |  [**15,619**](http://pantherdb.org/panther/index.jsp) family phylogenetic trees  |  [**143**](http://pantherdb.org/panther/summaryStats.jsp) species  |  [News](http://pantherdb.org/news/news20221215.jsp)   [Whole genome function views](http://pantherdb.org/servlet/GenomeFunctionChartServlet?chartType=1&listType=1&annotType=5&species=Homo%20sapiens) |

Analysis Summary: Please report in publication [Tips](javascript:;)

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| |  | | --- | | **Analysis Type:** PANTHER Overrepresentation Test (Released 20221013) | |  | |  | | **Annotation Version and Release Date:** GO Ontology database DOI: 10.5281/zenodo.6799722 Released 2022-07-01 | |  | | |  |  |  |  | | --- | --- | --- | --- | | **Analyzed List:** | |  | | --- | | upload\_1 (Homo sapiens) | | [Change](http://pantherdb.org/tools/uploadFiles.jsp) | |  | | | | **Reference List:** | |  | | --- | | Homo sapiens (all genes in database) | | [Change](javascript:uploadRefFile();) | | | |  |  | | **Annotation Data Set:** | | |

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| |  |  | | --- | --- | | [Tips](javascript:;) | | |  |  | | **Test Type:** Fisher's Exact   Binomial | | | |  |  |  | | **Correction:** Calculate False Discovery Rate   Use the Bonferroni correction for multiple testing  [Tips](javascript:;)   No correction | | | |

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|  | Reference list | upload\_1 |
| Uniquely Mapped IDS: | [20589](http://pantherdb.org/tools/gxIdsList.do?reflist=1) out of 20589 | [762](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 1328 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [677](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [678](http://pantherdb.org/tools/multipleMap.jsp?&listName=upload_1) |

Export  [Table](http://pantherdb.org/tools/compareToRefListTxt.jsp?sortOrder=-1&sortList=upload_1&sortField=hierarchy)  [XML with user input ids](http://pantherdb.org/tools/exportCompareToRefList.jsp?sortOrder=-1&sortList=upload_1&sortField=hierarchy&format=xml)  [JSON with user input ids](http://pantherdb.org/tools/exportCompareToRefList.jsp?sortOrder=-1&sortList=upload_1&sortField=hierarchy&format=json)   
  
Displaying only results for FDR P < 0.05, [click here to display all results](http://pantherdb.org/tools/compareToRefList.jsp?&showAll=true)

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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| |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | |  | [Homo sapiens](http://pantherdb.org/tools/gxIdsList.do?reflist=1) (REF) | [upload\_1](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) ( [Hierarchy](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1)  NEW! [Tips](javascript:;)) | | | | | | | [GO biological process complete](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=categories) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=Homo%20sapiens) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=num) | [expected](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=exp) | [Fold Enrichment](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=foldEnrich) | [+/-](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=rep) | [raw P value](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=pval) | [FDR](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=fdr) | | [positive regulation of mitochondrial DNA replication](http://amigo.geneontology.org/amigo/term/GO:0090297) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090297&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090297&list=upload_1&organism=Homo%20sapiens) | .19 | 15.50 | + | 3.86E-03 | 4.42E-02 | | [positive regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0045740) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045740&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045740&list=upload_1&organism=Homo%20sapiens) | 2.58 | 3.88 | + | 7.15E-04 | 1.13E-02 | | [positive regulation of DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051054) | [305](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 19.67 | 2.69 | + | 1.65E-09 | 8.82E-08 | | [positive regulation of nucleobase-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045935) | [2058](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&reflist=1) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 132.74 | 2.06 | + | 4.53E-28 | 1.78E-25 | | [positive regulation of nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051173) | [3174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&reflist=1) | [399](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 204.72 | 1.95 | + | 4.20E-38 | 6.59E-35 | | [positive regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0009893) | [3858](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&reflist=1) | [463](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 248.84 | 1.86 | + | 8.79E-41 | 1.97E-37 | | [positive regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0048518) | [6304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&reflist=1) | [665](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 406.61 | 1.64 | + | 3.85E-46 | 3.02E-42 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [971](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 761.49 | 1.28 | + | 5.95E-31 | 2.83E-28 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [1022](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 809.09 | 1.26 | + | 1.94E-33 | 1.45E-30 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [659](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 435.64 | 1.51 | + | 2.13E-34 | 1.97E-31 | | [regulation of nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051171) | [5709](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&reflist=1) | [581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 368.23 | 1.58 | + | 2.17E-33 | 1.54E-30 | | [positive regulation of cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0031325) | [3122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&reflist=1) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 201.37 | 1.94 | + | 8.12E-37 | 1.06E-33 | | [positive regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0048522) | [5670](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&reflist=1) | [617](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 365.72 | 1.69 | + | 1.79E-45 | 9.36E-42 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [942](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 721.57 | 1.31 | + | 3.58E-33 | 2.25E-30 | | [regulation of cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0031323) | [5647](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&reflist=1) | [572](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 364.23 | 1.57 | + | 4.25E-32 | 2.15E-29 | | [regulation of nucleobase-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019219) | [4067](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&reflist=1) | [414](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 262.32 | 1.58 | + | 1.84E-21 | 3.95E-19 | | [regulation of primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0080090) | [5872](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&reflist=1) | [593](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 378.75 | 1.57 | + | 1.64E-33 | 1.29E-30 | | [positive regulation of macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010604) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&reflist=1) | [433](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 228.46 | 1.90 | + | 2.99E-39 | 5.86E-36 | | [regulation of macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0060255) | [6214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&reflist=1) | [616](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 400.81 | 1.54 | + | 5.18E-33 | 3.01E-30 | | [regulation of DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051052) | [541](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 34.89 | 2.29 | + | 1.89E-10 | 1.12E-08 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 8.77 | 2.17 | + | 3.35E-03 | 3.94E-02 | | [positive regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010822) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010822&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010822&list=upload_1&organism=Homo%20sapiens) | 4.90 | 3.47 | + | 3.87E-05 | 9.44E-04 | | [regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010821) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&list=upload_1&organism=Homo%20sapiens) | 9.80 | 3.67 | + | 6.47E-10 | 3.66E-08 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 76.69 | 2.11 | + | 2.99E-17 | 4.07E-15 | | [regulation of cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0051128) | [2364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&reflist=1) | [274](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 152.48 | 1.80 | + | 3.79E-20 | 6.91E-18 | | [positive regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0010638) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&list=upload_1&organism=Homo%20sapiens) | 32.77 | 2.35 | + | 1.68E-10 | 1.02E-08 | | [positive regulation of cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0051130) | [1054](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 67.98 | 2.03 | + | 1.22E-13 | 1.05E-11 | | [regulation of centriole-centriole cohesion](http://amigo.geneontology.org/amigo/term/GO:0030997) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030997&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030997&list=upload_1&organism=Homo%20sapiens) | .19 | 15.50 | + | 3.86E-03 | 4.42E-02 | | [microtubule-based process](http://amigo.geneontology.org/amigo/term/GO:0007017) | [809](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&list=upload_1&organism=Homo%20sapiens) | 52.18 | 1.71 | + | 4.22E-06 | 1.29E-04 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [1201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 970.34 | 1.24 | + | 3.25E-53 | 5.09E-49 | | [microtubule cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0000226) | [547](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000226&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000226&list=upload_1&organism=Homo%20sapiens) | 35.28 | 1.90 | + | 2.87E-06 | 9.07E-05 | | [cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0007010) | [1240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&reflist=1) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&list=upload_1&organism=Homo%20sapiens) | 79.98 | 1.63 | + | 3.05E-07 | 1.17E-05 | | [organelle organization](http://amigo.geneontology.org/amigo/term/GO:0006996) | [3026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&reflist=1) | [307](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&list=upload_1&organism=Homo%20sapiens) | 195.18 | 1.57 | + | 4.13E-15 | 4.35E-13 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [516](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 356.24 | 1.45 | + | 3.32E-20 | 6.19E-18 | | [cellular component organization or biogenesis](http://amigo.geneontology.org/amigo/term/GO:0071840) | [5727](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&reflist=1) | [528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 369.39 | 1.43 | + | 1.48E-19 | 2.55E-17 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 54.24 | 1.62 | + | 3.04E-05 | 7.61E-04 | | [cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007049) | [1249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&reflist=1) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&list=upload_1&organism=Homo%20sapiens) | 80.56 | 1.80 | + | 1.16E-10 | 7.12E-09 | | [regulation of cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0010564) | [715](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&reflist=1) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 46.12 | 2.12 | + | 5.81E-11 | 3.77E-09 | | [regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051726) | [1122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&reflist=1) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 72.37 | 2.02 | + | 3.70E-14 | 3.37E-12 | | [protein targeting to lysosome involved in chaperone-mediated autophagy](http://amigo.geneontology.org/amigo/term/GO:0061740) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061740&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061740&list=upload_1&organism=Homo%20sapiens) | .19 | 15.50 | + | 3.86E-03 | 4.41E-02 | | [chaperone-mediated autophagy](http://amigo.geneontology.org/amigo/term/GO:0061684) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061684&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061684&list=upload_1&organism=Homo%20sapiens) | .52 | 11.63 | + | 9.63E-05 | 2.07E-03 | | [cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044248) | [1625](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&reflist=1) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&list=upload_1&organism=Homo%20sapiens) | 104.81 | 1.68 | + | 1.23E-10 | 7.50E-09 | | [catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009056) | [1974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&reflist=1) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&list=upload_1&organism=Homo%20sapiens) | 127.32 | 1.61 | + | 9.45E-11 | 5.90E-09 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [753](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 524.45 | 1.44 | + | 1.88E-34 | 1.84E-31 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [657](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 426.09 | 1.54 | + | 8.84E-37 | 1.07E-33 | | [protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0030163) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&list=upload_1&organism=Homo%20sapiens) | 48.76 | 1.97 | + | 4.51E-09 | 2.27E-07 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 252.84 | 1.62 | + | 2.98E-23 | 8.07E-21 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [594](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 383.20 | 1.55 | + | 2.51E-32 | 1.36E-29 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [723](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 496.46 | 1.46 | + | 3.80E-34 | 3.31E-31 | | [organonitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901564) | [5013](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&reflist=1) | [491](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 323.34 | 1.52 | + | 4.56E-23 | 1.21E-20 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [646](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 432.80 | 1.49 | + | 1.28E-31 | 6.26E-29 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [689](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 466.21 | 1.48 | + | 1.51E-33 | 1.25E-30 | | [organonitrogen compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901565) | [1112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&reflist=1) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&list=upload_1&organism=Homo%20sapiens) | 71.72 | 1.77 | + | 4.23E-09 | 2.15E-07 | | [organic substance catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901575) | [1679](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&reflist=1) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&list=upload_1&organism=Homo%20sapiens) | 108.30 | 1.69 | + | 2.98E-11 | 2.02E-09 | | [macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009057) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&reflist=1) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&list=upload_1&organism=Homo%20sapiens) | 63.79 | 2.05 | + | 2.60E-13 | 2.12E-11 | | [protein targeting to lysosome](http://amigo.geneontology.org/amigo/term/GO:0006622) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006622&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006622&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.13 | + | 1.70E-03 | 2.32E-02 | | [protein targeting](http://amigo.geneontology.org/amigo/term/GO:0006605) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006605&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006605&list=upload_1&organism=Homo%20sapiens) | 15.67 | 2.30 | + | 1.97E-05 | 5.19E-04 | | [intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0006886) | [682](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&list=upload_1&organism=Homo%20sapiens) | 43.99 | 2.09 | + | 4.76E-10 | 2.71E-08 | | [intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0046907) | [1360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&reflist=1) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&list=upload_1&organism=Homo%20sapiens) | 87.72 | 1.86 | + | 5.72E-13 | 4.58E-11 | | [establishment of localization in cell](http://amigo.geneontology.org/amigo/term/GO:0051649) | [1752](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&reflist=1) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&list=upload_1&organism=Homo%20sapiens) | 113.00 | 1.85 | + | 1.93E-16 | 2.39E-14 | | [cellular localization](http://amigo.geneontology.org/amigo/term/GO:0051641) | [2655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&reflist=1) | [298](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&list=upload_1&organism=Homo%20sapiens) | 171.25 | 1.74 | + | 3.27E-20 | 6.17E-18 | | [localization](http://amigo.geneontology.org/amigo/term/GO:0051179) | [4566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&reflist=1) | [442](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&list=upload_1&organism=Homo%20sapiens) | 294.51 | 1.50 | + | 3.36E-19 | 5.48E-17 | | [establishment of localization](http://amigo.geneontology.org/amigo/term/GO:0051234) | [3997](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&reflist=1) | [381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&list=upload_1&organism=Homo%20sapiens) | 257.81 | 1.48 | + | 3.79E-15 | 4.02E-13 | | [transport](http://amigo.geneontology.org/amigo/term/GO:0006810) | [3840](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&reflist=1) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&list=upload_1&organism=Homo%20sapiens) | 247.68 | 1.48 | + | 1.40E-14 | 1.34E-12 | | [protein localization](http://amigo.geneontology.org/amigo/term/GO:0008104) | [1919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&reflist=1) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&list=upload_1&organism=Homo%20sapiens) | 123.78 | 1.75 | + | 8.81E-15 | 8.63E-13 | | [cellular macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0070727) | [1925](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&reflist=1) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&list=upload_1&organism=Homo%20sapiens) | 124.16 | 1.75 | + | 1.37E-14 | 1.32E-12 | | [macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0033036) | [2345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&reflist=1) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&list=upload_1&organism=Homo%20sapiens) | 151.25 | 1.67 | + | 5.52E-15 | 5.66E-13 | | [protein transport](http://amigo.geneontology.org/amigo/term/GO:0015031) | [1179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&list=upload_1&organism=Homo%20sapiens) | 76.05 | 1.83 | + | 8.71E-11 | 5.48E-09 | | [establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:0045184) | [1267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&reflist=1) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&list=upload_1&organism=Homo%20sapiens) | 81.72 | 1.79 | + | 1.53E-10 | 9.29E-09 | | [nitrogen compound transport](http://amigo.geneontology.org/amigo/term/GO:0071705) | [1589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&reflist=1) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&list=upload_1&organism=Homo%20sapiens) | 102.49 | 1.75 | + | 4.45E-12 | 3.36E-10 | | [organic substance transport](http://amigo.geneontology.org/amigo/term/GO:0071702) | [1964](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&reflist=1) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&list=upload_1&organism=Homo%20sapiens) | 126.68 | 1.58 | + | 7.45E-10 | 4.16E-08 | | [establishment of protein localization to vacuole](http://amigo.geneontology.org/amigo/term/GO:0072666) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072666&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072666&list=upload_1&organism=Homo%20sapiens) | 3.93 | 2.80 | + | 3.88E-03 | 4.42E-02 | | [establishment of protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0072594) | [334](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&list=upload_1&organism=Homo%20sapiens) | 21.54 | 2.65 | + | 6.73E-10 | 3.80E-08 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 44.76 | 2.28 | + | 6.27E-13 | 4.99E-11 | | [protein localization to vacuole](http://amigo.geneontology.org/amigo/term/GO:0072665) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072665&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072665&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.62 | + | 2.95E-03 | 3.58E-02 | | [protein localization to lysosome](http://amigo.geneontology.org/amigo/term/GO:0061462) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061462&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061462&list=upload_1&organism=Homo%20sapiens) | 3.23 | 3.72 | + | 2.99E-04 | 5.47E-03 | | [cellular response to actinomycin D](http://amigo.geneontology.org/amigo/term/GO:0072717) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072717&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072717&list=upload_1&organism=Homo%20sapiens) | .26 | 15.50 | + | 7.71E-04 | 1.20E-02 | | [cellular response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901653) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&list=upload_1&organism=Homo%20sapiens) | 19.54 | 2.97 | + | 9.09E-12 | 6.51E-10 | | [cellular response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0071417) | [578](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 37.28 | 2.47 | + | 1.83E-13 | 1.53E-11 | | [cellular response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901699) | [641](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 41.34 | 2.42 | + | 3.98E-14 | 3.59E-12 | | [cellular response to chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0070887) | [2616](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&reflist=1) | [347](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 168.73 | 2.06 | + | 1.01E-36 | 1.14E-33 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [631](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 423.70 | 1.49 | + | 3.14E-30 | 1.37E-27 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 529.48 | 1.42 | + | 2.89E-33 | 1.97E-30 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [453](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 261.87 | 1.73 | + | 2.64E-32 | 1.38E-29 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 68.50 | 2.36 | + | 1.29E-21 | 2.85E-19 | | [response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0010243) | [968](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&reflist=1) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 62.44 | 2.42 | + | 6.21E-21 | 1.22E-18 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 174.41 | 2.12 | + | 8.64E-42 | 3.39E-38 | | [cellular response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0071310) | [2026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&reflist=1) | [285](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 130.68 | 2.18 | + | 2.92E-33 | 1.91E-30 | | [cellular response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0071495) | [1107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&reflist=1) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 71.40 | 2.38 | + | 5.87E-23 | 1.53E-20 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 88.43 | 2.28 | + | 2.74E-25 | 8.27E-23 | | [response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901652) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&list=upload_1&organism=Homo%20sapiens) | 28.70 | 2.58 | + | 8.77E-12 | 6.34E-10 | | [response to oxygen-containing compound](http://amigo.geneontology.org/amigo/term/GO:1901700) | [1551](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&reflist=1) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 100.04 | 2.26 | + | 7.69E-28 | 2.94E-25 | | [cellular response to oxygen-containing compound](http://amigo.geneontology.org/amigo/term/GO:1901701) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&reflist=1) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&list=upload_1&organism=Homo%20sapiens) | 68.31 | 2.34 | + | 4.65E-21 | 9.22E-19 | | [response to actinomycin D](http://amigo.geneontology.org/amigo/term/GO:0072716) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072716&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072716&list=upload_1&organism=Homo%20sapiens) | .32 | 12.40 | + | 1.32E-03 | 1.87E-02 | | [response to antibiotic](http://amigo.geneontology.org/amigo/term/GO:0046677) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046677&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046677&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.48 | + | 8.53E-04 | 1.30E-02 | | [cellular response to antibiotic](http://amigo.geneontology.org/amigo/term/GO:0071236) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071236&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071236&list=upload_1&organism=Homo%20sapiens) | .90 | 7.75 | + | 1.62E-04 | 3.28E-03 | | [positive regulation of autophagy of mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903599) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903599&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903599&list=upload_1&organism=Homo%20sapiens) | .84 | 10.73 | + | 2.59E-06 | 8.37E-05 | | [positive regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010508) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010508&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010508&list=upload_1&organism=Homo%20sapiens) | 9.42 | 2.12 | + | 2.94E-03 | 3.58E-02 | | [positive regulation of cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0031331) | [411](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031331&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031331&list=upload_1&organism=Homo%20sapiens) | 26.51 | 2.15 | + | 6.07E-07 | 2.25E-05 | | [positive regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009896) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009896&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009896&list=upload_1&organism=Homo%20sapiens) | 33.09 | 1.99 | + | 8.44E-07 | 3.04E-05 | | [regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009894) | [987](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&list=upload_1&organism=Homo%20sapiens) | 63.66 | 2.17 | + | 1.01E-15 | 1.14E-13 | | [regulation of cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0031329) | [786](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&list=upload_1&organism=Homo%20sapiens) | 50.70 | 2.23 | + | 1.09E-13 | 9.48E-12 | | [regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010506) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&list=upload_1&organism=Homo%20sapiens) | 22.25 | 2.11 | + | 8.36E-06 | 2.39E-04 | | [regulation of autophagy of mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903146) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903146&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903146&list=upload_1&organism=Homo%20sapiens) | 2.32 | 6.03 | + | 1.00E-06 | 3.55E-05 | | [response to indole-3-methanol](http://amigo.geneontology.org/amigo/term/GO:0071680) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071680&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071680&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.75E-02 | | [response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097305) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&list=upload_1&organism=Homo%20sapiens) | 16.38 | 2.01 | + | 4.05E-04 | 7.04E-03 | | [response to organic cyclic compound](http://amigo.geneontology.org/amigo/term/GO:0014070) | [879](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&reflist=1) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 56.70 | 2.40 | + | 9.83E-19 | 1.50E-16 | | [negative regulation of glucocorticoid receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2000323) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000323&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000323&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.74E-02 | | [negative regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033144) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&list=upload_1&organism=Homo%20sapiens) | 2.39 | 3.77 | + | 1.54E-03 | 2.13E-02 | | [negative regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009968) | [1257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&reflist=1) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 81.08 | 1.90 | + | 4.76E-13 | 3.83E-11 | | [regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009966) | [2989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&reflist=1) | [347](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 192.79 | 1.80 | + | 2.67E-26 | 8.37E-24 | | [regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048583) | [4034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&reflist=1) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 260.19 | 1.73 | + | 1.99E-32 | 1.11E-29 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 217.30 | 1.77 | + | 4.31E-28 | 1.73E-25 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 218.08 | 1.76 | + | 7.79E-28 | 2.91E-25 | | [negative regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010648) | [1357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 87.53 | 1.89 | + | 1.08E-13 | 9.43E-12 | | [negative regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0048523) | [4732](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&reflist=1) | [515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 305.22 | 1.69 | + | 2.05E-35 | 2.15E-32 | | [negative regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0048519) | [5314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&reflist=1) | [569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 342.76 | 1.66 | + | 1.36E-38 | 2.37E-35 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 87.91 | 1.89 | + | 7.92E-14 | 7.06E-12 | | [negative regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048585) | [1620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&reflist=1) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 104.49 | 1.96 | + | 1.08E-18 | 1.61E-16 | | [regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033143) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&list=upload_1&organism=Homo%20sapiens) | 4.71 | 3.19 | + | 2.44E-04 | 4.62E-03 | | [regulation of glucocorticoid receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2000322) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000322&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000322&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.75E-02 | | [cellular response to progesterone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071393) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071393&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071393&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.74E-02 | | [cellular response to steroid hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071383) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 9.80 | 4.18 | + | 1.30E-12 | 1.02E-10 | | [cellular response to organic cyclic compound](http://amigo.geneontology.org/amigo/term/GO:0071407) | [514](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 33.15 | 2.81 | + | 1.13E-16 | 1.48E-14 | | [cellular response to hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0032870) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 31.54 | 2.82 | + | 4.49E-16 | 5.29E-14 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 49.47 | 2.43 | + | 7.37E-17 | 9.80E-15 | | [cellular response to lipid](http://amigo.geneontology.org/amigo/term/GO:0071396) | [519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&list=upload_1&organism=Homo%20sapiens) | 33.48 | 2.48 | + | 1.95E-12 | 1.50E-10 | | [response to lipid](http://amigo.geneontology.org/amigo/term/GO:0033993) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&reflist=1) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&list=upload_1&organism=Homo%20sapiens) | 54.37 | 2.17 | + | 1.47E-13 | 1.24E-11 | | [response to steroid hormone](http://amigo.geneontology.org/amigo/term/GO:0048545) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 18.32 | 2.78 | + | 1.83E-09 | 9.70E-08 | | [cellular response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901655) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901655&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901655&list=upload_1&organism=Homo%20sapiens) | 6.84 | 3.51 | + | 8.94E-07 | 3.20E-05 | | [response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901654) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&list=upload_1&organism=Homo%20sapiens) | 13.29 | 2.78 | + | 2.13E-07 | 8.61E-06 | | [response to progesterone](http://amigo.geneontology.org/amigo/term/GO:0032570) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032570&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032570&list=upload_1&organism=Homo%20sapiens) | 2.52 | 3.58 | + | 2.10E-03 | 2.74E-02 | | [aggresome assembly](http://amigo.geneontology.org/amigo/term/GO:0070842) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070842&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070842&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.74E-02 | | [inclusion body assembly](http://amigo.geneontology.org/amigo/term/GO:0070841) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070841&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070841&list=upload_1&organism=Homo%20sapiens) | .45 | 11.07 | + | 4.48E-04 | 7.67E-03 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 154.41 | 1.68 | + | 8.32E-16 | 9.74E-14 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 169.83 | 1.62 | + | 7.83E-15 | 7.72E-13 | | [regulation of mitochondrial ATP synthesis coupled electron transport](http://amigo.geneontology.org/amigo/term/GO:1905446) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905446&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905446&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.74E-02 | | [regulation of generation of precursor metabolites and energy](http://amigo.geneontology.org/amigo/term/GO:0043467) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043467&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043467&list=upload_1&organism=Homo%20sapiens) | 8.51 | 2.94 | + | 8.60E-06 | 2.45E-04 | | [response to glycoside](http://amigo.geneontology.org/amigo/term/GO:1903416) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903416&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903416&list=upload_1&organism=Homo%20sapiens) | .39 | 10.34 | + | 2.10E-03 | 2.73E-02 | | [telomeric D-loop disassembly](http://amigo.geneontology.org/amigo/term/GO:0061820) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061820&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061820&list=upload_1&organism=Homo%20sapiens) | .52 | 9.69 | + | 6.92E-04 | 1.10E-02 | | [telomeric loop disassembly](http://amigo.geneontology.org/amigo/term/GO:0090657) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090657&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090657&list=upload_1&organism=Homo%20sapiens) | .65 | 9.30 | + | 2.31E-04 | 4.41E-03 | | [telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0000723) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&list=upload_1&organism=Homo%20sapiens) | 6.06 | 3.46 | + | 5.06E-06 | 1.52E-04 | | [telomere organization](http://amigo.geneontology.org/amigo/term/GO:0032200) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&list=upload_1&organism=Homo%20sapiens) | 6.64 | 3.46 | + | 1.84E-06 | 6.15E-05 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 28.64 | 2.27 | + | 1.43E-08 | 6.78E-07 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 51.21 | 1.95 | + | 2.75E-09 | 1.41E-07 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [287](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 162.41 | 1.77 | + | 3.36E-20 | 6.19E-18 | | [nucleic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090304) | [2276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&reflist=1) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 146.80 | 1.68 | + | 7.18E-15 | 7.27E-13 | | [nucleobase-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006139) | [2825](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&reflist=1) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 182.21 | 1.59 | + | 8.99E-15 | 8.70E-13 | | [organic cyclic compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901360) | [3292](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&reflist=1) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 212.34 | 1.56 | + | 4.33E-16 | 5.15E-14 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [305](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 193.44 | 1.58 | + | 4.36E-15 | 4.53E-13 | | [cellular aromatic compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006725) | [3050](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&reflist=1) | [309](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 196.73 | 1.57 | + | 4.82E-15 | 4.98E-13 | | [cellular nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034641) | [3573](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&reflist=1) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 230.46 | 1.60 | + | 9.42E-20 | 1.68E-17 | | [peptidyl-lysine deacetylation](http://amigo.geneontology.org/amigo/term/GO:0034983) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034983&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034983&list=upload_1&organism=Homo%20sapiens) | .52 | 9.69 | + | 6.92E-04 | 1.10E-02 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 56.89 | 1.88 | + | 4.56E-09 | 2.29E-07 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 171.44 | 1.64 | + | 9.31E-16 | 1.08E-13 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [296](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 185.95 | 1.59 | + | 4.16E-15 | 4.35E-13 | | [protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0006476) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&list=upload_1&organism=Homo%20sapiens) | 4.13 | 3.15 | + | 6.81E-04 | 1.09E-02 | | [protein deacylation](http://amigo.geneontology.org/amigo/term/GO:0035601) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&list=upload_1&organism=Homo%20sapiens) | 4.84 | 3.10 | + | 3.14E-04 | 5.68E-03 | | [macromolecule deacylation](http://amigo.geneontology.org/amigo/term/GO:0098732) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&list=upload_1&organism=Homo%20sapiens) | 5.10 | 2.94 | + | 5.09E-04 | 8.48E-03 | | [negative regulation of establishment of protein localization to mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903748) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903748&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903748&list=upload_1&organism=Homo%20sapiens) | .52 | 9.69 | + | 6.92E-04 | 1.10E-02 | | [negative regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:1904950) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904950&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904950&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.29 | + | 2.18E-03 | 2.82E-02 | | [regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:0070201) | [527](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&list=upload_1&organism=Homo%20sapiens) | 33.99 | 2.21 | + | 3.21E-09 | 1.64E-07 | | [regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:0032880) | [850](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&list=upload_1&organism=Homo%20sapiens) | 54.83 | 2.01 | + | 1.07E-10 | 6.61E-09 | | [regulation of cellular localization](http://amigo.geneontology.org/amigo/term/GO:0060341) | [962](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&list=upload_1&organism=Homo%20sapiens) | 62.05 | 1.98 | + | 1.48E-11 | 1.04E-09 | | [regulation of localization](http://amigo.geneontology.org/amigo/term/GO:0032879) | [2104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&reflist=1) | [246](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&list=upload_1&organism=Homo%20sapiens) | 135.71 | 1.81 | + | 2.25E-18 | 3.23E-16 | | [negative regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:1903828) | [196](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903828&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903828&list=upload_1&organism=Homo%20sapiens) | 12.64 | 1.98 | + | 2.56E-03 | 3.22E-02 | | [regulation of establishment of protein localization to mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903747) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903747&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903747&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.95 | + | 1.01E-04 | 2.15E-03 | | [SMAD protein complex assembly](http://amigo.geneontology.org/amigo/term/GO:0007183) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007183&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007183&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.75E-02 | | [enzyme-linked receptor protein signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007167) | [640](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&list=upload_1&organism=Homo%20sapiens) | 41.28 | 1.91 | + | 2.71E-07 | 1.06E-05 | | [cell surface receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007166) | [2174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&reflist=1) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 140.22 | 1.61 | + | 7.63E-12 | 5.59E-10 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 315.21 | 1.36 | + | 7.01E-12 | 5.19E-10 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 337.40 | 1.39 | + | 7.38E-15 | 7.37E-13 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [481](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 344.56 | 1.40 | + | 1.84E-15 | 2.01E-13 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 81.92 | 1.92 | + | 1.60E-13 | 1.34E-11 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 91.78 | 1.91 | + | 7.64E-15 | 7.58E-13 | | [cellular response to nicotine](http://amigo.geneontology.org/amigo/term/GO:0071316) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071316&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071316&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.75E-02 | | [response to nicotine](http://amigo.geneontology.org/amigo/term/GO:0035094) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035094&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035094&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.32E-02 | | [positive regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032075) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032075&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032075&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.75E-02 | | [regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032069) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&list=upload_1&organism=Homo%20sapiens) | 1.42 | 6.34 | + | 6.40E-05 | 1.46E-03 | | [regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051336) | [1020](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&list=upload_1&organism=Homo%20sapiens) | 65.79 | 1.73 | + | 8.85E-08 | 3.77E-06 | | [regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0050790) | [2373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&reflist=1) | [270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 153.06 | 1.76 | + | 7.30E-19 | 1.12E-16 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [356](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 199.56 | 1.78 | + | 1.64E-26 | 5.26E-24 | | [positive regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051345) | [589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&list=upload_1&organism=Homo%20sapiens) | 37.99 | 1.76 | + | 2.81E-05 | 7.13E-04 | | [positive regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0043085) | [1194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&reflist=1) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 77.01 | 1.84 | + | 3.25E-11 | 2.19E-09 | | [positive regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0044093) | [1590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&reflist=1) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 102.56 | 1.95 | + | 5.64E-18 | 7.97E-16 | | [negative regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032074) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032074&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032074&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.74E-02 | | [negative regulation of nucleobase-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045934) | [1562](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&reflist=1) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 100.75 | 1.89 | + | 1.01E-15 | 1.14E-13 | | [negative regulation of nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051172) | [2409](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&reflist=1) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 155.38 | 1.87 | + | 1.04E-23 | 2.86E-21 | | [negative regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0009892) | [2988](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&reflist=1) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 192.73 | 1.82 | + | 3.02E-27 | 1.08E-24 | | [negative regulation of cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0031324) | [2264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&reflist=1) | [270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 146.03 | 1.85 | + | 2.07E-21 | 4.34E-19 | | [negative regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0043086) | [781](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043086&reflist=1) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043086&list=upload_1&organism=Homo%20sapiens) | 50.37 | 1.79 | + | 6.63E-07 | 2.44E-05 | | [negative regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0044092) | [1150](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 74.18 | 1.89 | + | 9.78E-12 | 6.97E-10 | | [macrophage derived foam cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0010742) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010742&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010742&list=upload_1&organism=Homo%20sapiens) | .45 | 8.86 | + | 3.14E-03 | 3.74E-02 | | [foam cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0090077) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090077&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090077&list=upload_1&organism=Homo%20sapiens) | .52 | 7.75 | + | 4.48E-03 | 4.99E-02 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 226.98 | 1.51 | + | 1.88E-14 | 1.78E-12 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 228.46 | 1.51 | + | 6.75E-15 | 6.87E-13 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [537](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 366.17 | 1.47 | + | 1.60E-22 | 4.05E-20 | | [peptidyl-tyrosine autophosphorylation](http://amigo.geneontology.org/amigo/term/GO:0038083) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038083&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038083&list=upload_1&organism=Homo%20sapiens) | 1.16 | 8.61 | + | 3.09E-06 | 9.74E-05 | | [peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018108) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&list=upload_1&organism=Homo%20sapiens) | 10.84 | 3.14 | + | 5.64E-08 | 2.47E-06 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 46.38 | 2.13 | + | 3.82E-11 | 2.56E-09 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 59.21 | 1.91 | + | 7.41E-10 | 4.15E-08 | | [phosphate-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006796) | [1855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&reflist=1) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 119.65 | 1.70 | + | 1.34E-12 | 1.04E-10 | | [phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006793) | [1881](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&reflist=1) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&list=upload_1&organism=Homo%20sapiens) | 121.33 | 1.68 | + | 2.58E-12 | 1.97E-10 | | [peptidyl-tyrosine modification](http://amigo.geneontology.org/amigo/term/GO:0018212) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&list=upload_1&organism=Homo%20sapiens) | 10.97 | 3.10 | + | 7.22E-08 | 3.10E-06 | | [protein autophosphorylation](http://amigo.geneontology.org/amigo/term/GO:0046777) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046777&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046777&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.46 | + | 4.07E-05 | 9.84E-04 | | [RISC complex assembly](http://amigo.geneontology.org/amigo/term/GO:0070922) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070922&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070922&list=upload_1&organism=Homo%20sapiens) | .58 | 8.61 | + | 1.02E-03 | 1.51E-02 | | [gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0031047) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031047&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031047&list=upload_1&organism=Homo%20sapiens) | 6.19 | 2.42 | + | 3.80E-03 | 4.37E-02 | | [negative regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010629) | [902](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&reflist=1) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 58.18 | 2.23 | + | 9.35E-16 | 1.08E-13 | | [negative regulation of macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010605) | [2764](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&reflist=1) | [330](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 178.28 | 1.85 | + | 9.05E-27 | 3.02E-24 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [492](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 313.15 | 1.57 | + | 2.93E-26 | 9.02E-24 | | [ribonucleoprotein complex assembly](http://amigo.geneontology.org/amigo/term/GO:0022618) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.78 | + | 3.29E-07 | 1.25E-05 | | [ribonucleoprotein complex biogenesis](http://amigo.geneontology.org/amigo/term/GO:0022613) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&list=upload_1&organism=Homo%20sapiens) | 28.96 | 1.80 | + | 1.38E-04 | 2.86E-03 | | [ribonucleoprotein complex subunit organization](http://amigo.geneontology.org/amigo/term/GO:0071826) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071826&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071826&list=upload_1&organism=Homo%20sapiens) | 13.48 | 2.74 | + | 2.92E-07 | 1.14E-05 | | [progesterone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0050847) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050847&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050847&list=upload_1&organism=Homo%20sapiens) | .58 | 8.61 | + | 1.02E-03 | 1.51E-02 | | [intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030518) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&list=upload_1&organism=Homo%20sapiens) | 3.61 | 4.15 | + | 1.85E-05 | 4.89E-04 | | [intracellular receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030522) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&list=upload_1&organism=Homo%20sapiens) | 9.55 | 3.25 | + | 1.11E-07 | 4.68E-06 | | [steroid hormone mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0043401) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&list=upload_1&organism=Homo%20sapiens) | 4.97 | 3.62 | + | 1.39E-05 | 3.76E-04 | | [hormone-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0009755) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&list=upload_1&organism=Homo%20sapiens) | 8.45 | 2.60 | + | 2.08E-04 | 4.04E-03 | | [positive regulation of memory T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0043382) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043382&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043382&list=upload_1&organism=Homo%20sapiens) | .58 | 8.61 | + | 1.02E-03 | 1.51E-02 | | [positive regulation of T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045582) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&list=upload_1&organism=Homo%20sapiens) | 7.55 | 2.52 | + | 7.57E-04 | 1.19E-02 | | [positive regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045621) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 8.45 | 2.84 | + | 2.09E-05 | 5.47E-04 | | [regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045619) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 13.55 | 2.95 | + | 1.71E-08 | 8.01E-07 | | [regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902105) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 20.38 | 2.60 | + | 6.39E-09 | 3.19E-07 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 101.98 | 1.99 | + | 4.20E-19 | 6.73E-17 | | [regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0050793) | [2489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&reflist=1) | [293](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 160.54 | 1.83 | + | 1.07E-22 | 2.74E-20 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 25.67 | 2.77 | + | 9.50E-13 | 7.53E-11 | | [regulation of multicellular organismal development](http://amigo.geneontology.org/amigo/term/GO:2000026) | [1383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&reflist=1) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 89.20 | 1.92 | + | 8.93E-15 | 8.70E-13 | | [regulation of multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0051239) | [2750](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&reflist=1) | [328](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 177.38 | 1.85 | + | 1.20E-26 | 3.94E-24 | | [regulation of immune system process](http://amigo.geneontology.org/amigo/term/GO:0002682) | [1520](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&reflist=1) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 98.04 | 1.95 | + | 4.56E-17 | 6.11E-15 | | [regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051249) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&list=upload_1&organism=Homo%20sapiens) | 38.12 | 2.10 | + | 8.12E-09 | 3.99E-07 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 44.12 | 2.06 | + | 1.26E-09 | 6.83E-08 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 47.79 | 2.03 | + | 7.99E-10 | 4.43E-08 | | [positive regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902107) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&list=upload_1&organism=Homo%20sapiens) | 11.80 | 2.71 | + | 3.65E-06 | 1.13E-04 | | [positive regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045597) | [884](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 57.02 | 2.17 | + | 3.51E-14 | 3.22E-12 | | [positive regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0051094) | [1339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051094&reflist=1) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051094&list=upload_1&organism=Homo%20sapiens) | 86.37 | 2.10 | + | 5.41E-19 | 8.49E-17 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 11.80 | 2.71 | + | 3.65E-06 | 1.13E-04 | | [positive regulation of multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0051240) | [1515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&reflist=1) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 97.72 | 2.02 | + | 4.01E-19 | 6.48E-17 | | [positive regulation of immune system process](http://amigo.geneontology.org/amigo/term/GO:0002684) | [967](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 62.37 | 1.94 | + | 6.46E-11 | 4.15E-09 | | [positive regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051251) | [421](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051251&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051251&list=upload_1&organism=Homo%20sapiens) | 27.15 | 2.06 | + | 2.23E-06 | 7.31E-05 | | [positive regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002696) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&list=upload_1&organism=Homo%20sapiens) | 30.25 | 2.12 | + | 1.69E-07 | 6.96E-06 | | [positive regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050867) | [486](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&list=upload_1&organism=Homo%20sapiens) | 31.35 | 2.07 | + | 2.69E-07 | 1.06E-05 | | [positive regulation of T cell activation](http://amigo.geneontology.org/amigo/term/GO:0050870) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 16.32 | 2.51 | + | 7.27E-07 | 2.65E-05 | | [positive regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903039) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 17.80 | 2.70 | + | 1.00E-08 | 4.86E-07 | | [regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903037) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&list=upload_1&organism=Homo%20sapiens) | 23.80 | 2.35 | + | 4.51E-08 | 2.03E-06 | | [regulation of cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0022407) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&list=upload_1&organism=Homo%20sapiens) | 31.22 | 2.15 | + | 5.58E-08 | 2.45E-06 | | [regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0030155) | [789](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&reflist=1) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 50.89 | 2.12 | + | 8.26E-12 | 6.02E-10 | | [positive regulation of cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0022409) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 20.90 | 2.63 | + | 1.58E-09 | 8.51E-08 | | [positive regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0045785) | [488](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 31.48 | 2.41 | + | 7.20E-11 | 4.57E-09 | | [regulation of T cell activation](http://amigo.geneontology.org/amigo/term/GO:0050863) | [377](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&list=upload_1&organism=Homo%20sapiens) | 24.32 | 2.39 | + | 1.85E-08 | 8.62E-07 | | [regulation of T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045580) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&list=upload_1&organism=Homo%20sapiens) | 11.55 | 2.77 | + | 1.51E-06 | 5.11E-05 | | [regulation of memory T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0043380) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043380&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043380&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.72E-03 | 3.37E-02 | | [regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050776) | [935](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&list=upload_1&organism=Homo%20sapiens) | 60.31 | 1.99 | + | 1.98E-11 | 1.38E-09 | | [regulation of immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002697) | [386](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002697&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002697&list=upload_1&organism=Homo%20sapiens) | 24.90 | 1.93 | + | 5.97E-05 | 1.38E-03 | | [positive regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050778) | [590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050778&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050778&list=upload_1&organism=Homo%20sapiens) | 38.06 | 1.89 | + | 1.30E-06 | 4.50E-05 | | [positive regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048584) | [2223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&reflist=1) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 143.38 | 1.80 | + | 5.67E-19 | 8.80E-17 | | [positive regulation of immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002699) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002699&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002699&list=upload_1&organism=Homo%20sapiens) | 17.22 | 1.86 | + | 2.00E-03 | 2.66E-02 | | [positive regulation by host of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0044829) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044829&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044829&list=upload_1&organism=Homo%20sapiens) | .65 | 7.75 | + | 1.46E-03 | 2.03E-02 | | [modulation by host of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0044827) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044827&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044827&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.42E-03 | 1.98E-02 | | [modulation by host of viral process](http://amigo.geneontology.org/amigo/term/GO:0044788) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044788&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044788&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.13 | + | 1.29E-04 | 2.70E-03 | | [modulation by host of symbiont process](http://amigo.geneontology.org/amigo/term/GO:0051851) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&list=upload_1&organism=Homo%20sapiens) | 5.35 | 4.30 | + | 7.16E-08 | 3.08E-06 | | [biological process involved in interaction with symbiont](http://amigo.geneontology.org/amigo/term/GO:0051702) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 7.29 | 3.70 | + | 7.44E-08 | 3.19E-06 | | [biological process involved in symbiotic interaction](http://amigo.geneontology.org/amigo/term/GO:0044403) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 16.83 | 2.97 | + | 2.42E-10 | 1.42E-08 | | [biological process involved in interspecies interaction between organisms](http://amigo.geneontology.org/amigo/term/GO:0044419) | [1602](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&reflist=1) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&list=upload_1&organism=Homo%20sapiens) | 103.33 | 2.07 | + | 4.50E-22 | 1.04E-19 | | [positive regulation by host of viral process](http://amigo.geneontology.org/amigo/term/GO:0044794) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044794&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044794&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.17 | + | 1.13E-03 | 1.65E-02 | | [positive regulation of tumor necrosis factor-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:1903265) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903265&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903265&list=upload_1&organism=Homo%20sapiens) | .77 | 7.75 | + | 4.83E-04 | 8.15E-03 | | [positive regulation of cytokine-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0001961) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001961&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001961&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.54 | + | 2.61E-04 | 4.88E-03 | | [positive regulation of response to cytokine stimulus](http://amigo.geneontology.org/amigo/term/GO:0060760) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060760&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060760&list=upload_1&organism=Homo%20sapiens) | 4.13 | 3.15 | + | 6.81E-04 | 1.09E-02 | | [regulation of response to cytokine stimulus](http://amigo.geneontology.org/amigo/term/GO:0060759) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060759&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060759&list=upload_1&organism=Homo%20sapiens) | 10.51 | 2.47 | + | 8.45E-05 | 1.85E-03 | | [regulation of cytokine-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0001959) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001959&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001959&list=upload_1&organism=Homo%20sapiens) | 9.80 | 2.55 | + | 8.33E-05 | 1.83E-03 | | [positive regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009967) | [1528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&reflist=1) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 98.56 | 1.97 | + | 8.75E-18 | 1.23E-15 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 109.72 | 1.96 | + | 1.50E-19 | 2.55E-17 | | [positive regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010647) | [1696](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&reflist=1) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 109.39 | 1.97 | + | 1.28E-19 | 2.23E-17 | | [cellular response to epinephrine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071872) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071872&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071872&list=upload_1&organism=Homo%20sapiens) | .77 | 7.75 | + | 4.83E-04 | 8.15E-03 | | [response to epinephrine](http://amigo.geneontology.org/amigo/term/GO:0071871) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071871&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071871&list=upload_1&organism=Homo%20sapiens) | .97 | 6.20 | + | 1.21E-03 | 1.74E-02 | | [cellular response to catecholamine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071870) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071870&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071870&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.40 | + | 4.01E-03 | 4.54E-02 | | [cellular response to monoamine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071868) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071868&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071868&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.40 | + | 4.01E-03 | 4.53E-02 | | [positive regulation of natural killer cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0032825) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032825&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032825&list=upload_1&organism=Homo%20sapiens) | .52 | 7.75 | + | 4.48E-03 | 5.00E-02 | | [regulation of natural killer cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0032823) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032823&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032823&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.15E-02 | | [positive regulation of natural killer cell activation](http://amigo.geneontology.org/amigo/term/GO:0032816) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032816&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032816&list=upload_1&organism=Homo%20sapiens) | 1.81 | 3.88 | + | 4.44E-03 | 4.98E-02 | | [protein insertion into mitochondrial outer membrane](http://amigo.geneontology.org/amigo/term/GO:0045040) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045040&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045040&list=upload_1&organism=Homo%20sapiens) | .77 | 7.75 | + | 4.83E-04 | 8.13E-03 | | [protein insertion into membrane](http://amigo.geneontology.org/amigo/term/GO:0051205) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051205&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051205&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.20 | + | 5.99E-04 | 9.80E-03 | | [membrane organization](http://amigo.geneontology.org/amigo/term/GO:0061024) | [851](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061024&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061024&list=upload_1&organism=Homo%20sapiens) | 54.89 | 1.68 | + | 6.86E-06 | 2.00E-04 | | [protein localization to membrane](http://amigo.geneontology.org/amigo/term/GO:0072657) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072657&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072657&list=upload_1&organism=Homo%20sapiens) | 29.09 | 1.62 | + | 3.02E-03 | 3.66E-02 | | [localization within membrane](http://amigo.geneontology.org/amigo/term/GO:0051668) | [541](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051668&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051668&list=upload_1&organism=Homo%20sapiens) | 34.89 | 1.58 | + | 2.18E-03 | 2.82E-02 | | [establishment of protein localization to mitochondrial membrane](http://amigo.geneontology.org/amigo/term/GO:0090151) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090151&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090151&list=upload_1&organism=Homo%20sapiens) | 2.13 | 4.23 | + | 7.75E-04 | 1.20E-02 | | [mitochondrial membrane organization](http://amigo.geneontology.org/amigo/term/GO:0007006) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007006&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007006&list=upload_1&organism=Homo%20sapiens) | 7.42 | 2.83 | + | 6.98E-05 | 1.57E-03 | | [mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0007005) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007005&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007005&list=upload_1&organism=Homo%20sapiens) | 28.70 | 1.99 | + | 6.47E-06 | 1.90E-04 | | [establishment of protein localization to mitochondrion](http://amigo.geneontology.org/amigo/term/GO:0072655) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072655&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072655&list=upload_1&organism=Homo%20sapiens) | 4.84 | 2.69 | + | 2.41E-03 | 3.05E-02 | | [protein localization to mitochondrion](http://amigo.geneontology.org/amigo/term/GO:0070585) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070585&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070585&list=upload_1&organism=Homo%20sapiens) | 5.35 | 3.36 | + | 3.30E-05 | 8.22E-04 | | [mitochondrial transport](http://amigo.geneontology.org/amigo/term/GO:0006839) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006839&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006839&list=upload_1&organism=Homo%20sapiens) | 9.55 | 2.41 | + | 2.95E-04 | 5.42E-03 | | [outer mitochondrial membrane organization](http://amigo.geneontology.org/amigo/term/GO:0007008) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007008&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007008&list=upload_1&organism=Homo%20sapiens) | .77 | 7.75 | + | 4.83E-04 | 8.14E-03 | | [response to interleukin-15](http://amigo.geneontology.org/amigo/term/GO:0070672) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070672&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070672&list=upload_1&organism=Homo%20sapiens) | .52 | 7.75 | + | 4.48E-03 | 5.00E-02 | | [response to cytokine](http://amigo.geneontology.org/amigo/term/GO:0034097) | [808](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&list=upload_1&organism=Homo%20sapiens) | 52.12 | 2.55 | + | 2.69E-20 | 5.22E-18 | | [positive regulation of mitophagy in response to mitochondrial depolarization](http://amigo.geneontology.org/amigo/term/GO:0098779) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098779&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098779&list=upload_1&organism=Homo%20sapiens) | .52 | 7.75 | + | 4.48E-03 | 4.99E-02 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 103.14 | 2.21 | + | 7.45E-27 | 2.54E-24 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 223.56 | 1.83 | + | 3.66E-33 | 2.21E-30 | | [protein refolding](http://amigo.geneontology.org/amigo/term/GO:0042026) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042026&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042026&list=upload_1&organism=Homo%20sapiens) | 1.61 | 7.44 | + | 1.05E-06 | 3.68E-05 | | [protein folding](http://amigo.geneontology.org/amigo/term/GO:0006457) | [221](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&list=upload_1&organism=Homo%20sapiens) | 14.25 | 3.30 | + | 4.05E-11 | 2.69E-09 | | [response to muscle stretch](http://amigo.geneontology.org/amigo/term/GO:0035994) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035994&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035994&list=upload_1&organism=Homo%20sapiens) | 1.68 | 7.16 | + | 1.44E-06 | 4.95E-05 | | [response to mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0009612) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&list=upload_1&organism=Homo%20sapiens) | 14.06 | 3.06 | + | 2.02E-09 | 1.06E-07 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [291](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 159.25 | 1.83 | + | 1.68E-22 | 4.17E-20 | | [response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009628) | [1121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&reflist=1) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&list=upload_1&organism=Homo%20sapiens) | 72.31 | 2.42 | + | 2.38E-24 | 6.90E-22 | | [neurotrophin TRK receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0048011) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048011&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048011&list=upload_1&organism=Homo%20sapiens) | .84 | 7.16 | + | 6.69E-04 | 1.07E-02 | | [neurotrophin signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038179) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038179&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038179&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.77E-02 | | [cellular response to growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0071363) | [477](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 30.77 | 2.44 | + | 4.64E-11 | 3.05E-09 | | [response to growth factor](http://amigo.geneontology.org/amigo/term/GO:0070848) | [507](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 32.70 | 2.48 | + | 3.91E-12 | 2.96E-10 | | [transmembrane receptor protein tyrosine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007169) | [424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007169&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007169&list=upload_1&organism=Homo%20sapiens) | 27.35 | 2.12 | + | 5.78E-07 | 2.16E-05 | | [regulation of microtubule nucleation](http://amigo.geneontology.org/amigo/term/GO:0010968) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010968&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010968&list=upload_1&organism=Homo%20sapiens) | .71 | 7.05 | + | 2.02E-03 | 2.68E-02 | | [regulation of microtubule polymerization](http://amigo.geneontology.org/amigo/term/GO:0031113) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031113&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031113&list=upload_1&organism=Homo%20sapiens) | 3.55 | 4.51 | + | 4.06E-06 | 1.24E-04 | | [regulation of microtubule polymerization or depolymerization](http://amigo.geneontology.org/amigo/term/GO:0031110) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031110&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031110&list=upload_1&organism=Homo%20sapiens) | 5.61 | 3.56 | + | 5.85E-06 | 1.73E-04 | | [regulation of microtubule cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0070507) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070507&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070507&list=upload_1&organism=Homo%20sapiens) | 10.13 | 2.86 | + | 2.62E-06 | 8.43E-05 | | [regulation of cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0051493) | [540](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051493&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051493&list=upload_1&organism=Homo%20sapiens) | 34.83 | 1.98 | + | 6.40E-07 | 2.36E-05 | | [regulation of microtubule-based process](http://amigo.geneontology.org/amigo/term/GO:0032886) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032886&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032886&list=upload_1&organism=Homo%20sapiens) | 16.77 | 2.21 | + | 3.65E-05 | 8.98E-04 | | [regulation of supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:1902903) | [383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902903&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902903&list=upload_1&organism=Homo%20sapiens) | 24.70 | 2.23 | + | 2.72E-07 | 1.06E-05 | | [regulation of protein polymerization](http://amigo.geneontology.org/amigo/term/GO:0032271) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032271&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032271&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.47 | + | 1.97E-05 | 5.19E-04 | | [regulation of protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0043254) | [412](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&list=upload_1&organism=Homo%20sapiens) | 26.57 | 2.37 | + | 4.44E-09 | 2.25E-07 | | [regulation of cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044087) | [951](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 61.34 | 2.01 | + | 7.21E-12 | 5.31E-10 | | [cellular response to granulocyte macrophage colony-stimulating factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0097011) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097011&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097011&list=upload_1&organism=Homo%20sapiens) | .71 | 7.05 | + | 2.02E-03 | 2.67E-02 | | [cellular response to cytokine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071345) | [714](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&reflist=1) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 46.05 | 2.56 | + | 3.01E-18 | 4.29E-16 | | [response to granulocyte macrophage colony-stimulating factor](http://amigo.geneontology.org/amigo/term/GO:0097012) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097012&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097012&list=upload_1&organism=Homo%20sapiens) | .71 | 7.05 | + | 2.02E-03 | 2.68E-02 | | [regulation of attachment of spindle microtubules to kinetochore](http://amigo.geneontology.org/amigo/term/GO:0051988) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051988&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051988&list=upload_1&organism=Homo%20sapiens) | 1.16 | 6.89 | + | 1.04E-04 | 2.21E-03 | | [chaperone cofactor-dependent protein refolding](http://amigo.geneontology.org/amigo/term/GO:0051085) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051085&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051085&list=upload_1&organism=Homo%20sapiens) | 2.06 | 6.78 | + | 3.22E-07 | 1.23E-05 | | ['de novo' post-translational protein folding](http://amigo.geneontology.org/amigo/term/GO:0051084) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051084&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051084&list=upload_1&organism=Homo%20sapiens) | 2.39 | 6.29 | + | 2.69E-07 | 1.06E-05 | | ['de novo' protein folding](http://amigo.geneontology.org/amigo/term/GO:0006458) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006458&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006458&list=upload_1&organism=Homo%20sapiens) | 2.64 | 6.43 | + | 3.33E-08 | 1.52E-06 | | [chaperone-mediated protein folding](http://amigo.geneontology.org/amigo/term/GO:0061077) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061077&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061077&list=upload_1&organism=Homo%20sapiens) | 4.58 | 3.93 | + | 5.35E-06 | 1.59E-04 | | [negative regulation of stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:2000737) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000737&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000737&list=upload_1&organism=Homo%20sapiens) | 1.81 | 6.64 | + | 2.66E-06 | 8.55E-05 | | [regulation of stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:2000736) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&list=upload_1&organism=Homo%20sapiens) | 5.29 | 3.78 | + | 2.71E-06 | 8.70E-05 | | [negative regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045596) | [676](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 43.60 | 2.00 | + | 1.13E-08 | 5.43E-07 | | [negative regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0051093) | [923](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&list=upload_1&organism=Homo%20sapiens) | 59.53 | 1.90 | + | 8.68E-10 | 4.79E-08 | | [negative regulation of microtubule polymerization](http://amigo.geneontology.org/amigo/term/GO:0031115) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031115&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031115&list=upload_1&organism=Homo%20sapiens) | .90 | 6.64 | + | 9.08E-04 | 1.36E-02 | | [negative regulation of supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:1902904) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902904&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902904&list=upload_1&organism=Homo%20sapiens) | 10.45 | 2.58 | + | 3.61E-05 | 8.91E-04 | | [negative regulation of cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0051129) | [690](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 44.51 | 2.18 | + | 2.56E-11 | 1.76E-09 | | [negative regulation of microtubule polymerization or depolymerization](http://amigo.geneontology.org/amigo/term/GO:0031111) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031111&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031111&list=upload_1&organism=Homo%20sapiens) | 2.71 | 4.06 | + | 2.80E-04 | 5.21E-03 | | [negative regulation of cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0051494) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051494&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051494&list=upload_1&organism=Homo%20sapiens) | 10.19 | 2.36 | + | 4.15E-04 | 7.18E-03 | | [negative regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0010639) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&list=upload_1&organism=Homo%20sapiens) | 22.25 | 2.56 | + | 2.14E-09 | 1.11E-07 | | [negative regulation of protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0031333) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031333&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031333&list=upload_1&organism=Homo%20sapiens) | 9.22 | 2.71 | + | 2.83E-05 | 7.16E-04 | | [pre-miRNA processing](http://amigo.geneontology.org/amigo/term/GO:0031054) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031054&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031054&list=upload_1&organism=Homo%20sapiens) | .90 | 6.64 | + | 9.08E-04 | 1.36E-02 | | [miRNA processing](http://amigo.geneontology.org/amigo/term/GO:0035196) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035196&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035196&list=upload_1&organism=Homo%20sapiens) | 2.19 | 5.02 | + | 5.82E-05 | 1.35E-03 | | [small regulatory ncRNA processing](http://amigo.geneontology.org/amigo/term/GO:0070918) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070918&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070918&list=upload_1&organism=Homo%20sapiens) | 2.45 | 4.49 | + | 1.34E-04 | 2.77E-03 | | [RNA processing](http://amigo.geneontology.org/amigo/term/GO:0006396) | [868](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&list=upload_1&organism=Homo%20sapiens) | 55.99 | 1.50 | + | 4.96E-04 | 8.31E-03 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 149.25 | 1.65 | + | 3.22E-14 | 2.99E-12 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 105.46 | 1.56 | + | 5.32E-08 | 2.35E-06 | | [amyloid fibril formation](http://amigo.geneontology.org/amigo/term/GO:1990000) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990000&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990000&list=upload_1&organism=Homo%20sapiens) | 1.68 | 6.56 | + | 7.67E-06 | 2.21E-04 | | [supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:0097435) | [580](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097435&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097435&list=upload_1&organism=Homo%20sapiens) | 37.41 | 1.58 | + | 1.31E-03 | 1.86E-02 | | [regulation of helicase activity](http://amigo.geneontology.org/amigo/term/GO:0051095) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051095&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051095&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.72E-03 | 3.37E-02 | | [cellular response to interferon-alpha](http://amigo.geneontology.org/amigo/term/GO:0035457) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035457&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035457&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.72E-03 | 3.37E-02 | | [positive regulation of mitochondrial membrane potential](http://amigo.geneontology.org/amigo/term/GO:0010918) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010918&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010918&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.72E-03 | 3.37E-02 | | [regulation of mitochondrial membrane potential](http://amigo.geneontology.org/amigo/term/GO:0051881) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051881&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051881&list=upload_1&organism=Homo%20sapiens) | 4.58 | 3.06 | + | 5.57E-04 | 9.15E-03 | | [regulation of membrane potential](http://amigo.geneontology.org/amigo/term/GO:0042391) | [430](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042391&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042391&list=upload_1&organism=Homo%20sapiens) | 27.74 | 1.95 | + | 1.74E-05 | 4.60E-04 | | [regulation of biological quality](http://amigo.geneontology.org/amigo/term/GO:0065008) | [3677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&reflist=1) | [394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 237.17 | 1.66 | + | 3.89E-24 | 1.09E-21 | | [positive regulation of smooth muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0034393) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034393&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034393&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.72E-03 | 3.36E-02 | | [positive regulation of muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0010661) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010661&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010661&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.77 | + | 7.83E-04 | 1.21E-02 | | [regulation of muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0010660) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010660&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010660&list=upload_1&organism=Homo%20sapiens) | 4.39 | 3.42 | + | 1.24E-04 | 2.60E-03 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [219](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 94.69 | 2.31 | + | 3.82E-28 | 1.57E-25 | | [regulation of programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0043067) | [1498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&reflist=1) | [227](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 96.62 | 2.35 | + | 3.02E-30 | 1.35E-27 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [244](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 106.68 | 2.29 | + | 6.80E-31 | 3.14E-28 | | [positive regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043065) | [503](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&list=upload_1&organism=Homo%20sapiens) | 32.44 | 2.59 | + | 2.10E-13 | 1.73E-11 | | [positive regulation of programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0043068) | [516](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&list=upload_1&organism=Homo%20sapiens) | 33.28 | 2.61 | + | 5.55E-14 | 4.98E-12 | | [positive regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010942) | [583](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 37.60 | 2.50 | + | 3.70E-14 | 3.36E-12 | | [positive regulation by host of viral transcription](http://amigo.geneontology.org/amigo/term/GO:0043923) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&list=upload_1&organism=Homo%20sapiens) | 1.10 | 6.38 | + | 4.10E-04 | 7.11E-03 | | [lipoprotein transport](http://amigo.geneontology.org/amigo/term/GO:0042953) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042953&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042953&list=upload_1&organism=Homo%20sapiens) | 1.10 | 6.38 | + | 4.10E-04 | 7.11E-03 | | [lipoprotein localization](http://amigo.geneontology.org/amigo/term/GO:0044872) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044872&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044872&list=upload_1&organism=Homo%20sapiens) | 1.16 | 6.03 | + | 5.39E-04 | 8.89E-03 | | [chaperone-mediated protein complex assembly](http://amigo.geneontology.org/amigo/term/GO:0051131) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051131&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051131&list=upload_1&organism=Homo%20sapiens) | 1.42 | 6.34 | + | 6.40E-05 | 1.46E-03 | | [positive regulation of nitric-oxide synthase activity](http://amigo.geneontology.org/amigo/term/GO:0051000) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051000&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051000&list=upload_1&organism=Homo%20sapiens) | 1.42 | 6.34 | + | 6.40E-05 | 1.45E-03 | | [positive regulation of monooxygenase activity](http://amigo.geneontology.org/amigo/term/GO:0032770) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032770&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032770&list=upload_1&organism=Homo%20sapiens) | 2.06 | 5.33 | + | 3.69E-05 | 9.05E-04 | | [regulation of monooxygenase activity](http://amigo.geneontology.org/amigo/term/GO:0032768) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032768&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032768&list=upload_1&organism=Homo%20sapiens) | 3.29 | 4.26 | + | 2.77E-05 | 7.05E-04 | | [regulation of oxidoreductase activity](http://amigo.geneontology.org/amigo/term/GO:0051341) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&list=upload_1&organism=Homo%20sapiens) | 6.51 | 3.84 | + | 1.26E-07 | 5.30E-06 | | [positive regulation of oxidoreductase activity](http://amigo.geneontology.org/amigo/term/GO:0051353) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051353&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051353&list=upload_1&organism=Homo%20sapiens) | 3.87 | 4.39 | + | 2.76E-06 | 8.78E-05 | | [regulation of nitric-oxide synthase activity](http://amigo.geneontology.org/amigo/term/GO:0050999) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050999&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050999&list=upload_1&organism=Homo%20sapiens) | 2.45 | 4.08 | + | 5.09E-04 | 8.48E-03 | | [positive regulation of leukocyte adhesion to vascular endothelial cell](http://amigo.geneontology.org/amigo/term/GO:1904996) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904996&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904996&list=upload_1&organism=Homo%20sapiens) | 1.48 | 6.07 | + | 8.43E-05 | 1.85E-03 | | [regulation of leukocyte adhesion to vascular endothelial cell](http://amigo.geneontology.org/amigo/term/GO:1904994) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904994&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904994&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.65 | + | 4.34E-04 | 7.47E-03 | | [amyloid-beta clearance](http://amigo.geneontology.org/amigo/term/GO:0097242) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097242&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097242&list=upload_1&organism=Homo%20sapiens) | 1.48 | 6.07 | + | 8.43E-05 | 1.85E-03 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [583](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 424.48 | 1.37 | + | 1.47E-18 | 2.15E-16 | | [NIK/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0038061) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038061&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038061&list=upload_1&organism=Homo%20sapiens) | 2.32 | 6.03 | + | 1.00E-06 | 3.54E-05 | | [intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:0035556) | [1511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&reflist=1) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&list=upload_1&organism=Homo%20sapiens) | 97.46 | 2.00 | + | 1.44E-18 | 2.14E-16 | | [removal of superoxide radicals](http://amigo.geneontology.org/amigo/term/GO:0019430) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019430&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019430&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.16E-02 | | [response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0000302) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&list=upload_1&organism=Homo%20sapiens) | 10.77 | 3.62 | + | 1.80E-10 | 1.08E-08 | | [response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0006979) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 23.67 | 2.75 | + | 1.15E-11 | 8.18E-10 | | [response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0010035) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 34.38 | 2.30 | + | 2.51E-10 | 1.47E-08 | | [cellular response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0034614) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&list=upload_1&organism=Homo%20sapiens) | 7.55 | 4.11 | + | 1.01E-09 | 5.51E-08 | | [cellular response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0034599) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&list=upload_1&organism=Homo%20sapiens) | 14.32 | 3.35 | + | 1.53E-11 | 1.07E-09 | | [cellular response to chemical stress](http://amigo.geneontology.org/amigo/term/GO:0062197) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&list=upload_1&organism=Homo%20sapiens) | 17.61 | 3.12 | + | 5.65E-12 | 4.24E-10 | | [endodermal cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0001711) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001711&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001711&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.15E-02 | | [cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0045165) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&list=upload_1&organism=Homo%20sapiens) | 16.13 | 2.11 | + | 1.40E-04 | 2.90E-03 | | [formation of primary germ layer](http://amigo.geneontology.org/amigo/term/GO:0001704) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&list=upload_1&organism=Homo%20sapiens) | 7.74 | 2.97 | + | 1.64E-05 | 4.40E-04 | | [anatomical structure formation involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048646) | [941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&list=upload_1&organism=Homo%20sapiens) | 60.69 | 1.68 | + | 1.46E-06 | 4.98E-05 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 144.29 | 1.70 | + | 3.18E-15 | 3.39E-13 | | [anatomical structure development](http://amigo.geneontology.org/amigo/term/GO:0048856) | [5144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&reflist=1) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&list=upload_1&organism=Homo%20sapiens) | 331.79 | 1.46 | + | 4.27E-19 | 6.76E-17 | | [gastrulation](http://amigo.geneontology.org/amigo/term/GO:0007369) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&list=upload_1&organism=Homo%20sapiens) | 10.90 | 2.94 | + | 5.04E-07 | 1.89E-05 | | [embryonic morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048598) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&list=upload_1&organism=Homo%20sapiens) | 38.12 | 1.94 | + | 5.28E-07 | 1.98E-05 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 68.31 | 1.82 | + | 1.83E-09 | 9.72E-08 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [425](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 272.71 | 1.56 | + | 3.44E-21 | 6.92E-19 | | [endodermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0035987) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&list=upload_1&organism=Homo%20sapiens) | 2.84 | 5.29 | + | 1.60E-06 | 5.38E-05 | | [endoderm formation](http://amigo.geneontology.org/amigo/term/GO:0001706) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&list=upload_1&organism=Homo%20sapiens) | 3.48 | 5.17 | + | 1.95E-07 | 8.02E-06 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 5.22 | 4.79 | + | 3.20E-09 | 1.64E-07 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 111.33 | 1.71 | + | 6.30E-12 | 4.70E-10 | | [regulation of apoptotic process involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:1902337) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902337&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902337&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.15E-02 | | [regulation of apoptotic process involved in development](http://amigo.geneontology.org/amigo/term/GO:1904748) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904748&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904748&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.14E-02 | | [negative regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051974) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051974&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051974&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.15E-02 | | [negative regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051348) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&list=upload_1&organism=Homo%20sapiens) | 17.74 | 2.20 | + | 2.12E-05 | 5.54E-04 | | [regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051338) | [915](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&reflist=1) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 59.02 | 2.15 | + | 3.20E-14 | 2.99E-12 | | [negative regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000279) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000279&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000279&list=upload_1&organism=Homo%20sapiens) | 2.58 | 4.26 | + | 1.95E-04 | 3.85E-03 | | [negative regulation of macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010558) | [1533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&reflist=1) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 98.88 | 1.95 | + | 2.44E-17 | 3.36E-15 | | [negative regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009890) | [1624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&reflist=1) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 104.75 | 1.91 | + | 4.41E-17 | 5.96E-15 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [425](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 268.52 | 1.58 | + | 1.93E-22 | 4.73E-20 | | [regulation of macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010556) | [3938](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&reflist=1) | [407](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 254.00 | 1.60 | + | 3.12E-22 | 7.41E-20 | | [negative regulation of cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0031327) | [1594](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&reflist=1) | [196](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 102.81 | 1.91 | + | 1.32E-16 | 1.70E-14 | | [regulation of cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0031326) | [4102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&reflist=1) | [417](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 264.58 | 1.58 | + | 1.74E-21 | 3.78E-19 | | [regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000278) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&list=upload_1&organism=Homo%20sapiens) | 8.06 | 3.60 | + | 4.30E-08 | 1.94E-06 | | [regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051972) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&list=upload_1&organism=Homo%20sapiens) | 3.23 | 4.65 | + | 5.91E-06 | 1.75E-04 | | [cellular response to electrical stimulus](http://amigo.geneontology.org/amigo/term/GO:0071257) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071257&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071257&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.14E-02 | | [cellular response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071214) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 21.03 | 2.81 | + | 7.18E-11 | 4.60E-09 | | [cellular response to environmental stimulus](http://amigo.geneontology.org/amigo/term/GO:0104004) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&list=upload_1&organism=Homo%20sapiens) | 21.03 | 2.81 | + | 7.18E-11 | 4.58E-09 | | [response to electrical stimulus](http://amigo.geneontology.org/amigo/term/GO:0051602) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051602&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051602&list=upload_1&organism=Homo%20sapiens) | 2.84 | 4.93 | + | 6.87E-06 | 2.00E-04 | | [negative regulation of ubiquitin protein ligase activity](http://amigo.geneontology.org/amigo/term/GO:1904667) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904667&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904667&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.14E-02 | | [negative regulation of ubiquitin-protein transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051444) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051444&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051444&list=upload_1&organism=Homo%20sapiens) | 1.48 | 6.74 | + | 1.65E-05 | 4.41E-04 | | [negative regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031397) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&list=upload_1&organism=Homo%20sapiens) | 5.35 | 5.04 | + | 2.89E-10 | 1.69E-08 | | [negative regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903321) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&list=upload_1&organism=Homo%20sapiens) | 6.13 | 4.90 | + | 5.49E-11 | 3.59E-09 | | [negative regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031400) | [503](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 32.44 | 2.19 | + | 1.24E-08 | 5.90E-07 | | [negative regulation of protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051248) | [1042](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&reflist=1) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 67.21 | 2.11 | + | 2.79E-15 | 3.02E-13 | | [regulation of protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051246) | [2587](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&reflist=1) | [348](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&list=upload_1&organism=Homo%20sapiens) | 166.86 | 2.09 | + | 5.24E-38 | 7.47E-35 | | [regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031399) | [1563](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&reflist=1) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 100.81 | 2.15 | + | 3.34E-24 | 9.51E-22 | | [regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903320) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&list=upload_1&organism=Homo%20sapiens) | 16.32 | 3.43 | + | 1.34E-13 | 1.14E-11 | | [regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031396) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&list=upload_1&organism=Homo%20sapiens) | 13.61 | 3.31 | + | 9.70E-11 | 6.04E-09 | | [regulation of ubiquitin-protein transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051438) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051438&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051438&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.81 | + | 7.79E-05 | 1.73E-03 | | [regulation of ubiquitin protein ligase activity](http://amigo.geneontology.org/amigo/term/GO:1904666) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904666&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904666&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.77 | + | 7.83E-04 | 1.21E-02 | | [primary miRNA processing](http://amigo.geneontology.org/amigo/term/GO:0031053) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031053&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031053&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.13E-02 | | [negative regulation of alcohol biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1902931) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902931&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902931&list=upload_1&organism=Homo%20sapiens) | .84 | 5.96 | + | 3.57E-03 | 4.13E-02 | | [regulation of small molecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0062012) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062012&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062012&list=upload_1&organism=Homo%20sapiens) | 21.48 | 2.00 | + | 6.77E-05 | 1.53E-03 | | [negative regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902894) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902894&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902894&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.91 | + | 2.43E-04 | 4.60E-03 | | [negative regulation of DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0045892) | [1323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&reflist=1) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 85.33 | 1.89 | + | 2.07E-13 | 1.72E-11 | | [regulation of DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006355) | [3454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&reflist=1) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&list=upload_1&organism=Homo%20sapiens) | 222.78 | 1.55 | + | 3.23E-16 | 3.87E-14 | | [regulation of nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:1903506) | [3456](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&reflist=1) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&list=upload_1&organism=Homo%20sapiens) | 222.91 | 1.55 | + | 2.36E-16 | 2.86E-14 | | [regulation of RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2001141) | [3465](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&reflist=1) | [347](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 223.49 | 1.55 | + | 1.86E-16 | 2.32E-14 | | [regulation of RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051252) | [3752](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&reflist=1) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 242.01 | 1.54 | + | 2.05E-17 | 2.85E-15 | | [negative regulation of nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:1903507) | [1325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 85.46 | 1.90 | + | 1.32E-13 | 1.13E-11 | | [negative regulation of RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1902679) | [1327](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 85.59 | 1.89 | + | 1.41E-13 | 1.20E-11 | | [negative regulation of RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051253) | [1435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 92.56 | 1.88 | + | 3.47E-14 | 3.20E-12 | | [negative regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000629) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000629&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000629&list=upload_1&organism=Homo%20sapiens) | 1.42 | 5.64 | + | 3.13E-04 | 5.69E-03 | | [regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000628) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 4.77 | 4.61 | + | 4.85E-08 | 2.17E-06 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 4.06 | 4.92 | + | 8.04E-08 | 3.44E-06 | | [positive regulation of oxidative stress-induced cell death](http://amigo.geneontology.org/amigo/term/GO:1903209) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903209&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903209&list=upload_1&organism=Homo%20sapiens) | 1.42 | 5.64 | + | 3.13E-04 | 5.70E-03 | | [regulation of oxidative stress-induced cell death](http://amigo.geneontology.org/amigo/term/GO:1903201) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903201&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903201&list=upload_1&organism=Homo%20sapiens) | 4.71 | 3.61 | + | 2.49E-05 | 6.38E-04 | | [regulation of cellular response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:1900407) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900407&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900407&list=upload_1&organism=Homo%20sapiens) | 5.42 | 3.51 | + | 1.21E-05 | 3.33E-04 | | [regulation of cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0080135) | [709](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 45.73 | 2.03 | + | 1.51E-09 | 8.14E-08 | | [regulation of response to stress](http://amigo.geneontology.org/amigo/term/GO:0080134) | [1373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&reflist=1) | [177](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 88.56 | 2.00 | + | 7.51E-17 | 9.89E-15 | | [regulation of response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:1902882) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902882&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902882&list=upload_1&organism=Homo%20sapiens) | 6.06 | 3.13 | + | 4.67E-05 | 1.10E-03 | | [positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:1901522) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901522&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901522&list=upload_1&organism=Homo%20sapiens) | 1.42 | 5.64 | + | 3.13E-04 | 5.68E-03 | | [positive regulation of transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0045944) | [1259](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&reflist=1) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&list=upload_1&organism=Homo%20sapiens) | 81.21 | 2.17 | + | 8.72E-20 | 1.57E-17 | | [positive regulation of DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0045893) | [1715](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&reflist=1) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 110.62 | 2.02 | + | 1.08E-21 | 2.43E-19 | | [positive regulation of nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:1903508) | [1715](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&reflist=1) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 110.62 | 2.02 | + | 1.08E-21 | 2.46E-19 | | [positive regulation of RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1902680) | [1721](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&reflist=1) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 111.01 | 2.01 | + | 1.91E-21 | 4.06E-19 | | [positive regulation of RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051254) | [1848](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&reflist=1) | [237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 119.20 | 1.99 | + | 2.97E-22 | 7.18E-20 | | [positive regulation of cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0031328) | [2048](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&reflist=1) | [270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 132.10 | 2.04 | + | 2.72E-27 | 9.92E-25 | | [positive regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009891) | [2087](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&reflist=1) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 134.61 | 2.05 | + | 3.37E-28 | 1.43E-25 | | [positive regulation of macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010557) | [1943](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&reflist=1) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 125.32 | 2.07 | + | 3.95E-27 | 1.38E-24 | | [regulation of transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0006357) | [2606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&reflist=1) | [266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 168.09 | 1.58 | + | 3.82E-13 | 3.11E-11 | | [myelination in peripheral nervous system](http://amigo.geneontology.org/amigo/term/GO:0022011) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022011&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022011&list=upload_1&organism=Homo%20sapiens) | 2.00 | 5.50 | + | 2.90E-05 | 7.30E-04 | | [myelination](http://amigo.geneontology.org/amigo/term/GO:0042552) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042552&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042552&list=upload_1&organism=Homo%20sapiens) | 7.42 | 2.43 | + | 1.36E-03 | 1.92E-02 | | [axon ensheathment](http://amigo.geneontology.org/amigo/term/GO:0008366) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008366&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008366&list=upload_1&organism=Homo%20sapiens) | 7.55 | 2.52 | + | 7.57E-04 | 1.18E-02 | | [ensheathment of neurons](http://amigo.geneontology.org/amigo/term/GO:0007272) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007272&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007272&list=upload_1&organism=Homo%20sapiens) | 7.55 | 2.52 | + | 7.57E-04 | 1.18E-02 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 141.32 | 1.63 | + | 1.80E-12 | 1.39E-10 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 247.55 | 1.55 | + | 2.22E-18 | 3.22E-16 | | [Schwann cell development](http://amigo.geneontology.org/amigo/term/GO:0014044) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014044&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014044&list=upload_1&organism=Homo%20sapiens) | 2.19 | 5.47 | + | 1.32E-05 | 3.59E-04 | | [glial cell development](http://amigo.geneontology.org/amigo/term/GO:0021782) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021782&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021782&list=upload_1&organism=Homo%20sapiens) | 7.29 | 3.98 | + | 6.40E-09 | 3.19E-07 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 111.26 | 1.58 | + | 8.24E-09 | 4.04E-07 | | [glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0010001) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010001&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010001&list=upload_1&organism=Homo%20sapiens) | 12.06 | 3.15 | + | 8.63E-09 | 4.22E-07 | | [gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0042063) | [246](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&list=upload_1&organism=Homo%20sapiens) | 15.87 | 2.65 | + | 1.27E-07 | 5.33E-06 | | [neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0022008) | [1290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&list=upload_1&organism=Homo%20sapiens) | 83.21 | 1.60 | + | 4.95E-07 | 1.87E-05 | | [Schwann cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0014037) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014037&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014037&list=upload_1&organism=Homo%20sapiens) | 2.52 | 5.17 | + | 9.64E-06 | 2.70E-04 | | [peripheral nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007422) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007422&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007422&list=upload_1&organism=Homo%20sapiens) | 5.35 | 3.74 | + | 3.18E-06 | 9.97E-05 | | [peripheral nervous system axon ensheathment](http://amigo.geneontology.org/amigo/term/GO:0032292) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032292&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032292&list=upload_1&organism=Homo%20sapiens) | 2.00 | 5.50 | + | 2.90E-05 | 7.29E-04 | | [natural killer cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0001779) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001779&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001779&list=upload_1&organism=Homo%20sapiens) | 1.10 | 5.47 | + | 2.02E-03 | 2.68E-02 | | [lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0030098) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&list=upload_1&organism=Homo%20sapiens) | 18.06 | 2.60 | + | 3.32E-08 | 1.52E-06 | | [mononuclear cell differentiation](http://amigo.geneontology.org/amigo/term/GO:1903131) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&list=upload_1&organism=Homo%20sapiens) | 21.03 | 2.66 | + | 7.82E-10 | 4.35E-08 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 25.80 | 2.48 | + | 6.92E-10 | 3.89E-08 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 42.57 | 2.11 | + | 4.37E-10 | 2.50E-08 | | [hematopoietic or lymphoid organ development](http://amigo.geneontology.org/amigo/term/GO:0048534) | [710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 45.80 | 2.07 | + | 3.73E-10 | 2.15E-08 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 48.83 | 2.07 | + | 1.15E-10 | 7.07E-09 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 156.67 | 1.62 | + | 1.06E-13 | 9.30E-12 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [331](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 209.88 | 1.58 | + | 1.65E-16 | 2.09E-14 | | [lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0046649) | [465](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&list=upload_1&organism=Homo%20sapiens) | 29.99 | 2.23 | + | 1.77E-08 | 8.27E-07 | | [leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0045321) | [581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&list=upload_1&organism=Homo%20sapiens) | 37.47 | 2.16 | + | 1.41E-09 | 7.61E-08 | | [cell activation](http://amigo.geneontology.org/amigo/term/GO:0001775) | [700](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&list=upload_1&organism=Homo%20sapiens) | 45.15 | 2.15 | + | 3.97E-11 | 2.65E-09 | | [natural killer cell activation](http://amigo.geneontology.org/amigo/term/GO:0030101) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030101&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030101&list=upload_1&organism=Homo%20sapiens) | 4.26 | 2.82 | + | 2.46E-03 | 3.12E-02 | | [pulmonary valve morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003184) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003184&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003184&list=upload_1&organism=Homo%20sapiens) | 1.10 | 5.47 | + | 2.02E-03 | 2.67E-02 | | [pulmonary valve development](http://amigo.geneontology.org/amigo/term/GO:0003177) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003177&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003177&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.91 | + | 2.43E-04 | 4.61E-03 | | [semi-lunar valve development](http://amigo.geneontology.org/amigo/term/GO:1905314) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&list=upload_1&organism=Homo%20sapiens) | 2.64 | 3.40 | + | 2.82E-03 | 3.47E-02 | | [heart valve development](http://amigo.geneontology.org/amigo/term/GO:0003170) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&list=upload_1&organism=Homo%20sapiens) | 4.19 | 3.10 | + | 7.73E-04 | 1.20E-02 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 35.80 | 2.07 | + | 3.87E-08 | 1.75E-06 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 58.63 | 1.60 | + | 2.41E-05 | 6.19E-04 | | [regulation of translational elongation](http://amigo.geneontology.org/amigo/term/GO:0006448) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006448&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006448&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.36E-02 | | [regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0006417) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&list=upload_1&organism=Homo%20sapiens) | 26.45 | 2.38 | + | 3.90E-09 | 1.99E-07 | | [regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034248) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&list=upload_1&organism=Homo%20sapiens) | 30.25 | 2.45 | + | 5.74E-11 | 3.73E-09 | | [regulation of cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000112) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&list=upload_1&organism=Homo%20sapiens) | 31.80 | 2.30 | + | 9.85E-10 | 5.40E-08 | | [post-transcriptional regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010608) | [498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010608&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010608&list=upload_1&organism=Homo%20sapiens) | 32.12 | 2.40 | + | 5.96E-11 | 3.85E-09 | | [cellular response to gonadotropin stimulus](http://amigo.geneontology.org/amigo/term/GO:0071371) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071371&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071371&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.35E-02 | | [response to muramyl dipeptide](http://amigo.geneontology.org/amigo/term/GO:0032495) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032495&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032495&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.35E-02 | | [necroptotic process](http://amigo.geneontology.org/amigo/term/GO:0070266) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070266&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070266&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.35E-02 | | [programmed necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0097300) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097300&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097300&list=upload_1&organism=Homo%20sapiens) | 1.61 | 5.58 | + | 1.41E-04 | 2.91E-03 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 69.27 | 2.15 | + | 1.19E-16 | 1.54E-14 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 71.47 | 2.13 | + | 1.78E-16 | 2.23E-14 | | [necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0070265) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070265&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070265&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.98 | + | 2.84E-04 | 5.27E-03 | | [membrane repolarization during cardiac muscle cell action potential](http://amigo.geneontology.org/amigo/term/GO:0086013) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086013&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086013&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.35E-02 | | [cardiac muscle cell membrane repolarization](http://amigo.geneontology.org/amigo/term/GO:0099622) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099622&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099622&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.43 | + | 8.96E-04 | 1.35E-02 | | [membrane repolarization](http://amigo.geneontology.org/amigo/term/GO:0086009) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086009&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086009&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.77E-02 | | [membrane repolarization during action potential](http://amigo.geneontology.org/amigo/term/GO:0086011) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086011&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086011&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.42E-03 | 1.98E-02 | | [cardiac muscle cell action potential](http://amigo.geneontology.org/amigo/term/GO:0086001) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086001&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086001&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.33E-02 | | [negative regulation of oxidative stress-induced neuron death](http://amigo.geneontology.org/amigo/term/GO:1903204) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903204&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903204&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.17 | + | 1.13E-03 | 1.66E-02 | | [negative regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901215) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&list=upload_1&organism=Homo%20sapiens) | 14.19 | 2.82 | + | 5.21E-08 | 2.31E-06 | | [regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901214) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&list=upload_1&organism=Homo%20sapiens) | 20.96 | 2.72 | + | 3.00E-10 | 1.75E-08 | | [negative regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0060548) | [1022](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&reflist=1) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&list=upload_1&organism=Homo%20sapiens) | 65.92 | 2.32 | + | 1.11E-19 | 1.96E-17 | | [negative regulation of oxidative stress-induced cell death](http://amigo.geneontology.org/amigo/term/GO:1903202) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903202&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903202&list=upload_1&organism=Homo%20sapiens) | 3.03 | 3.63 | + | 6.33E-04 | 1.03E-02 | | [regulation of oxidative stress-induced neuron death](http://amigo.geneontology.org/amigo/term/GO:1903203) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903203&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903203&list=upload_1&organism=Homo%20sapiens) | 2.00 | 4.50 | + | 5.30E-04 | 8.78E-03 | | [ERBB2 signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038128) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038128&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038128&list=upload_1&organism=Homo%20sapiens) | 1.16 | 5.17 | + | 2.56E-03 | 3.22E-02 | | [ERBB signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038127) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038127&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038127&list=upload_1&organism=Homo%20sapiens) | 4.00 | 4.25 | + | 4.01E-06 | 1.23E-04 | | [negative regulation of release of cytochrome c from mitochondria](http://amigo.geneontology.org/amigo/term/GO:0090201) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090201&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090201&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.17 | + | 1.13E-03 | 1.65E-02 | | [negative regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010823) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010823&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010823&list=upload_1&organism=Homo%20sapiens) | 3.42 | 4.39 | + | 1.06E-05 | 2.96E-04 | | [negative regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001234) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&list=upload_1&organism=Homo%20sapiens) | 14.77 | 2.98 | + | 2.65E-09 | 1.37E-07 | | [negative regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043066) | [898](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 57.92 | 2.38 | + | 1.05E-18 | 1.58E-16 | | [negative regulation of programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0043069) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&reflist=1) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 59.21 | 2.40 | + | 2.02E-19 | 3.37E-17 | | [regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001233) | [364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&list=upload_1&organism=Homo%20sapiens) | 23.48 | 2.60 | + | 3.74E-10 | 2.15E-08 | | [regulation of release of cytochrome c from mitochondria](http://amigo.geneontology.org/amigo/term/GO:0090199) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090199&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090199&list=upload_1&organism=Homo%20sapiens) | 3.03 | 3.63 | + | 6.33E-04 | 1.03E-02 | | [negative regulation of telomere maintenance via telomerase](http://amigo.geneontology.org/amigo/term/GO:0032211) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032211&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032211&list=upload_1&organism=Homo%20sapiens) | 1.35 | 5.17 | + | 1.13E-03 | 1.65E-02 | | [regulation of telomere maintenance via telomerase](http://amigo.geneontology.org/amigo/term/GO:0032210) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032210&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032210&list=upload_1&organism=Homo%20sapiens) | 3.48 | 3.45 | + | 5.44E-04 | 8.96E-03 | | [regulation of telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:1904356) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904356&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904356&list=upload_1&organism=Homo%20sapiens) | 4.00 | 3.25 | + | 5.25E-04 | 8.70E-03 | | [regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032204) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&list=upload_1&organism=Homo%20sapiens) | 6.51 | 3.22 | + | 1.31E-05 | 3.58E-04 | | [regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0033044) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 16.25 | 2.58 | + | 2.12E-07 | 8.60E-06 | | [negative regulation of telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:1904357) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904357&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904357&list=upload_1&organism=Homo%20sapiens) | 1.81 | 3.88 | + | 4.44E-03 | 4.98E-02 | | [negative regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032205) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032205&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032205&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.45 | + | 4.47E-03 | 5.00E-02 | | [negative regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001251) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001251&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001251&list=upload_1&organism=Homo%20sapiens) | 5.29 | 2.84 | + | 7.14E-04 | 1.13E-02 | | [regulation of inclusion body assembly](http://amigo.geneontology.org/amigo/term/GO:0090083) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090083&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090083&list=upload_1&organism=Homo%20sapiens) | 1.16 | 5.17 | + | 2.56E-03 | 3.22E-02 | | [negative regulation of steroid biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010894) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010894&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010894&list=upload_1&organism=Homo%20sapiens) | 1.55 | 5.17 | + | 5.06E-04 | 8.44E-03 | | [regulation of lipid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019216) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019216&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019216&list=upload_1&organism=Homo%20sapiens) | 22.32 | 2.11 | + | 8.71E-06 | 2.48E-04 | | [regulation of lipid biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0046890) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046890&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046890&list=upload_1&organism=Homo%20sapiens) | 11.16 | 2.06 | + | 2.26E-03 | 2.90E-02 | | [regulation of steroid biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0050810) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050810&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050810&list=upload_1&organism=Homo%20sapiens) | 4.52 | 2.88 | + | 1.40E-03 | 1.96E-02 | | [negative regulation of steroid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045939) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045939&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045939&list=upload_1&organism=Homo%20sapiens) | 1.74 | 4.59 | + | 9.62E-04 | 1.43E-02 | | [adrenal gland development](http://amigo.geneontology.org/amigo/term/GO:0030325) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030325&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030325&list=upload_1&organism=Homo%20sapiens) | 1.74 | 5.17 | + | 2.27E-04 | 4.34E-03 | | [gland development](http://amigo.geneontology.org/amigo/term/GO:0048732) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&list=upload_1&organism=Homo%20sapiens) | 27.22 | 2.46 | + | 3.36E-10 | 1.95E-08 | | [endocrine system development](http://amigo.geneontology.org/amigo/term/GO:0035270) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&list=upload_1&organism=Homo%20sapiens) | 8.39 | 2.74 | + | 4.96E-05 | 1.17E-03 | | [mammary gland epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060644) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060644&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060644&list=upload_1&organism=Homo%20sapiens) | 1.16 | 5.17 | + | 2.56E-03 | 3.22E-02 | | [mammary gland epithelium development](http://amigo.geneontology.org/amigo/term/GO:0061180) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061180&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061180&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.69 | + | 5.93E-05 | 1.37E-03 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 69.14 | 1.81 | + | 1.63E-09 | 8.71E-08 | | [epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030855) | [620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&list=upload_1&organism=Homo%20sapiens) | 39.99 | 1.75 | + | 2.19E-05 | 5.70E-04 | | [negative regulation of transcription elongation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0034244) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034244&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034244&list=upload_1&organism=Homo%20sapiens) | 1.16 | 5.17 | + | 2.56E-03 | 3.21E-02 | | [neuroepithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060563) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060563&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060563&list=upload_1&organism=Homo%20sapiens) | 2.00 | 5.00 | + | 1.28E-04 | 2.68E-03 | | [columnar/cuboidal epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002065) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&list=upload_1&organism=Homo%20sapiens) | 6.77 | 3.10 | + | 2.18E-05 | 5.69E-04 | | [cellular response to dexamethasone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071549) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071549&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071549&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.98 | + | 2.84E-04 | 5.27E-03 | | [response to dexamethasone](http://amigo.geneontology.org/amigo/term/GO:0071548) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&list=upload_1&organism=Homo%20sapiens) | 2.84 | 4.23 | + | 1.08E-04 | 2.28E-03 | | [response to glucocorticoid](http://amigo.geneontology.org/amigo/term/GO:0051384) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&list=upload_1&organism=Homo%20sapiens) | 9.22 | 2.60 | + | 9.98E-05 | 2.14E-03 | | [response to corticosteroid](http://amigo.geneontology.org/amigo/term/GO:0031960) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.43 | + | 1.07E-04 | 2.26E-03 | | [cellular response to glucocorticoid stimulus](http://amigo.geneontology.org/amigo/term/GO:0071385) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071385&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071385&list=upload_1&organism=Homo%20sapiens) | 3.61 | 4.71 | + | 1.25E-06 | 4.35E-05 | | [cellular response to corticosteroid stimulus](http://amigo.geneontology.org/amigo/term/GO:0071384) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071384&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071384&list=upload_1&organism=Homo%20sapiens) | 4.19 | 4.05 | + | 6.84E-06 | 2.00E-04 | | [regulation of hormone biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0046885) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046885&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046885&list=upload_1&organism=Homo%20sapiens) | 1.61 | 4.96 | + | 6.32E-04 | 1.03E-02 | | [regulation of hormone metabolic process](http://amigo.geneontology.org/amigo/term/GO:0032350) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032350&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032350&list=upload_1&organism=Homo%20sapiens) | 2.58 | 3.88 | + | 7.15E-04 | 1.13E-02 | | [regulation of hormone levels](http://amigo.geneontology.org/amigo/term/GO:0010817) | [528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010817&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010817&list=upload_1&organism=Homo%20sapiens) | 34.06 | 1.94 | + | 1.89E-06 | 6.29E-05 | | [positive regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902895) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&list=upload_1&organism=Homo%20sapiens) | 3.03 | 4.95 | + | 3.15E-06 | 9.89E-05 | | [positive regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000630) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&list=upload_1&organism=Homo%20sapiens) | 3.42 | 4.68 | + | 2.72E-06 | 8.70E-05 | | [DNA unwinding involved in DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006268) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.42E-03 | 1.98E-02 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 5.93 | 3.03 | + | 1.05E-04 | 2.23E-03 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 6.32 | 3.01 | + | 7.61E-05 | 1.69E-03 | | [DNA conformation change](http://amigo.geneontology.org/amigo/term/GO:0071103) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&list=upload_1&organism=Homo%20sapiens) | 6.90 | 2.75 | + | 2.08E-04 | 4.02E-03 | | [DNA-templated DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006261) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006261&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006261&list=upload_1&organism=Homo%20sapiens) | 8.97 | 2.23 | + | 2.07E-03 | 2.72E-02 | | [DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006260) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&list=upload_1&organism=Homo%20sapiens) | 13.22 | 2.12 | + | 4.85E-04 | 8.17E-03 | | [regulation of monocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045655) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045655&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045655&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.90 | + | 3.20E-03 | 3.80E-02 | | [regulation of myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002761) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002761&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002761&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.29 | + | 2.18E-03 | 2.82E-02 | | [regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045637) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.79 | + | 2.96E-07 | 1.15E-05 | | [negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:1902176) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902176&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902176&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.90 | + | 3.20E-03 | 3.79E-02 | | [regulation of oxidative stress-induced intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:1902175) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902175&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902175&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.28 | + | 1.42E-03 | 1.98E-02 | | [regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001242) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.97 | + | 4.00E-07 | 1.52E-05 | | [regulation of intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:1902531) | [1721](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 111.01 | 1.95 | + | 2.42E-19 | 3.99E-17 | | [negative regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001243) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001243&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001243&list=upload_1&organism=Homo%20sapiens) | 6.39 | 3.29 | + | 1.01E-05 | 2.82E-04 | | [negative regulation of intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:1902532) | [518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&list=upload_1&organism=Homo%20sapiens) | 33.41 | 1.95 | + | 2.30E-06 | 7.52E-05 | | [cellular response to heat](http://amigo.geneontology.org/amigo/term/GO:0034605) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&list=upload_1&organism=Homo%20sapiens) | 3.48 | 4.88 | + | 8.23E-07 | 2.98E-05 | | [response to heat](http://amigo.geneontology.org/amigo/term/GO:0009408) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&list=upload_1&organism=Homo%20sapiens) | 6.64 | 4.06 | + | 1.45E-08 | 6.82E-07 | | [response to temperature stimulus](http://amigo.geneontology.org/amigo/term/GO:0009266) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.96 | + | 1.87E-07 | 7.71E-06 | | [negative regulation of blood vessel endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0043537) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043537&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043537&list=upload_1&organism=Homo%20sapiens) | 2.26 | 4.87 | + | 7.23E-05 | 1.62E-03 | | [regulation of blood vessel endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0043535) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&list=upload_1&organism=Homo%20sapiens) | 5.87 | 3.58 | + | 3.27E-06 | 1.02E-04 | | [regulation of endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010594) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&list=upload_1&organism=Homo%20sapiens) | 10.90 | 2.02 | + | 3.43E-03 | 4.03E-02 | | [regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010632) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&list=upload_1&organism=Homo%20sapiens) | 14.77 | 2.10 | + | 3.26E-04 | 5.89E-03 | | [regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030334) | [929](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 59.92 | 1.67 | + | 2.46E-06 | 8.00E-05 | | [regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000145) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&list=upload_1&organism=Homo%20sapiens) | 63.79 | 1.65 | + | 2.50E-06 | 8.11E-05 | | [regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040012) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&list=upload_1&organism=Homo%20sapiens) | 66.69 | 1.65 | + | 1.54E-06 | 5.19E-05 | | [negative regulation of endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010596) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010596&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010596&list=upload_1&organism=Homo%20sapiens) | 3.42 | 3.22 | + | 1.48E-03 | 2.05E-02 | | [negative regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010633) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010633&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010633&list=upload_1&organism=Homo%20sapiens) | 4.39 | 2.74 | + | 3.06E-03 | 3.70E-02 | | [negative regulation of multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0051241) | [1039](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&list=upload_1&organism=Homo%20sapiens) | 67.02 | 1.73 | + | 5.94E-08 | 2.60E-06 | | [regulation of bicellular tight junction assembly](http://amigo.geneontology.org/amigo/term/GO:2000810) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000810&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000810&list=upload_1&organism=Homo%20sapiens) | 1.29 | 4.65 | + | 3.95E-03 | 4.48E-02 | | [hematopoietic stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060218) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060218&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060218&list=upload_1&organism=Homo%20sapiens) | 1.29 | 4.65 | + | 3.95E-03 | 4.48E-02 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 11.80 | 2.63 | + | 7.23E-06 | 2.10E-04 | | [positive regulation of amyloid-beta formation](http://amigo.geneontology.org/amigo/term/GO:1902004) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902004&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902004&list=upload_1&organism=Homo%20sapiens) | 1.29 | 4.65 | + | 3.95E-03 | 4.48E-02 | | [positive regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034250) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034250&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034250&list=upload_1&organism=Homo%20sapiens) | 11.16 | 2.87 | + | 7.90E-07 | 2.86E-05 | | [regulation of amyloid-beta formation](http://amigo.geneontology.org/amigo/term/GO:1902003) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902003&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902003&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.88 | + | 1.31E-03 | 1.86E-02 | | [regulation of amyloid precursor protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902991) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902991&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902991&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.61 | + | 1.15E-03 | 1.68E-02 | | [positive regulation of amyloid precursor protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902993) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902993&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902993&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.77 | + | 7.83E-04 | 1.21E-02 | | [positive regulation of protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051247) | [1515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&reflist=1) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 97.72 | 2.19 | + | 8.06E-25 | 2.38E-22 | | [negative regulation of miRNA-mediated gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060965) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060965&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060965&list=upload_1&organism=Homo%20sapiens) | 1.29 | 4.65 | + | 3.95E-03 | 4.47E-02 | | [regulation of miRNA-mediated gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060964) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.69 | + | 9.87E-04 | 1.46E-02 | | [regulation of post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:1900368) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.52 | + | 1.34E-03 | 1.89E-02 | | [regulation of post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060147) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&list=upload_1&organism=Homo%20sapiens) | 2.90 | 3.45 | + | 1.55E-03 | 2.13E-02 | | [regulation of gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0060966) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&list=upload_1&organism=Homo%20sapiens) | 2.97 | 3.71 | + | 5.42E-04 | 8.93E-03 | | [positive regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010628) | [1151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&reflist=1) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 74.24 | 2.32 | + | 3.80E-22 | 8.90E-20 | | [phasic smooth muscle contraction](http://amigo.geneontology.org/amigo/term/GO:0014821) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014821&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014821&list=upload_1&organism=Homo%20sapiens) | 1.29 | 4.65 | + | 3.95E-03 | 4.47E-02 | | [muscle contraction](http://amigo.geneontology.org/amigo/term/GO:0006936) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006936&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006936&list=upload_1&organism=Homo%20sapiens) | 14.84 | 2.16 | + | 1.97E-04 | 3.87E-03 | | [muscle system process](http://amigo.geneontology.org/amigo/term/GO:0003012) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003012&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003012&list=upload_1&organism=Homo%20sapiens) | 18.19 | 2.25 | + | 8.73E-06 | 2.47E-04 | | [system process](http://amigo.geneontology.org/amigo/term/GO:0003008) | [2079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003008&reflist=1) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003008&list=upload_1&organism=Homo%20sapiens) | 134.10 | 1.31 | + | 3.89E-04 | 6.86E-03 | | [positive regulation of histone H3-K4 methylation](http://amigo.geneontology.org/amigo/term/GO:0051571) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051571&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051571&list=upload_1&organism=Homo%20sapiens) | 1.74 | 4.59 | + | 9.62E-04 | 1.43E-02 | | [regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031056) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.23 | + | 3.74E-04 | 6.63E-03 | | [positive regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031062) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031062&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031062&list=upload_1&organism=Homo%20sapiens) | 3.35 | 2.98 | + | 3.88E-03 | 4.42E-02 | | [positive regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031058) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 6.90 | 2.75 | + | 2.08E-04 | 4.02E-03 | | [positive regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031401) | [1019](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&reflist=1) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 65.73 | 2.15 | + | 1.39E-15 | 1.54E-13 | | [mismatch repair](http://amigo.geneontology.org/amigo/term/GO:0006298) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&list=upload_1&organism=Homo%20sapiens) | 2.19 | 4.56 | + | 2.41E-04 | 4.57E-03 | | [DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006281) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&list=upload_1&organism=Homo%20sapiens) | 32.77 | 1.92 | + | 4.45E-06 | 1.35E-04 | | [cellular response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:0006974) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 48.76 | 1.99 | + | 1.87E-09 | 9.86E-08 | | [Fc-epsilon receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038095) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038095&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038095&list=upload_1&organism=Homo%20sapiens) | 1.55 | 4.52 | + | 2.15E-03 | 2.78E-02 | | [Fc receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038093) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&list=upload_1&organism=Homo%20sapiens) | 3.35 | 3.88 | + | 1.20E-04 | 2.51E-03 | | [immune response-regulating signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002764) | [397](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&list=upload_1&organism=Homo%20sapiens) | 25.61 | 1.76 | + | 7.91E-04 | 1.22E-02 | | [positive regulation of erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045648) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045648&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045648&list=upload_1&organism=Homo%20sapiens) | 2.00 | 4.50 | + | 5.30E-04 | 8.77E-03 | | [positive regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045639) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 6.45 | 3.41 | + | 3.77E-06 | 1.16E-04 | | [regulation of erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045646) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.82 | + | 8.51E-06 | 2.43E-04 | | [positive regulation of interleukin-17 production](http://amigo.geneontology.org/amigo/term/GO:0032740) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032740&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032740&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.43 | + | 1.17E-03 | 1.70E-02 | | [positive regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001819) | [481](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 31.02 | 2.16 | + | 5.02E-08 | 2.23E-06 | | [regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001817) | [742](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&list=upload_1&organism=Homo%20sapiens) | 47.86 | 2.13 | + | 2.67E-11 | 1.82E-09 | | [base-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006284) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006284&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006284&list=upload_1&organism=Homo%20sapiens) | 2.71 | 4.43 | + | 7.43E-05 | 1.65E-03 | | [negative regulation of cardiac muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0010614) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010614&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010614&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.43 | + | 1.17E-03 | 1.70E-02 | | [negative regulation of muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014741) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014741&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014741&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.13 | + | 1.70E-03 | 2.31E-02 | | [regulation of system process](http://amigo.geneontology.org/amigo/term/GO:0044057) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044057&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044057&list=upload_1&organism=Homo%20sapiens) | 36.64 | 1.75 | + | 6.04E-05 | 1.39E-03 | | [regulation of muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043502) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&list=upload_1&organism=Homo%20sapiens) | 5.16 | 2.52 | + | 3.94E-03 | 4.48E-02 | | [cytoplasmic pattern recognition receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002753) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002753&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002753&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.43 | + | 1.17E-03 | 1.70E-02 | | [pattern recognition receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002221) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002221&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002221&list=upload_1&organism=Homo%20sapiens) | 6.39 | 2.51 | + | 2.29E-03 | 2.93E-02 | | [I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0007249) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007249&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007249&list=upload_1&organism=Homo%20sapiens) | 4.32 | 4.40 | + | 7.19E-07 | 2.63E-05 | | [cellular senescence](http://amigo.geneontology.org/amigo/term/GO:0090398) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&list=upload_1&organism=Homo%20sapiens) | 3.87 | 4.39 | + | 2.76E-06 | 8.80E-05 | | [intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0042771) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042771&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042771&list=upload_1&organism=Homo%20sapiens) | 2.06 | 4.36 | + | 6.43E-04 | 1.04E-02 | | [intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097193) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&list=upload_1&organism=Homo%20sapiens) | 10.51 | 2.47 | + | 8.45E-05 | 1.85E-03 | | [apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097190) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&list=upload_1&organism=Homo%20sapiens) | 20.38 | 2.26 | + | 1.95E-06 | 6.45E-05 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 66.63 | 2.18 | + | 1.52E-16 | 1.94E-14 | | [intrinsic apoptotic signaling pathway in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:0008630) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&list=upload_1&organism=Homo%20sapiens) | 4.77 | 3.77 | + | 8.72E-06 | 2.47E-04 | | [positive regulation of microtubule polymerization](http://amigo.geneontology.org/amigo/term/GO:0031116) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031116&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031116&list=upload_1&organism=Homo%20sapiens) | 2.06 | 4.36 | + | 6.43E-04 | 1.04E-02 | | [positive regulation of microtubule polymerization or depolymerization](http://amigo.geneontology.org/amigo/term/GO:0031112) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031112&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031112&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.88 | + | 1.31E-03 | 1.86E-02 | | [positive regulation of cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0051495) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051495&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051495&list=upload_1&organism=Homo%20sapiens) | 12.58 | 2.31 | + | 1.06E-04 | 2.24E-03 | | [positive regulation of protein polymerization](http://amigo.geneontology.org/amigo/term/GO:0032273) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032273&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032273&list=upload_1&organism=Homo%20sapiens) | 5.93 | 3.20 | + | 3.62E-05 | 8.91E-04 | | [positive regulation of protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0031334) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031334&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031334&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.56 | + | 7.37E-06 | 2.13E-04 | | [positive regulation of cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044089) | [501](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044089&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044089&list=upload_1&organism=Homo%20sapiens) | 32.31 | 2.01 | + | 6.67E-07 | 2.45E-05 | | [positive regulation of supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:1902905) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902905&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902905&list=upload_1&organism=Homo%20sapiens) | 11.35 | 2.47 | + | 4.63E-05 | 1.10E-03 | | [regulation of protein export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0046825) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046825&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046825&list=upload_1&organism=Homo%20sapiens) | 2.06 | 4.36 | + | 6.43E-04 | 1.04E-02 | | [regulation of intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0033157) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033157&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033157&list=upload_1&organism=Homo%20sapiens) | 14.90 | 2.42 | + | 6.65E-06 | 1.95E-04 | | [regulation of protein transport](http://amigo.geneontology.org/amigo/term/GO:0051223) | [502](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&list=upload_1&organism=Homo%20sapiens) | 32.38 | 2.16 | + | 2.07E-08 | 9.60E-07 | | [regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051049) | [1766](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&reflist=1) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&list=upload_1&organism=Homo%20sapiens) | 113.91 | 1.81 | + | 2.84E-15 | 3.05E-13 | | [regulation of intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0032386) | [342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&list=upload_1&organism=Homo%20sapiens) | 22.06 | 2.27 | + | 5.82E-07 | 2.17E-05 | | [regulation of nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0046822) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.91 | + | 5.00E-05 | 1.17E-03 | | [cellular response to epidermal growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0071364) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071364&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071364&list=upload_1&organism=Homo%20sapiens) | 2.77 | 4.33 | + | 8.98E-05 | 1.95E-03 | | [response to epidermal growth factor](http://amigo.geneontology.org/amigo/term/GO:0070849) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070849&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070849&list=upload_1&organism=Homo%20sapiens) | 3.03 | 4.29 | + | 4.99E-05 | 1.17E-03 | | [protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0043491) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043491&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043491&list=upload_1&organism=Homo%20sapiens) | 3.48 | 4.31 | + | 1.29E-05 | 3.52E-04 | | [negative regulation of extrinsic apoptotic signaling pathway via death domain receptors](http://amigo.geneontology.org/amigo/term/GO:1902042) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902042&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902042&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.28 | + | 1.42E-03 | 1.98E-02 | | [regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001236) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.72 | + | 1.32E-05 | 3.59E-04 | | [negative regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001237) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&list=upload_1&organism=Homo%20sapiens) | 6.32 | 3.48 | + | 2.84E-06 | 8.99E-05 | | [regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay](http://amigo.geneontology.org/amigo/term/GO:1900151) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900151&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900151&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.77E-02 | | [regulation of mRNA stability](http://amigo.geneontology.org/amigo/term/GO:0043488) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&list=upload_1&organism=Homo%20sapiens) | 10.51 | 2.28 | + | 5.18E-04 | 8.61E-03 | | [regulation of RNA stability](http://amigo.geneontology.org/amigo/term/GO:0043487) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&list=upload_1&organism=Homo%20sapiens) | 11.29 | 2.21 | + | 5.22E-04 | 8.66E-03 | | [regulation of mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0061013) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061013&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061013&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.23 | + | 3.74E-04 | 6.62E-03 | | [regulation of mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903311) | [301](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&list=upload_1&organism=Homo%20sapiens) | 19.41 | 2.01 | + | 1.27E-04 | 2.66E-03 | | [regulation of telomere capping](http://amigo.geneontology.org/amigo/term/GO:1904353) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904353&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904353&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.76E-02 | | [muscle cell cellular homeostasis](http://amigo.geneontology.org/amigo/term/GO:0046716) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046716&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046716&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.76E-02 | | [cellular homeostasis](http://amigo.geneontology.org/amigo/term/GO:0019725) | [641](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019725&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019725&list=upload_1&organism=Homo%20sapiens) | 41.34 | 1.72 | + | 4.02E-05 | 9.73E-04 | | [homeostatic process](http://amigo.geneontology.org/amigo/term/GO:0042592) | [1424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&reflist=1) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&list=upload_1&organism=Homo%20sapiens) | 91.85 | 1.70 | + | 9.17E-10 | 5.04E-08 | | [anatomical structure homeostasis](http://amigo.geneontology.org/amigo/term/GO:0060249) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&list=upload_1&organism=Homo%20sapiens) | 19.54 | 2.35 | + | 6.65E-07 | 2.44E-05 | | [regulation of miRNA maturation](http://amigo.geneontology.org/amigo/term/GO:1903798) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903798&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903798&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.76E-02 | | [regulation of production of small RNA involved in gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0070920) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070920&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070920&list=upload_1&organism=Homo%20sapiens) | 1.74 | 4.02 | + | 3.75E-03 | 4.31E-02 | | [regulation of necroptotic process](http://amigo.geneontology.org/amigo/term/GO:0060544) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060544&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060544&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.17 | + | 3.14E-03 | 3.76E-02 | | [regulation of programmed necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0062098) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062098&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062098&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.28 | + | 1.42E-03 | 1.98E-02 | | [regulation of necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0010939) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010939&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010939&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.24 | + | 3.71E-03 | 4.28E-02 | | [positive regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051973) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051973&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051973&list=upload_1&organism=Homo%20sapiens) | 2.19 | 4.10 | + | 9.28E-04 | 1.39E-02 | | [positive regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000573) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000573&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000573&list=upload_1&organism=Homo%20sapiens) | 4.84 | 3.51 | + | 3.35E-05 | 8.33E-04 | | [positive regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051347) | [590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&list=upload_1&organism=Homo%20sapiens) | 38.06 | 2.08 | + | 1.30E-08 | 6.18E-07 | | [tumor necrosis factor-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033209) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033209&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033209&list=upload_1&organism=Homo%20sapiens) | 3.68 | 4.08 | + | 2.21E-05 | 5.73E-04 | | [cellular response to tumor necrosis factor](http://amigo.geneontology.org/amigo/term/GO:0071356) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&list=upload_1&organism=Homo%20sapiens) | 11.48 | 3.75 | + | 8.26E-12 | 6.00E-10 | | [response to tumor necrosis factor](http://amigo.geneontology.org/amigo/term/GO:0034612) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&list=upload_1&organism=Homo%20sapiens) | 13.03 | 3.45 | + | 2.81E-11 | 1.91E-09 | | [cytokine-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0019221) | [366](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&list=upload_1&organism=Homo%20sapiens) | 23.61 | 2.20 | + | 7.73E-07 | 2.81E-05 | | [reactive nitrogen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2001057) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001057&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001057&list=upload_1&organism=Homo%20sapiens) | 1.74 | 4.02 | + | 3.75E-03 | 4.32E-02 | | [regulation of superoxide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090322) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090322&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090322&list=upload_1&organism=Homo%20sapiens) | 2.00 | 4.00 | + | 2.03E-03 | 2.68E-02 | | [regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000377) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000377&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000377&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.91 | + | 4.49E-06 | 1.36E-04 | | [striated muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014897) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014897&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014897&list=upload_1&organism=Homo%20sapiens) | 2.00 | 4.00 | + | 2.03E-03 | 2.68E-02 | | [muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014896) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014896&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014896&list=upload_1&organism=Homo%20sapiens) | 2.13 | 3.76 | + | 2.83E-03 | 3.47E-02 | | [cellular response to hydrogen peroxide](http://amigo.geneontology.org/amigo/term/GO:0070301) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070301&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070301&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.99 | + | 8.12E-06 | 2.33E-04 | | [response to hydrogen peroxide](http://amigo.geneontology.org/amigo/term/GO:0042542) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&list=upload_1&organism=Homo%20sapiens) | 6.64 | 3.16 | + | 1.70E-05 | 4.51E-04 | | [regulation of regulatory T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045589) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045589&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045589&list=upload_1&organism=Homo%20sapiens) | 2.26 | 3.99 | + | 1.10E-03 | 1.62E-02 | | [lipopolysaccharide-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0031663) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031663&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031663&list=upload_1&organism=Homo%20sapiens) | 2.52 | 3.98 | + | 6.05E-04 | 9.88E-03 | | [cellular response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0071222) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.40 | + | 4.99E-05 | 1.17E-03 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 20.19 | 2.33 | + | 9.30E-07 | 3.32E-05 | | [response to molecule of bacterial origin](http://amigo.geneontology.org/amigo/term/GO:0002237) | [331](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&list=upload_1&organism=Homo%20sapiens) | 21.35 | 2.30 | + | 6.04E-07 | 2.25E-05 | | [response to external biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0043207) | [1432](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&reflist=1) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&list=upload_1&organism=Homo%20sapiens) | 92.36 | 1.94 | + | 1.00E-15 | 1.15E-13 | | [response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009607) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&reflist=1) | [185](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&list=upload_1&organism=Homo%20sapiens) | 95.33 | 1.94 | + | 1.94E-16 | 2.38E-14 | | [response to bacterium](http://amigo.geneontology.org/amigo/term/GO:0009617) | [754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&list=upload_1&organism=Homo%20sapiens) | 48.63 | 1.79 | + | 9.37E-07 | 3.34E-05 | | [response to other organism](http://amigo.geneontology.org/amigo/term/GO:0051707) | [1429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&reflist=1) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&list=upload_1&organism=Homo%20sapiens) | 92.17 | 1.93 | + | 1.48E-15 | 1.62E-13 | | [cellular response to molecule of bacterial origin](http://amigo.geneontology.org/amigo/term/GO:0071219) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&list=upload_1&organism=Homo%20sapiens) | 13.16 | 2.36 | + | 4.44E-05 | 1.06E-03 | | [cellular response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071216) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&list=upload_1&organism=Homo%20sapiens) | 14.90 | 2.48 | + | 3.31E-06 | 1.03E-04 | | [positive regulation of nitric oxide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0045429) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045429&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045429&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.97 | + | 3.32E-04 | 5.95E-03 | | [positive regulation of nitric oxide metabolic process](http://amigo.geneontology.org/amigo/term/GO:1904407) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904407&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904407&list=upload_1&organism=Homo%20sapiens) | 2.90 | 3.79 | + | 4.63E-04 | 7.85E-03 | | [regulation of nitric oxide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0045428) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045428&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045428&list=upload_1&organism=Homo%20sapiens) | 3.81 | 2.89 | + | 3.10E-03 | 3.73E-02 | | [negative regulation of lipid localization](http://amigo.geneontology.org/amigo/term/GO:1905953) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905953&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905953&list=upload_1&organism=Homo%20sapiens) | 3.03 | 3.96 | + | 1.83E-04 | 3.66E-03 | | [regulation of lipid localization](http://amigo.geneontology.org/amigo/term/GO:1905952) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905952&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905952&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.04 | + | 3.14E-03 | 3.74E-02 | | [negative regulation of myoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045662) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045662&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045662&list=upload_1&organism=Homo%20sapiens) | 1.81 | 3.88 | + | 4.44E-03 | 4.98E-02 | | [regulation of myoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045661) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045661&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045661&list=upload_1&organism=Homo%20sapiens) | 4.97 | 3.02 | + | 4.01E-04 | 7.02E-03 | | [negative regulation of extrinsic apoptotic signaling pathway in absence of ligand](http://amigo.geneontology.org/amigo/term/GO:2001240) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001240&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001240&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.88 | + | 1.31E-03 | 1.86E-02 | | [regulation of extrinsic apoptotic signaling pathway in absence of ligand](http://amigo.geneontology.org/amigo/term/GO:2001239) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001239&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001239&list=upload_1&organism=Homo%20sapiens) | 2.97 | 3.37 | + | 1.78E-03 | 2.41E-02 | | [negative regulation of signal transduction in absence of ligand](http://amigo.geneontology.org/amigo/term/GO:1901099) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901099&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901099&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.88 | + | 1.31E-03 | 1.86E-02 | | [translational elongation](http://amigo.geneontology.org/amigo/term/GO:0006414) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006414&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006414&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.88 | + | 3.93E-04 | 6.91E-03 | | [cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0034645) | [773](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034645&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034645&list=upload_1&organism=Homo%20sapiens) | 49.86 | 1.66 | + | 2.04E-05 | 5.35E-04 | | [cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044249) | [2464](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&reflist=1) | [262](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&list=upload_1&organism=Homo%20sapiens) | 158.93 | 1.65 | + | 7.23E-15 | 7.26E-13 | | [biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009058) | [2603](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&reflist=1) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&list=upload_1&organism=Homo%20sapiens) | 167.89 | 1.64 | + | 1.45E-15 | 1.60E-13 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 95.91 | 1.75 | + | 2.03E-11 | 1.40E-09 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 163.44 | 1.63 | + | 1.52E-14 | 1.45E-12 | | [translation](http://amigo.geneontology.org/amigo/term/GO:0006412) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006412&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006412&list=upload_1&organism=Homo%20sapiens) | 24.45 | 2.25 | + | 2.17E-07 | 8.72E-06 | | [peptide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0043043) | [408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043043&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043043&list=upload_1&organism=Homo%20sapiens) | 26.32 | 2.20 | + | 1.96E-07 | 8.03E-06 | | [peptide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006518) | [537](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006518&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006518&list=upload_1&organism=Homo%20sapiens) | 34.64 | 2.02 | + | 2.39E-07 | 9.58E-06 | | [cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043603) | [802](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043603&reflist=1) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043603&list=upload_1&organism=Homo%20sapiens) | 51.73 | 1.74 | + | 1.87E-06 | 6.23E-05 | | [amide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0043604) | [527](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043604&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043604&list=upload_1&organism=Homo%20sapiens) | 33.99 | 2.12 | + | 2.68E-08 | 1.23E-06 | | [cellular nitrogen compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044271) | [1588](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&reflist=1) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 102.43 | 1.89 | + | 3.03E-16 | 3.65E-14 | | [organonitrogen compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901566) | [1333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901566&reflist=1) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901566&list=upload_1&organism=Homo%20sapiens) | 85.98 | 1.54 | + | 3.95E-06 | 1.21E-04 | | [positive regulation of RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0033120) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033120&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033120&list=upload_1&organism=Homo%20sapiens) | 2.58 | 3.88 | + | 7.15E-04 | 1.13E-02 | | [regulation of RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0043484) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.06 | + | 1.79E-03 | 2.41E-02 | | [positive regulation of G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:1900087) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900087&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900087&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.88 | + | 3.93E-04 | 6.90E-03 | | [regulation of G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:2000045) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000045&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000045&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.84 | + | 2.11E-06 | 6.94E-05 | | [regulation of cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:1902806) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 12.38 | 2.66 | + | 2.94E-06 | 9.29E-05 | | [regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901987) | [431](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&list=upload_1&organism=Homo%20sapiens) | 27.80 | 2.16 | + | 2.41E-07 | 9.62E-06 | | [regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901990) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&list=upload_1&organism=Homo%20sapiens) | 21.41 | 2.43 | + | 5.56E-08 | 2.45E-06 | | [regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007346) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 31.80 | 2.39 | + | 8.88E-11 | 5.57E-09 | | [positive regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901992) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901992&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901992&list=upload_1&organism=Homo%20sapiens) | 5.93 | 3.37 | + | 1.19E-05 | 3.30E-04 | | [positive regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901989) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901989&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901989&list=upload_1&organism=Homo%20sapiens) | 7.42 | 3.10 | + | 9.03E-06 | 2.54E-04 | | [positive regulation of cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0090068) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&list=upload_1&organism=Homo%20sapiens) | 16.19 | 2.47 | + | 1.30E-06 | 4.51E-05 | | [positive regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045787) | [353](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 22.77 | 2.33 | + | 1.40E-07 | 5.83E-06 | | [positive regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045931) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&list=upload_1&organism=Homo%20sapiens) | 7.80 | 3.08 | + | 6.57E-06 | 1.93E-04 | | [positive regulation of cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:1902808) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902808&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902808&list=upload_1&organism=Homo%20sapiens) | 3.74 | 3.47 | + | 3.02E-04 | 5.52E-03 | | [positive regulation of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0045070) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045070&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045070&list=upload_1&organism=Homo%20sapiens) | 2.06 | 3.88 | + | 2.40E-03 | 3.05E-02 | | [positive regulation of viral process](http://amigo.geneontology.org/amigo/term/GO:0048524) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048524&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048524&list=upload_1&organism=Homo%20sapiens) | 4.19 | 3.58 | + | 8.04E-05 | 1.77E-03 | | [regulation of viral process](http://amigo.geneontology.org/amigo/term/GO:0050792) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.36 | + | 2.91E-04 | 5.38E-03 | | [regulation of viral life cycle](http://amigo.geneontology.org/amigo/term/GO:1903900) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903900&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903900&list=upload_1&organism=Homo%20sapiens) | 9.16 | 2.29 | + | 1.30E-03 | 1.85E-02 | | [regulation of protein targeting to mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903214) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903214&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903214&list=upload_1&organism=Homo%20sapiens) | 2.90 | 3.79 | + | 4.63E-04 | 7.86E-03 | | [regulation of protein targeting](http://amigo.geneontology.org/amigo/term/GO:1903533) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903533&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903533&list=upload_1&organism=Homo%20sapiens) | 5.16 | 2.71 | + | 1.54E-03 | 2.12E-02 | | [positive regulation of interferon-beta production](http://amigo.geneontology.org/amigo/term/GO:0032728) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032728&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032728&list=upload_1&organism=Homo%20sapiens) | 2.64 | 3.78 | + | 8.42E-04 | 1.29E-02 | | [positive regulation of type I interferon production](http://amigo.geneontology.org/amigo/term/GO:0032481) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032481&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032481&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.45 | + | 1.94E-04 | 3.82E-03 | | [regulation of type I interferon production](http://amigo.geneontology.org/amigo/term/GO:0032479) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032479&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032479&list=upload_1&organism=Homo%20sapiens) | 6.64 | 3.16 | + | 1.70E-05 | 4.51E-04 | | [regulation of interferon-beta production](http://amigo.geneontology.org/amigo/term/GO:0032648) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032648&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032648&list=upload_1&organism=Homo%20sapiens) | 3.74 | 3.74 | + | 9.14E-05 | 1.98E-03 | | [regulation of transcription from RNA polymerase II promoter in response to stress](http://amigo.geneontology.org/amigo/term/GO:0043618) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043618&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043618&list=upload_1&organism=Homo%20sapiens) | 2.64 | 3.78 | + | 8.42E-04 | 1.28E-02 | | [regulation of DNA-templated transcription in response to stress](http://amigo.geneontology.org/amigo/term/GO:0043620) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043620&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043620&list=upload_1&organism=Homo%20sapiens) | 3.03 | 3.63 | + | 6.33E-04 | 1.03E-02 | | [negative regulation of proteasomal ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0032435) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032435&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032435&list=upload_1&organism=Homo%20sapiens) | 2.39 | 3.77 | + | 1.54E-03 | 2.13E-02 | | [negative regulation of proteasomal protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901799) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901799&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901799&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.34E-02 | | [negative regulation of protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0042177) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042177&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042177&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.82 | + | 1.08E-04 | 2.28E-03 | | [regulation of protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0042176) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&list=upload_1&organism=Homo%20sapiens) | 23.67 | 2.41 | + | 1.43E-08 | 6.79E-07 | | [negative regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009895) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&list=upload_1&organism=Homo%20sapiens) | 21.03 | 2.38 | + | 1.62E-07 | 6.70E-06 | | [regulation of proteasomal protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0061136) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061136&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061136&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.88 | + | 1.54E-07 | 6.40E-06 | | [regulation of proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1903050) | [228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&list=upload_1&organism=Homo%20sapiens) | 14.71 | 2.92 | + | 6.50E-09 | 3.22E-07 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 47.92 | 2.19 | + | 2.12E-12 | 1.62E-10 | | [negative regulation of proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1903051) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903051&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903051&list=upload_1&organism=Homo%20sapiens) | 4.19 | 3.58 | + | 8.04E-05 | 1.78E-03 | | [negative regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0045861) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045861&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045861&list=upload_1&organism=Homo%20sapiens) | 22.25 | 1.98 | + | 6.18E-05 | 1.42E-03 | | [regulation of proteasomal ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0032434) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&list=upload_1&organism=Homo%20sapiens) | 9.16 | 3.28 | + | 1.50E-07 | 6.25E-06 | | [regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000058) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&list=upload_1&organism=Homo%20sapiens) | 11.09 | 3.24 | + | 1.09E-08 | 5.25E-07 | | [negative regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000059) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.95 | + | 1.01E-04 | 2.16E-03 | | [negative regulation of cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0031330) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 15.61 | 2.37 | + | 6.73E-06 | 1.97E-04 | | [aortic valve development](http://amigo.geneontology.org/amigo/term/GO:0003176) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&list=upload_1&organism=Homo%20sapiens) | 2.39 | 3.77 | + | 1.54E-03 | 2.12E-02 | | [protein export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0006611) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006611&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006611&list=upload_1&organism=Homo%20sapiens) | 2.13 | 3.76 | + | 2.83E-03 | 3.47E-02 | | [nuclear export](http://amigo.geneontology.org/amigo/term/GO:0051168) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051168&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051168&list=upload_1&organism=Homo%20sapiens) | 8.58 | 2.68 | + | 6.74E-05 | 1.53E-03 | | [nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0006913) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&list=upload_1&organism=Homo%20sapiens) | 16.00 | 2.69 | + | 6.61E-08 | 2.88E-06 | | [nuclear transport](http://amigo.geneontology.org/amigo/term/GO:0051169) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&list=upload_1&organism=Homo%20sapiens) | 16.00 | 2.69 | + | 6.61E-08 | 2.87E-06 | | [mammary gland duct morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060603) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060603&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060603&list=upload_1&organism=Homo%20sapiens) | 2.13 | 3.76 | + | 2.83E-03 | 3.47E-02 | | [epithelial tube morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060562) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060562&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060562&list=upload_1&organism=Homo%20sapiens) | 20.51 | 1.95 | + | 1.90E-04 | 3.76E-03 | | [morphogenesis of an epithelium](http://amigo.geneontology.org/amigo/term/GO:0002009) | [459](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002009&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002009&list=upload_1&organism=Homo%20sapiens) | 29.61 | 2.03 | + | 1.49E-06 | 5.06E-05 | | [tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048729) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&list=upload_1&organism=Homo%20sapiens) | 36.64 | 1.88 | + | 2.79E-06 | 8.86E-05 | | [tube morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0035239) | [673](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&list=upload_1&organism=Homo%20sapiens) | 43.41 | 1.66 | + | 8.54E-05 | 1.87E-03 | | [tube development](http://amigo.geneontology.org/amigo/term/GO:0035295) | [885](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&list=upload_1&organism=Homo%20sapiens) | 57.08 | 1.59 | + | 4.64E-05 | 1.10E-03 | | [animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009887) | [1003](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&list=upload_1&organism=Homo%20sapiens) | 64.69 | 1.76 | + | 3.47E-08 | 1.58E-06 | | [positive regulation of NIK/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:1901224) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901224&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901224&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.70 | + | 3.29E-05 | 8.21E-04 | | [positive regulation of intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:1902533) | [999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 64.44 | 2.16 | + | 1.30E-15 | 1.45E-13 | | [regulation of NIK/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:1901222) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901222&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901222&list=upload_1&organism=Homo%20sapiens) | 6.45 | 3.41 | + | 3.77E-06 | 1.16E-04 | | [type I interferon signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0060337) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060337&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060337&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.69 | + | 9.87E-04 | 1.46E-02 | | [cellular response to type I interferon](http://amigo.geneontology.org/amigo/term/GO:0071357) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071357&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071357&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.88 | + | 3.93E-04 | 6.91E-03 | | [response to type I interferon](http://amigo.geneontology.org/amigo/term/GO:0034340) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034340&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034340&list=upload_1&organism=Homo%20sapiens) | 3.35 | 3.88 | + | 1.20E-04 | 2.51E-03 | | [innate immune response](http://amigo.geneontology.org/amigo/term/GO:0045087) | [832](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&list=upload_1&organism=Homo%20sapiens) | 53.66 | 1.84 | + | 4.68E-08 | 2.10E-06 | | [defense response to other organism](http://amigo.geneontology.org/amigo/term/GO:0098542) | [1068](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098542&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098542&list=upload_1&organism=Homo%20sapiens) | 68.89 | 1.77 | + | 9.61E-09 | 4.68E-07 | | [defense response](http://amigo.geneontology.org/amigo/term/GO:0006952) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&reflist=1) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&list=upload_1&organism=Homo%20sapiens) | 95.33 | 1.75 | + | 1.90E-11 | 1.32E-09 | | [immune response](http://amigo.geneontology.org/amigo/term/GO:0006955) | [1621](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&reflist=1) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&list=upload_1&organism=Homo%20sapiens) | 104.56 | 1.54 | + | 1.99E-07 | 8.09E-06 | | [columnar/cuboidal epithelial cell development](http://amigo.geneontology.org/amigo/term/GO:0002066) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002066&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002066&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.69 | + | 9.87E-04 | 1.46E-02 | | [epithelial cell development](http://amigo.geneontology.org/amigo/term/GO:0002064) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002064&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002064&list=upload_1&organism=Homo%20sapiens) | 12.32 | 2.19 | + | 4.63E-04 | 7.85E-03 | | [positive regulation of protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0042307) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042307&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042307&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.69 | + | 9.87E-04 | 1.46E-02 | | [positive regulation of nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0046824) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046824&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046824&list=upload_1&organism=Homo%20sapiens) | 4.13 | 3.39 | + | 2.23E-04 | 4.27E-03 | | [positive regulation of intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0032388) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032388&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032388&list=upload_1&organism=Homo%20sapiens) | 13.09 | 2.29 | + | 8.63E-05 | 1.88E-03 | | [positive regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051050) | [919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&reflist=1) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&list=upload_1&organism=Homo%20sapiens) | 59.28 | 1.99 | + | 2.37E-11 | 1.63E-09 | | [positive regulation of intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0090316) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090316&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090316&list=upload_1&organism=Homo%20sapiens) | 10.32 | 2.52 | + | 6.75E-05 | 1.53E-03 | | [positive regulation of protein transport](http://amigo.geneontology.org/amigo/term/GO:0051222) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051222&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051222&list=upload_1&organism=Homo%20sapiens) | 19.61 | 2.29 | + | 2.06E-06 | 6.80E-05 | | [positive regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:1904951) | [320](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&list=upload_1&organism=Homo%20sapiens) | 20.64 | 2.28 | + | 1.25E-06 | 4.36E-05 | | [positive regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:1903829) | [462](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903829&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903829&list=upload_1&organism=Homo%20sapiens) | 29.80 | 2.15 | + | 1.32E-07 | 5.54E-06 | | [regulation of protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0042306) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042306&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042306&list=upload_1&organism=Homo%20sapiens) | 4.00 | 2.75 | + | 4.32E-03 | 4.85E-02 | | [positive regulation of lamellipodium organization](http://amigo.geneontology.org/amigo/term/GO:1902745) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902745&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902745&list=upload_1&organism=Homo%20sapiens) | 2.45 | 3.67 | + | 1.80E-03 | 2.42E-02 | | [regulation of plasma membrane bounded cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0120035) | [640](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&list=upload_1&organism=Homo%20sapiens) | 41.28 | 1.60 | + | 5.22E-04 | 8.66E-03 | | [regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031344) | [656](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&list=upload_1&organism=Homo%20sapiens) | 42.31 | 1.56 | + | 8.25E-04 | 1.26E-02 | | [positive regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031346) | [351](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&list=upload_1&organism=Homo%20sapiens) | 22.64 | 1.86 | + | 3.71E-04 | 6.58E-03 | | [cellular response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0071276) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071276&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071276&list=upload_1&organism=Homo%20sapiens) | 2.45 | 3.67 | + | 1.80E-03 | 2.42E-02 | | [response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0046686) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&list=upload_1&organism=Homo%20sapiens) | 3.93 | 3.81 | + | 4.32E-05 | 1.03E-03 | | [response to metal ion](http://amigo.geneontology.org/amigo/term/GO:0010038) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&list=upload_1&organism=Homo%20sapiens) | 23.41 | 2.01 | + | 2.43E-05 | 6.23E-04 | | [cellular response to metal ion](http://amigo.geneontology.org/amigo/term/GO:0071248) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071248&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071248&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.17 | + | 3.75E-04 | 6.64E-03 | | [cellular response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0071241) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&list=upload_1&organism=Homo%20sapiens) | 14.84 | 2.16 | + | 1.97E-04 | 3.87E-03 | | [dendritic cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0097028) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097028&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097028&list=upload_1&organism=Homo%20sapiens) | 2.45 | 3.67 | + | 1.80E-03 | 2.41E-02 | | [antigen processing and presentation of peptide or polysaccharide antigen via MHC class II](http://amigo.geneontology.org/amigo/term/GO:0002504) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002504&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002504&list=upload_1&organism=Homo%20sapiens) | 2.19 | 3.65 | + | 3.31E-03 | 3.91E-02 | | [antigen processing and presentation](http://amigo.geneontology.org/amigo/term/GO:0019882) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019882&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019882&list=upload_1&organism=Homo%20sapiens) | 6.19 | 2.75 | + | 4.52E-04 | 7.72E-03 | | [cytoplasmic translational initiation](http://amigo.geneontology.org/amigo/term/GO:0002183) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002183&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002183&list=upload_1&organism=Homo%20sapiens) | 2.19 | 3.65 | + | 3.31E-03 | 3.91E-02 | | [cytoplasmic translation](http://amigo.geneontology.org/amigo/term/GO:0002181) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&list=upload_1&organism=Homo%20sapiens) | 8.00 | 3.13 | + | 3.31E-06 | 1.03E-04 | | [translational initiation](http://amigo.geneontology.org/amigo/term/GO:0006413) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006413&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006413&list=upload_1&organism=Homo%20sapiens) | 4.52 | 3.99 | + | 4.52E-06 | 1.37E-04 | | [postreplication repair](http://amigo.geneontology.org/amigo/term/GO:0006301) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006301&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006301&list=upload_1&organism=Homo%20sapiens) | 2.19 | 3.65 | + | 3.31E-03 | 3.91E-02 | | [positive regulation of glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045687) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045687&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045687&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.61 | + | 1.15E-03 | 1.68E-02 | | [positive regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014015) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.29 | + | 2.93E-04 | 5.40E-03 | | [regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014013) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&list=upload_1&organism=Homo%20sapiens) | 6.51 | 3.07 | + | 3.84E-05 | 9.39E-04 | | [regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050767) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&list=upload_1&organism=Homo%20sapiens) | 24.06 | 2.04 | + | 1.18E-05 | 3.27E-04 | | [regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051960) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&list=upload_1&organism=Homo%20sapiens) | 29.15 | 1.82 | + | 9.52E-05 | 2.06E-03 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 33.09 | 1.96 | + | 1.40E-06 | 4.83E-05 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 14.90 | 2.28 | + | 3.91E-05 | 9.51E-04 | | [positive regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051962) | [279](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&list=upload_1&organism=Homo%20sapiens) | 18.00 | 2.00 | + | 2.89E-04 | 5.34E-03 | | [positive regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0010720) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 19.87 | 2.11 | + | 2.25E-05 | 5.82E-04 | | [regulation of glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045685) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&list=upload_1&organism=Homo%20sapiens) | 4.77 | 2.72 | + | 2.17E-03 | 2.81E-02 | | [regulation of protein localization to cell surface](http://amigo.geneontology.org/amigo/term/GO:2000008) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000008&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000008&list=upload_1&organism=Homo%20sapiens) | 2.52 | 3.58 | + | 2.10E-03 | 2.74E-02 | | [post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0016441) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016441&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016441&list=upload_1&organism=Homo%20sapiens) | 2.52 | 3.58 | + | 2.10E-03 | 2.73E-02 | | [digestive tract morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048546) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&list=upload_1&organism=Homo%20sapiens) | 3.10 | 3.55 | + | 7.36E-04 | 1.15E-02 | | [digestive tract development](http://amigo.geneontology.org/amigo/term/GO:0048565) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048565&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048565&list=upload_1&organism=Homo%20sapiens) | 8.51 | 2.23 | + | 2.82E-03 | 3.47E-02 | | [digestive system development](http://amigo.geneontology.org/amigo/term/GO:0055123) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&list=upload_1&organism=Homo%20sapiens) | 9.22 | 2.28 | + | 1.34E-03 | 1.90E-02 | | [regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060251) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 2.26 | 3.54 | + | 3.86E-03 | 4.42E-02 | | [regulation of cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0042127) | [1674](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&reflist=1) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 107.97 | 1.99 | + | 3.03E-20 | 5.79E-18 | | [negative regulation of striated muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051154) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051154&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051154&list=upload_1&organism=Homo%20sapiens) | 2.26 | 3.54 | + | 3.86E-03 | 4.42E-02 | | [negative regulation of muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051148) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051148&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051148&list=upload_1&organism=Homo%20sapiens) | 3.81 | 3.42 | + | 3.48E-04 | 6.21E-03 | | [regulation of muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051147) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051147&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051147&list=upload_1&organism=Homo%20sapiens) | 8.77 | 2.17 | + | 3.35E-03 | 3.94E-02 | | [muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043500) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043500&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043500&list=upload_1&organism=Homo%20sapiens) | 2.26 | 3.54 | + | 3.86E-03 | 4.42E-02 | | [positive regulation of peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0033138) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033138&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033138&list=upload_1&organism=Homo%20sapiens) | 7.10 | 3.52 | + | 5.02E-07 | 1.89E-05 | | [positive regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001934) | [748](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&list=upload_1&organism=Homo%20sapiens) | 48.25 | 2.07 | + | 1.42E-10 | 8.61E-09 | | [regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001932) | [1105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&reflist=1) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 71.27 | 2.03 | + | 2.43E-14 | 2.29E-12 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 80.50 | 2.16 | + | 1.82E-19 | 3.06E-17 | | [regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019220) | [1404](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&reflist=1) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 90.56 | 2.14 | + | 2.30E-21 | 4.74E-19 | | [regulation of phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051174) | [1405](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&reflist=1) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 90.62 | 2.14 | + | 2.38E-21 | 4.84E-19 | | [positive regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042327) | [826](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&list=upload_1&organism=Homo%20sapiens) | 53.28 | 2.14 | + | 1.12E-12 | 8.84E-11 | | [positive regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045937) | [911](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&list=upload_1&organism=Homo%20sapiens) | 58.76 | 2.13 | + | 8.95E-14 | 7.88E-12 | | [positive regulation of phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010562) | [911](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&list=upload_1&organism=Homo%20sapiens) | 58.76 | 2.13 | + | 8.95E-14 | 7.93E-12 | | [regulation of peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0033135) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033135&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033135&list=upload_1&organism=Homo%20sapiens) | 9.22 | 3.04 | + | 1.44E-06 | 4.95E-05 | | [cardiac muscle cell contraction](http://amigo.geneontology.org/amigo/term/GO:0086003) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086003&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086003&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.52 | + | 1.34E-03 | 1.89E-02 | | [cardiac muscle contraction](http://amigo.geneontology.org/amigo/term/GO:0060048) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060048&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060048&list=upload_1&organism=Homo%20sapiens) | 4.90 | 2.86 | + | 1.00E-03 | 1.48E-02 | | [striated muscle contraction](http://amigo.geneontology.org/amigo/term/GO:0006941) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006941&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006941&list=upload_1&organism=Homo%20sapiens) | 7.03 | 2.42 | + | 1.95E-03 | 2.60E-02 | | [heart contraction](http://amigo.geneontology.org/amigo/term/GO:0060047) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060047&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060047&list=upload_1&organism=Homo%20sapiens) | 6.00 | 3.17 | + | 4.11E-05 | 9.92E-04 | | [heart process](http://amigo.geneontology.org/amigo/term/GO:0003015) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003015&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003015&list=upload_1&organism=Homo%20sapiens) | 7.03 | 3.13 | + | 1.24E-05 | 3.40E-04 | | [circulatory system process](http://amigo.geneontology.org/amigo/term/GO:0003013) | [498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003013&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003013&list=upload_1&organism=Homo%20sapiens) | 32.12 | 1.84 | + | 2.94E-05 | 7.39E-04 | | [blood circulation](http://amigo.geneontology.org/amigo/term/GO:0008015) | [408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008015&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008015&list=upload_1&organism=Homo%20sapiens) | 26.32 | 1.98 | + | 1.65E-05 | 4.41E-04 | | [actin-mediated cell contraction](http://amigo.geneontology.org/amigo/term/GO:0070252) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070252&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070252&list=upload_1&organism=Homo%20sapiens) | 4.39 | 2.74 | + | 3.06E-03 | 3.70E-02 | | [actin filament-based process](http://amigo.geneontology.org/amigo/term/GO:0030029) | [611](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030029&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030029&list=upload_1&organism=Homo%20sapiens) | 39.41 | 1.60 | + | 7.16E-04 | 1.13E-02 | | [cellular response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0071456) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&list=upload_1&organism=Homo%20sapiens) | 8.26 | 3.51 | + | 6.68E-08 | 2.88E-06 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 17.87 | 2.91 | + | 2.00E-10 | 1.19E-08 | | [response to decreased oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0036293) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 18.71 | 2.83 | + | 3.12E-10 | 1.81E-08 | | [response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0070482) | [319](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 20.58 | 2.67 | + | 1.00E-09 | 5.47E-08 | | [cellular response to decreased oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0036294) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&list=upload_1&organism=Homo%20sapiens) | 8.77 | 3.42 | + | 6.64E-08 | 2.88E-06 | | [cellular response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0071453) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&list=upload_1&organism=Homo%20sapiens) | 9.87 | 3.14 | + | 2.10E-07 | 8.52E-06 | | [circadian regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0032922) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032922&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032922&list=upload_1&organism=Homo%20sapiens) | 4.58 | 3.49 | + | 6.00E-05 | 1.38E-03 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 8.90 | 3.26 | + | 2.65E-07 | 1.05E-05 | | [rhythmic process](http://amigo.geneontology.org/amigo/term/GO:0048511) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 17.54 | 3.02 | + | 4.05E-11 | 2.68E-09 | | [epidermal growth factor receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007173) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007173&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007173&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.48 | + | 8.53E-04 | 1.30E-02 | | [positive regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0043388) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&list=upload_1&organism=Homo%20sapiens) | 3.74 | 3.47 | + | 3.02E-04 | 5.52E-03 | | [regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0051101) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 8.00 | 2.88 | + | 2.60E-05 | 6.64E-04 | | [regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051098) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&list=upload_1&organism=Homo%20sapiens) | 24.12 | 2.74 | + | 8.89E-12 | 6.40E-10 | | [positive regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051099) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.57 | + | 1.36E-05 | 3.68E-04 | | [neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0051402) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&list=upload_1&organism=Homo%20sapiens) | 6.06 | 3.46 | + | 5.06E-06 | 1.51E-04 | | [neuron death](http://amigo.geneontology.org/amigo/term/GO:0070997) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070997&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070997&list=upload_1&organism=Homo%20sapiens) | 6.77 | 3.40 | + | 2.44E-06 | 7.92E-05 | | [regulation of endothelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045601) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045601&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045601&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.45 | + | 4.47E-03 | 5.01E-02 | | [regulation of epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030856) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&list=upload_1&organism=Homo%20sapiens) | 9.80 | 2.75 | + | 1.07E-05 | 2.97E-04 | | [fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048144) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048144&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048144&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.45 | + | 4.47E-03 | 5.00E-02 | | [cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008283) | [718](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&list=upload_1&organism=Homo%20sapiens) | 46.31 | 1.96 | + | 1.15E-08 | 5.50E-07 | | [glial cell activation](http://amigo.geneontology.org/amigo/term/GO:0061900) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061900&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061900&list=upload_1&organism=Homo%20sapiens) | 2.32 | 3.45 | + | 4.47E-03 | 5.00E-02 | | [inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0006954) | [540](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&list=upload_1&organism=Homo%20sapiens) | 34.83 | 1.98 | + | 6.40E-07 | 2.37E-05 | | [positive regulation of blood vessel endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0043536) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043536&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043536&list=upload_1&organism=Homo%20sapiens) | 3.48 | 3.45 | + | 5.44E-04 | 8.95E-03 | | [positive regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010634) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&list=upload_1&organism=Homo%20sapiens) | 9.74 | 2.16 | + | 1.99E-03 | 2.64E-02 | | [positive regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030335) | [532](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&list=upload_1&organism=Homo%20sapiens) | 34.31 | 1.95 | + | 1.31E-06 | 4.53E-05 | | [positive regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000147) | [558](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&list=upload_1&organism=Homo%20sapiens) | 35.99 | 1.86 | + | 5.35E-06 | 1.59E-04 | | [positive regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040017) | [574](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&list=upload_1&organism=Homo%20sapiens) | 37.02 | 1.81 | + | 1.50E-05 | 4.04E-04 | | [SMAD protein signal transduction](http://amigo.geneontology.org/amigo/term/GO:0060395) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060395&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060395&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.45 | + | 1.94E-04 | 3.83E-03 | | [phosphatidylinositol 3-kinase signaling](http://amigo.geneontology.org/amigo/term/GO:0014065) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014065&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014065&list=upload_1&organism=Homo%20sapiens) | 2.90 | 3.45 | + | 1.55E-03 | 2.13E-02 | | [phosphatidylinositol-mediated signaling](http://amigo.geneontology.org/amigo/term/GO:0048015) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048015&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048015&list=upload_1&organism=Homo%20sapiens) | 5.22 | 2.68 | + | 1.71E-03 | 2.32E-02 | | [inositol lipid-mediated signaling](http://amigo.geneontology.org/amigo/term/GO:0048017) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048017&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048017&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.55 | + | 2.54E-03 | 3.20E-02 | | [regulation of interleukin-12 production](http://amigo.geneontology.org/amigo/term/GO:0032655) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032655&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032655&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.45 | + | 1.94E-04 | 3.82E-03 | | [ventricular septum morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060412) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060412&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060412&list=upload_1&organism=Homo%20sapiens) | 2.64 | 3.40 | + | 2.82E-03 | 3.47E-02 | | [cardiac septum morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060411) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060411&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060411&list=upload_1&organism=Homo%20sapiens) | 4.52 | 2.88 | + | 1.40E-03 | 1.97E-02 | | [heart morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003007) | [249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&list=upload_1&organism=Homo%20sapiens) | 16.06 | 1.87 | + | 2.21E-03 | 2.84E-02 | | [regulation of T cell mediated cytotoxicity](http://amigo.geneontology.org/amigo/term/GO:0001914) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001914&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001914&list=upload_1&organism=Homo%20sapiens) | 2.64 | 3.40 | + | 2.82E-03 | 3.47E-02 | | [regulation of T cell mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002709) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002709&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002709&list=upload_1&organism=Homo%20sapiens) | 5.74 | 2.96 | + | 2.08E-04 | 4.03E-03 | | [regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains](http://amigo.geneontology.org/amigo/term/GO:0002822) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002822&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002822&list=upload_1&organism=Homo%20sapiens) | 11.74 | 2.39 | + | 1.01E-04 | 2.15E-03 | | [regulation of adaptive immune response](http://amigo.geneontology.org/amigo/term/GO:0002819) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002819&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002819&list=upload_1&organism=Homo%20sapiens) | 12.77 | 2.35 | + | 6.24E-05 | 1.43E-03 | | [regulation of lymphocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002706) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002706&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002706&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.35 | + | 1.57E-04 | 3.21E-03 | | [regulation of leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002703) | [241](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002703&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002703&list=upload_1&organism=Homo%20sapiens) | 15.54 | 2.38 | + | 6.25E-06 | 1.84E-04 | | [regulation of leukocyte mediated cytotoxicity](http://amigo.geneontology.org/amigo/term/GO:0001910) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001910&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001910&list=upload_1&organism=Homo%20sapiens) | 5.61 | 2.67 | + | 1.21E-03 | 1.75E-02 | | [regulation of cell killing](http://amigo.geneontology.org/amigo/term/GO:0031341) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031341&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031341&list=upload_1&organism=Homo%20sapiens) | 6.64 | 2.71 | + | 3.59E-04 | 6.39E-03 | | [ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070371) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070371&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070371&list=upload_1&organism=Homo%20sapiens) | 3.55 | 3.38 | + | 6.27E-04 | 1.02E-02 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 14.19 | 3.03 | + | 2.57E-09 | 1.33E-07 | | [cellular response to nerve growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:1990090) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990090&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990090&list=upload_1&organism=Homo%20sapiens) | 2.97 | 3.37 | + | 1.78E-03 | 2.40E-02 | | [response to nerve growth factor](http://amigo.geneontology.org/amigo/term/GO:1990089) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990089&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990089&list=upload_1&organism=Homo%20sapiens) | 3.10 | 3.23 | + | 2.34E-03 | 2.99E-02 | | [regulation of T-helper cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045622) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045622&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045622&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.32 | + | 3.24E-03 | 3.85E-02 | | [nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006289) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.32 | + | 7.20E-04 | 1.13E-02 | | [mRNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0048255) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.32 | + | 7.20E-04 | 1.13E-02 | | [negative regulation of mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902373) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902373&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902373&list=upload_1&organism=Homo%20sapiens) | 4.32 | 2.78 | + | 2.75E-03 | 3.40E-02 | | [negative regulation of mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903312) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903312&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903312&list=upload_1&organism=Homo%20sapiens) | 5.93 | 2.86 | + | 2.93E-04 | 5.40E-03 | | [RNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0043489) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&list=upload_1&organism=Homo%20sapiens) | 4.19 | 2.86 | + | 2.20E-03 | 2.84E-02 | | [extrinsic apoptotic signaling pathway via death domain receptors](http://amigo.geneontology.org/amigo/term/GO:0008625) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008625&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008625&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.32 | + | 3.24E-03 | 3.84E-02 | | [extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097191) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097191&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097191&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.54 | + | 1.04E-03 | 1.53E-02 | | [regulation of heart rate by cardiac conduction](http://amigo.geneontology.org/amigo/term/GO:0086091) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086091&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0086091&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.32 | + | 3.24E-03 | 3.84E-02 | | [cardiac conduction](http://amigo.geneontology.org/amigo/term/GO:0061337) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061337&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061337&list=upload_1&organism=Homo%20sapiens) | 4.45 | 3.37 | + | 1.43E-04 | 2.94E-03 | | [multicellular organismal signaling](http://amigo.geneontology.org/amigo/term/GO:0035637) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035637&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035637&list=upload_1&organism=Homo%20sapiens) | 8.06 | 2.73 | + | 7.67E-05 | 1.70E-03 | | [regulation of heart contraction](http://amigo.geneontology.org/amigo/term/GO:0008016) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008016&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008016&list=upload_1&organism=Homo%20sapiens) | 13.03 | 2.15 | + | 4.14E-04 | 7.17E-03 | | [regulation of blood circulation](http://amigo.geneontology.org/amigo/term/GO:1903522) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903522&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903522&list=upload_1&organism=Homo%20sapiens) | 16.19 | 1.85 | + | 2.36E-03 | 3.01E-02 | | [regulation of heart rate](http://amigo.geneontology.org/amigo/term/GO:0002027) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002027&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002027&list=upload_1&organism=Homo%20sapiens) | 6.71 | 2.68 | + | 3.97E-04 | 6.96E-03 | | [cellular response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0071479) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&list=upload_1&organism=Homo%20sapiens) | 4.84 | 3.31 | + | 1.05E-04 | 2.23E-03 | | [cellular response to radiation](http://amigo.geneontology.org/amigo/term/GO:0071478) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 11.74 | 2.90 | + | 2.95E-07 | 1.15E-05 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 28.96 | 2.18 | + | 8.94E-08 | 3.80E-06 | | [response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0010212) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.15 | + | 2.64E-03 | 3.30E-02 | | [positive regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001244) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001244&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001244&list=upload_1&organism=Homo%20sapiens) | 3.93 | 3.30 | + | 4.59E-04 | 7.82E-03 | | [positive regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001235) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001235&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001235&list=upload_1&organism=Homo%20sapiens) | 8.39 | 2.39 | + | 8.27E-04 | 1.27E-02 | | [adherens junction organization](http://amigo.geneontology.org/amigo/term/GO:0034332) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034332&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034332&list=upload_1&organism=Homo%20sapiens) | 3.03 | 3.30 | + | 2.05E-03 | 2.69E-02 | | [cell junction organization](http://amigo.geneontology.org/amigo/term/GO:0034330) | [498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034330&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034330&list=upload_1&organism=Homo%20sapiens) | 32.12 | 1.71 | + | 2.83E-04 | 5.27E-03 | | [positive regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032206) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.29 | + | 2.93E-04 | 5.39E-03 | | [positive regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001252) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 6.84 | 2.49 | + | 1.65E-03 | 2.26E-02 | | [regulation of morphogenesis of a branching structure](http://amigo.geneontology.org/amigo/term/GO:0060688) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060688&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060688&list=upload_1&organism=Homo%20sapiens) | 3.35 | 3.28 | + | 1.30E-03 | 1.85E-02 | | [regulation of anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0022603) | [924](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&list=upload_1&organism=Homo%20sapiens) | 59.60 | 1.61 | + | 1.55E-05 | 4.17E-04 | | [protein stabilization](http://amigo.geneontology.org/amigo/term/GO:0050821) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&list=upload_1&organism=Homo%20sapiens) | 14.06 | 3.27 | + | 8.17E-11 | 5.17E-09 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 21.48 | 3.03 | + | 2.31E-13 | 1.90E-11 | | [cellular response to cAMP](http://amigo.geneontology.org/amigo/term/GO:0071320) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071320&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071320&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.26 | + | 8.25E-04 | 1.27E-02 | | [response to cAMP](http://amigo.geneontology.org/amigo/term/GO:0051591) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.83 | + | 3.28E-04 | 5.88E-03 | | [response to purine-containing compound](http://amigo.geneontology.org/amigo/term/GO:0014074) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&list=upload_1&organism=Homo%20sapiens) | 9.48 | 2.64 | + | 6.28E-05 | 1.43E-03 | | [response to organophosphorus](http://amigo.geneontology.org/amigo/term/GO:0046683) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&list=upload_1&organism=Homo%20sapiens) | 8.51 | 2.58 | + | 2.18E-04 | 4.18E-03 | | [cellular response to mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0071260) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071260&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071260&list=upload_1&organism=Homo%20sapiens) | 4.90 | 3.26 | + | 1.20E-04 | 2.52E-03 | | [cellular response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0071496) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&list=upload_1&organism=Homo%20sapiens) | 20.96 | 2.34 | + | 4.63E-07 | 1.75E-05 | | [synaptic vesicle endocytosis](http://amigo.geneontology.org/amigo/term/GO:0048488) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048488&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048488&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.26 | + | 8.25E-04 | 1.27E-02 | | [synaptic vesicle recycling](http://amigo.geneontology.org/amigo/term/GO:0036465) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036465&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036465&list=upload_1&organism=Homo%20sapiens) | 4.26 | 2.82 | + | 2.46E-03 | 3.12E-02 | | [synaptic vesicle cycle](http://amigo.geneontology.org/amigo/term/GO:0099504) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099504&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099504&list=upload_1&organism=Homo%20sapiens) | 8.13 | 2.34 | + | 1.34E-03 | 1.90E-02 | | [vesicle-mediated transport in synapse](http://amigo.geneontology.org/amigo/term/GO:0099003) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099003&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099003&list=upload_1&organism=Homo%20sapiens) | 8.71 | 2.18 | + | 3.20E-03 | 3.80E-02 | | [vesicle-mediated transport](http://amigo.geneontology.org/amigo/term/GO:0016192) | [1382](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016192&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016192&list=upload_1&organism=Homo%20sapiens) | 89.14 | 1.49 | + | 1.25E-05 | 3.43E-04 | | [presynaptic endocytosis](http://amigo.geneontology.org/amigo/term/GO:0140238) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140238&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140238&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.26 | + | 8.25E-04 | 1.27E-02 | | [endocytosis](http://amigo.geneontology.org/amigo/term/GO:0006897) | [528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006897&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006897&list=upload_1&organism=Homo%20sapiens) | 34.06 | 2.03 | + | 3.04E-07 | 1.17E-05 | | [oligodendrocyte development](http://amigo.geneontology.org/amigo/term/GO:0014003) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014003&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014003&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.24 | + | 3.71E-03 | 4.29E-02 | | [central nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007417) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 66.69 | 1.69 | + | 2.99E-07 | 1.15E-05 | | [animal organ regeneration](http://amigo.geneontology.org/amigo/term/GO:0031100) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.24 | + | 3.35E-04 | 6.00E-03 | | [regeneration](http://amigo.geneontology.org/amigo/term/GO:0031099) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.62 | + | 4.58E-05 | 1.09E-03 | | [autonomic nervous system development](http://amigo.geneontology.org/amigo/term/GO:0048483) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048483&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048483&list=upload_1&organism=Homo%20sapiens) | 3.10 | 3.23 | + | 2.34E-03 | 2.99E-02 | | [negative regulation of fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045599) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&list=upload_1&organism=Homo%20sapiens) | 3.42 | 3.22 | + | 1.48E-03 | 2.06E-02 | | [regulation of fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045598) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&list=upload_1&organism=Homo%20sapiens) | 8.71 | 2.64 | + | 1.32E-04 | 2.74E-03 | | [substrate adhesion-dependent cell spreading](http://amigo.geneontology.org/amigo/term/GO:0034446) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034446&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034446&list=upload_1&organism=Homo%20sapiens) | 3.74 | 3.21 | + | 9.41E-04 | 1.41E-02 | | [cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0031589) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031589&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031589&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.00 | + | 2.38E-03 | 3.04E-02 | | [cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0007155) | [969](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007155&reflist=1) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007155&list=upload_1&organism=Homo%20sapiens) | 62.50 | 1.44 | + | 1.17E-03 | 1.70E-02 | | [cell morphogenesis involved in differentiation](http://amigo.geneontology.org/amigo/term/GO:0000904) | [556](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000904&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000904&list=upload_1&organism=Homo%20sapiens) | 35.86 | 1.81 | + | 1.67E-05 | 4.46E-04 | | [cell morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0000902) | [713](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&list=upload_1&organism=Homo%20sapiens) | 45.99 | 1.72 | + | 1.31E-05 | 3.59E-04 | | [positive regulation of myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002763) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002763&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002763&list=upload_1&organism=Homo%20sapiens) | 3.74 | 3.21 | + | 9.41E-04 | 1.41E-02 | | [insulin receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0008286) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008286&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008286&list=upload_1&organism=Homo%20sapiens) | 4.06 | 3.20 | + | 5.99E-04 | 9.79E-03 | | [cellular response to insulin stimulus](http://amigo.geneontology.org/amigo/term/GO:0032869) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&list=upload_1&organism=Homo%20sapiens) | 9.48 | 2.95 | + | 2.31E-06 | 7.52E-05 | | [response to insulin](http://amigo.geneontology.org/amigo/term/GO:0032868) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&list=upload_1&organism=Homo%20sapiens) | 13.74 | 2.69 | + | 5.88E-07 | 2.19E-05 | | [response to peptide hormone](http://amigo.geneontology.org/amigo/term/GO:0043434) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&list=upload_1&organism=Homo%20sapiens) | 23.41 | 2.43 | + | 1.07E-08 | 5.17E-07 | | [cellular response to peptide hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071375) | [241](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071375&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071375&list=upload_1&organism=Homo%20sapiens) | 15.54 | 2.83 | + | 1.02E-08 | 4.93E-07 | | [activation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006919) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&list=upload_1&organism=Homo%20sapiens) | 5.35 | 3.18 | + | 9.99E-05 | 2.14E-03 | | [positive regulation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043280) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043280&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043280&list=upload_1&organism=Homo%20sapiens) | 8.32 | 3.00 | + | 6.07E-06 | 1.79E-04 | | [regulation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043281) | [208](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&list=upload_1&organism=Homo%20sapiens) | 13.42 | 2.61 | + | 1.93E-06 | 6.39E-05 | | [regulation of cysteine-type endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:2000116) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000116&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000116&list=upload_1&organism=Homo%20sapiens) | 15.42 | 2.53 | + | 1.36E-06 | 4.68E-05 | | [regulation of endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:0052548) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052548&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052548&list=upload_1&organism=Homo%20sapiens) | 27.22 | 1.91 | + | 3.53E-05 | 8.75E-04 | | [regulation of peptidase activity](http://amigo.geneontology.org/amigo/term/GO:0052547) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052547&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052547&list=upload_1&organism=Homo%20sapiens) | 29.15 | 1.89 | + | 2.81E-05 | 7.12E-04 | | [positive regulation of cysteine-type endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:2001056) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001056&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001056&list=upload_1&organism=Homo%20sapiens) | 9.55 | 2.93 | + | 2.59E-06 | 8.37E-05 | | [positive regulation of endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:0010950) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010950&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010950&list=upload_1&organism=Homo%20sapiens) | 11.22 | 2.85 | + | 8.82E-07 | 3.16E-05 | | [positive regulation of peptidase activity](http://amigo.geneontology.org/amigo/term/GO:0010952) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&list=upload_1&organism=Homo%20sapiens) | 12.45 | 2.73 | + | 9.63E-07 | 3.42E-05 | | [positive regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0045862) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&list=upload_1&organism=Homo%20sapiens) | 24.06 | 2.49 | + | 2.31E-09 | 1.20E-07 | | [negative regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000378) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000378&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000378&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.17 | + | 4.24E-03 | 4.77E-02 | | [cellular response to virus](http://amigo.geneontology.org/amigo/term/GO:0098586) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&list=upload_1&organism=Homo%20sapiens) | 5.68 | 3.17 | + | 6.41E-05 | 1.45E-03 | | [response to virus](http://amigo.geneontology.org/amigo/term/GO:0009615) | [357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&list=upload_1&organism=Homo%20sapiens) | 23.03 | 2.87 | + | 1.31E-12 | 1.02E-10 | | [positive regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901216) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&list=upload_1&organism=Homo%20sapiens) | 6.00 | 3.17 | + | 4.11E-05 | 9.91E-04 | | [axon extension](http://amigo.geneontology.org/amigo/term/GO:0048675) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048675&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048675&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.34E-02 | | [neuron projection extension](http://amigo.geneontology.org/amigo/term/GO:1990138) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990138&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990138&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.62 | + | 2.95E-03 | 3.58E-02 | | [developmental cell growth](http://amigo.geneontology.org/amigo/term/GO:0048588) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048588&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048588&list=upload_1&organism=Homo%20sapiens) | 6.64 | 2.41 | + | 2.79E-03 | 3.44E-02 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 26.64 | 2.18 | + | 2.54E-07 | 1.01E-05 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 26.64 | 2.18 | + | 2.54E-07 | 1.01E-05 | | [cell growth](http://amigo.geneontology.org/amigo/term/GO:0016049) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016049&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016049&list=upload_1&organism=Homo%20sapiens) | 6.77 | 2.36 | + | 3.14E-03 | 3.76E-02 | | [neuron projection morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048812) | [479](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048812&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048812&list=upload_1&organism=Homo%20sapiens) | 30.90 | 1.65 | + | 1.16E-03 | 1.69E-02 | | [neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0031175) | [677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&list=upload_1&organism=Homo%20sapiens) | 43.67 | 1.53 | + | 1.27E-03 | 1.83E-02 | | [neuron development](http://amigo.geneontology.org/amigo/term/GO:0048666) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&list=upload_1&organism=Homo%20sapiens) | 54.37 | 1.54 | + | 2.36E-04 | 4.50E-03 | | [neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0030182) | [1065](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&list=upload_1&organism=Homo%20sapiens) | 68.69 | 1.48 | + | 1.88E-04 | 3.73E-03 | | [generation of neurons](http://amigo.geneontology.org/amigo/term/GO:0048699) | [1134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&list=upload_1&organism=Homo%20sapiens) | 73.14 | 1.52 | + | 3.87E-05 | 9.43E-04 | | [cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0030030) | [1161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030030&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030030&list=upload_1&organism=Homo%20sapiens) | 74.89 | 1.36 | + | 2.86E-03 | 3.49E-02 | | [plasma membrane bounded cell projection morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0120039) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120039&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120039&list=upload_1&organism=Homo%20sapiens) | 31.22 | 1.63 | + | 1.27E-03 | 1.82E-02 | | [cell projection morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048858) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048858&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048858&list=upload_1&organism=Homo%20sapiens) | 31.54 | 1.68 | + | 6.74E-04 | 1.08E-02 | | [cell part morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032990) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032990&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032990&list=upload_1&organism=Homo%20sapiens) | 32.77 | 1.71 | + | 3.10E-04 | 5.65E-03 | | [cellular component morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032989) | [604](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&list=upload_1&organism=Homo%20sapiens) | 38.96 | 1.69 | + | 9.95E-05 | 2.13E-03 | | [developmental growth involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060560) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060560&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060560&list=upload_1&organism=Homo%20sapiens) | 8.45 | 2.49 | + | 4.15E-04 | 7.19E-03 | | [axonogenesis](http://amigo.geneontology.org/amigo/term/GO:0007409) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007409&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007409&list=upload_1&organism=Homo%20sapiens) | 23.54 | 1.74 | + | 1.47E-03 | 2.05E-02 | | [cell morphogenesis involved in neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0048667) | [440](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048667&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048667&list=upload_1&organism=Homo%20sapiens) | 28.38 | 1.76 | + | 3.47E-04 | 6.21E-03 | | [axon development](http://amigo.geneontology.org/amigo/term/GO:0061564) | [404](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061564&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061564&list=upload_1&organism=Homo%20sapiens) | 26.06 | 1.77 | + | 6.08E-04 | 9.93E-03 | | [thymus development](http://amigo.geneontology.org/amigo/term/GO:0048538) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048538&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048538&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.33E-02 | | [negative regulation of epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030857) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030857&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030857&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.33E-02 | | [negative regulation of dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035305) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035305&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035305&list=upload_1&organism=Homo%20sapiens) | 3.16 | 3.16 | + | 2.67E-03 | 3.33E-02 | | [negative regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045936) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&list=upload_1&organism=Homo%20sapiens) | 27.22 | 1.95 | + | 2.27E-05 | 5.87E-04 | | [negative regulation of phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010563) | [423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&list=upload_1&organism=Homo%20sapiens) | 27.28 | 1.94 | + | 2.31E-05 | 5.97E-04 | | [regulation of dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035303) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035303&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035303&list=upload_1&organism=Homo%20sapiens) | 8.71 | 2.53 | + | 2.57E-04 | 4.82E-03 | | [ovulation cycle](http://amigo.geneontology.org/amigo/term/GO:0042698) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042698&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042698&list=upload_1&organism=Homo%20sapiens) | 4.45 | 3.15 | + | 4.34E-04 | 7.47E-03 | | [reproductive process](http://amigo.geneontology.org/amigo/term/GO:0022414) | [1437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&list=upload_1&organism=Homo%20sapiens) | 92.69 | 1.34 | + | 1.68E-03 | 2.30E-02 | | [reproduction](http://amigo.geneontology.org/amigo/term/GO:0000003) | [1447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&list=upload_1&organism=Homo%20sapiens) | 93.33 | 1.34 | + | 1.72E-03 | 2.33E-02 | | [protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0006606) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006606&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006606&list=upload_1&organism=Homo%20sapiens) | 7.42 | 3.10 | + | 9.03E-06 | 2.55E-04 | | [protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:0034504) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.64 | + | 3.34E-06 | 1.04E-04 | | [import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0051170) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&list=upload_1&organism=Homo%20sapiens) | 7.68 | 3.13 | + | 5.13E-06 | 1.53E-04 | | [positive regulation of phosphatidylinositol 3-kinase signaling](http://amigo.geneontology.org/amigo/term/GO:0014068) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014068&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014068&list=upload_1&organism=Homo%20sapiens) | 5.16 | 3.10 | + | 2.01E-04 | 3.94E-03 | | [regulation of phosphatidylinositol 3-kinase signaling](http://amigo.geneontology.org/amigo/term/GO:0014066) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014066&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014066&list=upload_1&organism=Homo%20sapiens) | 6.97 | 2.58 | + | 9.62E-04 | 1.43E-02 | | [positive regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000379) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000379&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000379&list=upload_1&organism=Homo%20sapiens) | 4.52 | 3.10 | + | 4.92E-04 | 8.28E-03 | | [regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:2000036) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&list=upload_1&organism=Homo%20sapiens) | 4.52 | 3.10 | + | 4.92E-04 | 8.27E-03 | | [axonal transport](http://amigo.geneontology.org/amigo/term/GO:0098930) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098930&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098930&list=upload_1&organism=Homo%20sapiens) | 3.87 | 3.10 | + | 1.22E-03 | 1.75E-02 | | [axo-dendritic transport](http://amigo.geneontology.org/amigo/term/GO:0008088) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008088&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008088&list=upload_1&organism=Homo%20sapiens) | 4.71 | 3.19 | + | 2.44E-04 | 4.61E-03 | | [transport along microtubule](http://amigo.geneontology.org/amigo/term/GO:0010970) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&list=upload_1&organism=Homo%20sapiens) | 10.38 | 2.60 | + | 3.39E-05 | 8.42E-04 | | [cytoskeleton-dependent intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0030705) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&list=upload_1&organism=Homo%20sapiens) | 12.84 | 2.34 | + | 6.64E-05 | 1.50E-03 | | [microtubule-based transport](http://amigo.geneontology.org/amigo/term/GO:0099111) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099111&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099111&list=upload_1&organism=Homo%20sapiens) | 13.09 | 2.14 | + | 4.36E-04 | 7.49E-03 | | [cellular response to unfolded protein](http://amigo.geneontology.org/amigo/term/GO:0034620) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034620&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034620&list=upload_1&organism=Homo%20sapiens) | 5.16 | 3.10 | + | 2.01E-04 | 3.93E-03 | | [cellular response to topologically incorrect protein](http://amigo.geneontology.org/amigo/term/GO:0035967) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035967&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035967&list=upload_1&organism=Homo%20sapiens) | 6.45 | 2.95 | + | 9.62E-05 | 2.07E-03 | | [response to topologically incorrect protein](http://amigo.geneontology.org/amigo/term/GO:0035966) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035966&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035966&list=upload_1&organism=Homo%20sapiens) | 9.35 | 3.21 | + | 2.22E-07 | 8.91E-06 | | [response to unfolded protein](http://amigo.geneontology.org/amigo/term/GO:0006986) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006986&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006986&list=upload_1&organism=Homo%20sapiens) | 7.93 | 3.28 | + | 9.86E-07 | 3.50E-05 | | [neuroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0007405) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007405&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007405&list=upload_1&organism=Homo%20sapiens) | 3.23 | 3.10 | + | 3.03E-03 | 3.68E-02 | | [neural precursor cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0061351) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061351&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061351&list=upload_1&organism=Homo%20sapiens) | 6.45 | 2.64 | + | 6.81E-04 | 1.09E-02 | | [negative regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043524) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043524&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043524&list=upload_1&organism=Homo%20sapiens) | 10.00 | 3.10 | + | 2.69E-07 | 1.06E-05 | | [regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043523) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043523&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043523&list=upload_1&organism=Homo%20sapiens) | 14.06 | 2.84 | + | 4.19E-08 | 1.89E-06 | | [glandular epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002067) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002067&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002067&list=upload_1&organism=Homo%20sapiens) | 4.19 | 3.10 | + | 7.73E-04 | 1.20E-02 | | [liver development](http://amigo.geneontology.org/amigo/term/GO:0001889) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&list=upload_1&organism=Homo%20sapiens) | 8.45 | 3.08 | + | 2.73E-06 | 8.71E-05 | | [hepaticobiliary system development](http://amigo.geneontology.org/amigo/term/GO:0061008) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&list=upload_1&organism=Homo%20sapiens) | 8.64 | 3.01 | + | 3.91E-06 | 1.20E-04 | | [somatic stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0035019) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.05 | + | 2.17E-03 | 2.81E-02 | | [stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0019827) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&list=upload_1&organism=Homo%20sapiens) | 7.35 | 2.72 | + | 1.66E-04 | 3.35E-03 | | [maintenance of cell number](http://amigo.geneontology.org/amigo/term/GO:0098727) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&list=upload_1&organism=Homo%20sapiens) | 7.61 | 2.76 | + | 9.63E-05 | 2.07E-03 | | [mitotic spindle assembly](http://amigo.geneontology.org/amigo/term/GO:0090307) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090307&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090307&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.04 | + | 3.44E-03 | 4.04E-02 | | [mitotic spindle organization](http://amigo.geneontology.org/amigo/term/GO:0007052) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.72 | + | 5.02E-04 | 8.41E-03 | | [spindle organization](http://amigo.geneontology.org/amigo/term/GO:0007051) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007051&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007051&list=upload_1&organism=Homo%20sapiens) | 10.32 | 2.33 | + | 4.49E-04 | 7.68E-03 | | [microtubule cytoskeleton organization involved in mitosis](http://amigo.geneontology.org/amigo/term/GO:1902850) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&list=upload_1&organism=Homo%20sapiens) | 8.32 | 2.76 | + | 4.46E-05 | 1.06E-03 | | [mitotic cell cycle process](http://amigo.geneontology.org/amigo/term/GO:1903047) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&list=upload_1&organism=Homo%20sapiens) | 34.38 | 1.89 | + | 4.90E-06 | 1.47E-04 | | [mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000278) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&list=upload_1&organism=Homo%20sapiens) | 40.44 | 2.03 | + | 2.09E-08 | 9.63E-07 | | [spindle assembly](http://amigo.geneontology.org/amigo/term/GO:0051225) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051225&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051225&list=upload_1&organism=Homo%20sapiens) | 6.19 | 2.58 | + | 1.16E-03 | 1.69E-02 | | [non-membrane-bounded organelle assembly](http://amigo.geneontology.org/amigo/term/GO:0140694) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&list=upload_1&organism=Homo%20sapiens) | 20.38 | 2.06 | + | 4.38E-05 | 1.05E-03 | | [organelle assembly](http://amigo.geneontology.org/amigo/term/GO:0070925) | [803](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070925&reflist=1) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070925&list=upload_1&organism=Homo%20sapiens) | 51.79 | 1.51 | + | 8.66E-04 | 1.32E-02 | | [mitotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0140014) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&list=upload_1&organism=Homo%20sapiens) | 11.16 | 2.06 | + | 2.26E-03 | 2.91E-02 | | [protein autoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0051865) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&list=upload_1&organism=Homo%20sapiens) | 4.97 | 3.02 | + | 4.01E-04 | 7.01E-03 | | [protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016567) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016567&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016567&list=upload_1&organism=Homo%20sapiens) | 44.12 | 1.68 | + | 5.00E-05 | 1.17E-03 | | [protein modification by small protein conjugation](http://amigo.geneontology.org/amigo/term/GO:0032446) | [753](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032446&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032446&list=upload_1&organism=Homo%20sapiens) | 48.57 | 1.69 | + | 1.56E-05 | 4.20E-04 | | [protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:0070647) | [898](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070647&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070647&list=upload_1&organism=Homo%20sapiens) | 57.92 | 1.54 | + | 1.63E-04 | 3.31E-03 | | [ureteric bud development](http://amigo.geneontology.org/amigo/term/GO:0001657) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001657&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001657&list=upload_1&organism=Homo%20sapiens) | 5.68 | 3.00 | + | 1.85E-04 | 3.69E-03 | | [mesonephric tubule development](http://amigo.geneontology.org/amigo/term/GO:0072164) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072164&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072164&list=upload_1&organism=Homo%20sapiens) | 5.74 | 2.96 | + | 2.08E-04 | 4.04E-03 | | [mesonephric epithelium development](http://amigo.geneontology.org/amigo/term/GO:0072163) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072163&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072163&list=upload_1&organism=Homo%20sapiens) | 5.74 | 2.96 | + | 2.08E-04 | 4.03E-03 | | [mesonephros development](http://amigo.geneontology.org/amigo/term/GO:0001823) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001823&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001823&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.83 | + | 3.28E-04 | 5.91E-03 | | [kidney development](http://amigo.geneontology.org/amigo/term/GO:0001822) | [299](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&list=upload_1&organism=Homo%20sapiens) | 19.29 | 1.87 | + | 1.07E-03 | 1.57E-02 | | [renal system development](http://amigo.geneontology.org/amigo/term/GO:0072001) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&list=upload_1&organism=Homo%20sapiens) | 19.87 | 1.81 | + | 1.32E-03 | 1.87E-02 | | [urogenital system development](http://amigo.geneontology.org/amigo/term/GO:0001655) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&list=upload_1&organism=Homo%20sapiens) | 22.58 | 1.77 | + | 1.18E-03 | 1.71E-02 | | [kidney epithelium development](http://amigo.geneontology.org/amigo/term/GO:0072073) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072073&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072073&list=upload_1&organism=Homo%20sapiens) | 8.84 | 2.72 | + | 3.95E-05 | 9.58E-04 | | [regulation of phosphatidylinositol 3-kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043551) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043551&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043551&list=upload_1&organism=Homo%20sapiens) | 3.68 | 2.99 | + | 2.45E-03 | 3.11E-02 | | [regulation of lipid kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043550) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043550&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043550&list=upload_1&organism=Homo%20sapiens) | 4.45 | 2.92 | + | 1.25E-03 | 1.79E-02 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 50.50 | 2.00 | + | 5.94E-10 | 3.37E-08 | | [positive regulation of NF-kappaB transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051092) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051092&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051092&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.98 | + | 8.55E-07 | 3.08E-05 | | [positive regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051091) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&list=upload_1&organism=Homo%20sapiens) | 17.29 | 2.78 | + | 6.06E-09 | 3.04E-07 | | [regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051090) | [438](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&list=upload_1&organism=Homo%20sapiens) | 28.25 | 2.48 | + | 1.04E-10 | 6.45E-09 | | [negative regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0032091) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.97 | + | 1.33E-04 | 2.77E-03 | | [negative regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051100) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 10.51 | 2.57 | + | 3.86E-05 | 9.42E-04 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.85 | + | 1.24E-07 | 5.24E-06 | | [T cell differentiation in thymus](http://amigo.geneontology.org/amigo/term/GO:0033077) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033077&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033077&list=upload_1&organism=Homo%20sapiens) | 4.06 | 2.95 | + | 1.75E-03 | 2.37E-02 | | [T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030217) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030217&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030217&list=upload_1&organism=Homo%20sapiens) | 10.90 | 2.39 | + | 1.96E-04 | 3.86E-03 | | [T cell activation](http://amigo.geneontology.org/amigo/term/GO:0042110) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&list=upload_1&organism=Homo%20sapiens) | 19.35 | 2.02 | + | 1.23E-04 | 2.57E-03 | | [regulation of epidermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045604) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045604&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045604&list=upload_1&organism=Homo%20sapiens) | 3.74 | 2.94 | + | 2.76E-03 | 3.41E-02 | | [regulation of epidermis development](http://amigo.geneontology.org/amigo/term/GO:0045682) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045682&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045682&list=upload_1&organism=Homo%20sapiens) | 4.19 | 2.86 | + | 2.20E-03 | 2.84E-02 | | [positive regulation of protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0051897) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&list=upload_1&organism=Homo%20sapiens) | 7.48 | 2.94 | + | 2.87E-05 | 7.24E-04 | | [regulation of protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0051896) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051896&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051896&list=upload_1&organism=Homo%20sapiens) | 10.97 | 2.37 | + | 2.04E-04 | 3.99E-03 | | [positive regulation of proteasomal ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0032436) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032436&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032436&list=upload_1&organism=Homo%20sapiens) | 6.13 | 2.94 | + | 1.50E-04 | 3.07E-03 | | [positive regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000060) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000060&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000060&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.65 | + | 3.14E-04 | 5.68E-03 | | [positive regulation of proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1903052) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903052&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903052&list=upload_1&organism=Homo%20sapiens) | 8.84 | 2.38 | + | 6.30E-04 | 1.03E-02 | | [positive regulation of proteasomal protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901800) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901800&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901800&list=upload_1&organism=Homo%20sapiens) | 7.68 | 2.61 | + | 4.37E-04 | 7.50E-03 | | [positive regulation of protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0045732) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045732&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045732&list=upload_1&organism=Homo%20sapiens) | 13.87 | 2.09 | + | 5.86E-04 | 9.60E-03 | | [cellular response to fibroblast growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0044344) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044344&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044344&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.92 | + | 3.65E-04 | 6.50E-03 | | [response to fibroblast growth factor](http://amigo.geneontology.org/amigo/term/GO:0071774) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071774&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071774&list=upload_1&organism=Homo%20sapiens) | 5.87 | 2.73 | + | 7.04E-04 | 1.12E-02 | | [positive regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048661) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.92 | + | 3.65E-04 | 6.49E-03 | | [positive regulation of cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008284) | [949](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 61.21 | 2.01 | + | 6.92E-12 | 5.14E-10 | | [regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048660) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&list=upload_1&organism=Homo%20sapiens) | 9.16 | 2.95 | + | 3.58E-06 | 1.11E-04 | | [adult locomotory behavior](http://amigo.geneontology.org/amigo/term/GO:0008344) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008344&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008344&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.92 | + | 3.65E-04 | 6.48E-03 | | [locomotory behavior](http://amigo.geneontology.org/amigo/term/GO:0007626) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007626&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007626&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.39 | + | 3.72E-05 | 9.10E-04 | | [behavior](http://amigo.geneontology.org/amigo/term/GO:0007610) | [606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007610&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007610&list=upload_1&organism=Homo%20sapiens) | 39.09 | 1.82 | + | 5.81E-06 | 1.73E-04 | | [adult behavior](http://amigo.geneontology.org/amigo/term/GO:0030534) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030534&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030534&list=upload_1&organism=Homo%20sapiens) | 9.55 | 2.20 | + | 1.69E-03 | 2.30E-02 | | [response to estradiol](http://amigo.geneontology.org/amigo/term/GO:0032355) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&list=upload_1&organism=Homo%20sapiens) | 7.93 | 2.90 | + | 2.32E-05 | 5.98E-04 | | [protein localization to chromosome](http://amigo.geneontology.org/amigo/term/GO:0034502) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&list=upload_1&organism=Homo%20sapiens) | 4.84 | 2.89 | + | 8.94E-04 | 1.35E-02 | | [leukocyte mediated cytotoxicity](http://amigo.geneontology.org/amigo/term/GO:0001909) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001909&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001909&list=upload_1&organism=Homo%20sapiens) | 3.81 | 2.89 | + | 3.10E-03 | 3.74E-02 | | [leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002443) | [310](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&list=upload_1&organism=Homo%20sapiens) | 20.00 | 1.90 | + | 4.04E-04 | 7.04E-03 | | [immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002252) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&list=upload_1&organism=Homo%20sapiens) | 30.32 | 1.78 | + | 1.30E-04 | 2.70E-03 | | [toll-like receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002224) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002224&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002224&list=upload_1&organism=Homo%20sapiens) | 3.81 | 2.89 | + | 3.10E-03 | 3.73E-02 | | [regulation of epithelial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1904035) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904035&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904035&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.85 | + | 2.10E-04 | 4.05E-03 | | [positive regulation of protein localization to plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1903078) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903078&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903078&list=upload_1&organism=Homo%20sapiens) | 3.87 | 2.84 | + | 3.47E-03 | 4.06E-02 | | [regulation of protein localization to plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1903076) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903076&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903076&list=upload_1&organism=Homo%20sapiens) | 6.77 | 2.51 | + | 1.58E-03 | 2.16E-02 | | [regulation of protein localization to cell periphery](http://amigo.geneontology.org/amigo/term/GO:1904375) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904375&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904375&list=upload_1&organism=Homo%20sapiens) | 8.19 | 2.44 | + | 6.73E-04 | 1.08E-02 | | [regulation of protein localization to membrane](http://amigo.geneontology.org/amigo/term/GO:1905475) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905475&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905475&list=upload_1&organism=Homo%20sapiens) | 11.35 | 2.20 | + | 8.37E-04 | 1.28E-02 | | [positive regulation of protein localization to membrane](http://amigo.geneontology.org/amigo/term/GO:1905477) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905477&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905477&list=upload_1&organism=Homo%20sapiens) | 6.71 | 2.83 | + | 1.51E-04 | 3.09E-03 | | [positive regulation of protein localization to cell periphery](http://amigo.geneontology.org/amigo/term/GO:1904377) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904377&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904377&list=upload_1&organism=Homo%20sapiens) | 4.39 | 2.74 | + | 3.06E-03 | 3.70E-02 | | [regulation of interleukin-10 production](http://amigo.geneontology.org/amigo/term/GO:0032653) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032653&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032653&list=upload_1&organism=Homo%20sapiens) | 3.87 | 2.84 | + | 3.47E-03 | 4.06E-02 | | [astrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0048708) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048708&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048708&list=upload_1&organism=Homo%20sapiens) | 3.87 | 2.84 | + | 3.47E-03 | 4.06E-02 | | [histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0016575) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&list=upload_1&organism=Homo%20sapiens) | 3.87 | 2.84 | + | 3.47E-03 | 4.05E-02 | | [histone modification](http://amigo.geneontology.org/amigo/term/GO:0016570) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&list=upload_1&organism=Homo%20sapiens) | 23.54 | 1.95 | + | 5.95E-05 | 1.38E-03 | | [positive regulation of T cell mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002711) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002711&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002711&list=upload_1&organism=Homo%20sapiens) | 3.87 | 2.84 | + | 3.47E-03 | 4.05E-02 | | [positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains](http://amigo.geneontology.org/amigo/term/GO:0002824) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002824&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002824&list=upload_1&organism=Homo%20sapiens) | 7.35 | 2.58 | + | 6.61E-04 | 1.06E-02 | | [positive regulation of adaptive immune response](http://amigo.geneontology.org/amigo/term/GO:0002821) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002821&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002821&list=upload_1&organism=Homo%20sapiens) | 7.74 | 2.45 | + | 8.99E-04 | 1.35E-02 | | [positive regulation of leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002705) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002705&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002705&list=upload_1&organism=Homo%20sapiens) | 9.03 | 2.10 | + | 4.10E-03 | 4.64E-02 | | [positive regulation of cell division](http://amigo.geneontology.org/amigo/term/GO:0051781) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051781&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051781&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.83 | + | 3.28E-04 | 5.90E-03 | | [regulation of cell division](http://amigo.geneontology.org/amigo/term/GO:0051302) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051302&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051302&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.13 | + | 7.66E-04 | 1.19E-02 | | [receptor internalization](http://amigo.geneontology.org/amigo/term/GO:0031623) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031623&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031623&list=upload_1&organism=Homo%20sapiens) | 4.64 | 2.80 | + | 1.75E-03 | 2.36E-02 | | [receptor-mediated endocytosis](http://amigo.geneontology.org/amigo/term/GO:0006898) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006898&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006898&list=upload_1&organism=Homo%20sapiens) | 11.03 | 2.81 | + | 1.69E-06 | 5.67E-05 | | [negative regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045638) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045638&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045638&list=upload_1&organism=Homo%20sapiens) | 5.42 | 2.77 | + | 8.88E-04 | 1.35E-02 | | [positive regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0045727) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045727&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045727&list=upload_1&organism=Homo%20sapiens) | 9.42 | 2.76 | + | 1.49E-05 | 4.02E-04 | | [dicarboxylic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043648) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043648&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043648&list=upload_1&organism=Homo%20sapiens) | 5.81 | 2.76 | + | 6.34E-04 | 1.03E-02 | | [carboxylic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019752) | [822](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019752&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019752&list=upload_1&organism=Homo%20sapiens) | 53.02 | 1.43 | + | 3.30E-03 | 3.90E-02 | | [small molecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044281) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044281&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044281&list=upload_1&organism=Homo%20sapiens) | 106.68 | 1.40 | + | 8.64E-05 | 1.88E-03 | | [antigen processing and presentation of peptide antigen](http://amigo.geneontology.org/amigo/term/GO:0048002) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048002&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048002&list=upload_1&organism=Homo%20sapiens) | 4.00 | 2.75 | + | 4.32E-03 | 4.86E-02 | | [regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035065) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&list=upload_1&organism=Homo%20sapiens) | 4.39 | 2.74 | + | 3.06E-03 | 3.69E-02 | | [regulation of peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:2000756) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000756&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000756&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.62 | + | 2.95E-03 | 3.59E-02 | | [regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901983) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&list=upload_1&organism=Homo%20sapiens) | 5.74 | 2.61 | + | 1.48E-03 | 2.05E-02 | | [regulation of stress fiber assembly](http://amigo.geneontology.org/amigo/term/GO:0051492) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051492&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051492&list=upload_1&organism=Homo%20sapiens) | 5.93 | 2.70 | + | 7.81E-04 | 1.21E-02 | | [regulation of actin filament bundle assembly](http://amigo.geneontology.org/amigo/term/GO:0032231) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032231&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032231&list=upload_1&organism=Homo%20sapiens) | 6.77 | 2.51 | + | 1.58E-03 | 2.16E-02 | | [regulation of actomyosin structure organization](http://amigo.geneontology.org/amigo/term/GO:0110020) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110020&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110020&list=upload_1&organism=Homo%20sapiens) | 6.51 | 2.46 | + | 2.51E-03 | 3.17E-02 | | [regulation of signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1901796) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 6.71 | 2.68 | + | 3.97E-04 | 6.96E-03 | | [ubiquitin-dependent ERAD pathway](http://amigo.geneontology.org/amigo/term/GO:0030433) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030433&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030433&list=upload_1&organism=Homo%20sapiens) | 5.22 | 2.68 | + | 1.71E-03 | 2.32E-02 | | [ERAD pathway](http://amigo.geneontology.org/amigo/term/GO:0036503) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036503&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036503&list=upload_1&organism=Homo%20sapiens) | 6.39 | 2.51 | + | 2.29E-03 | 2.93E-02 | | [proteasomal protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0010498) | [378](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010498&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010498&list=upload_1&organism=Homo%20sapiens) | 24.38 | 2.17 | + | 1.03E-06 | 3.64E-05 | | [proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0051603) | [647](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051603&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051603&list=upload_1&organism=Homo%20sapiens) | 41.73 | 1.85 | + | 1.56E-06 | 5.26E-05 | | [proteolysis](http://amigo.geneontology.org/amigo/term/GO:0006508) | [1266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&list=upload_1&organism=Homo%20sapiens) | 81.66 | 1.49 | + | 2.71E-05 | 6.92E-04 | | [response to endoplasmic reticulum stress](http://amigo.geneontology.org/amigo/term/GO:0034976) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034976&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034976&list=upload_1&organism=Homo%20sapiens) | 14.32 | 2.16 | + | 1.72E-04 | 3.46E-03 | | [proteasome-mediated ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0043161) | [347](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043161&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043161&list=upload_1&organism=Homo%20sapiens) | 22.38 | 2.32 | + | 1.97E-07 | 8.02E-06 | | [ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006511) | [575](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006511&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006511&list=upload_1&organism=Homo%20sapiens) | 37.09 | 1.89 | + | 2.14E-06 | 7.02E-05 | | [modification-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0019941) | [586](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019941&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019941&list=upload_1&organism=Homo%20sapiens) | 37.80 | 1.90 | + | 1.14E-06 | 3.98E-05 | | [modification-dependent macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0043632) | [598](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043632&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043632&list=upload_1&organism=Homo%20sapiens) | 38.57 | 1.87 | + | 2.19E-06 | 7.20E-05 | | [cellular macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044265) | [785](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&list=upload_1&organism=Homo%20sapiens) | 50.63 | 2.07 | + | 5.37E-11 | 3.53E-09 | | [aging](http://amigo.geneontology.org/amigo/term/GO:0007568) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&list=upload_1&organism=Homo%20sapiens) | 11.22 | 2.67 | + | 8.71E-06 | 2.47E-04 | | [myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002573) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.66 | + | 7.46E-05 | 1.66E-03 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 17.03 | 2.41 | + | 1.52E-06 | 5.14E-05 | | [positive regulation of canonical Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0090263) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090263&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090263&list=upload_1&organism=Homo%20sapiens) | 6.77 | 2.66 | + | 4.40E-04 | 7.54E-03 | | [regulation of canonical Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0060828) | [255](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060828&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060828&list=upload_1&organism=Homo%20sapiens) | 16.45 | 2.19 | + | 5.31E-05 | 1.23E-03 | | [regulation of Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030111) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030111&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030111&list=upload_1&organism=Homo%20sapiens) | 21.41 | 1.91 | + | 2.52E-04 | 4.74E-03 | | [positive regulation of Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030177) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030177&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030177&list=upload_1&organism=Homo%20sapiens) | 9.16 | 2.18 | + | 2.38E-03 | 3.03E-02 | | [stress-activated MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0051403) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051403&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051403&list=upload_1&organism=Homo%20sapiens) | 4.90 | 2.65 | + | 2.66E-03 | 3.33E-02 | | [stress-activated protein kinase signaling cascade](http://amigo.geneontology.org/amigo/term/GO:0031098) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031098&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031098&list=upload_1&organism=Homo%20sapiens) | 5.16 | 2.52 | + | 3.94E-03 | 4.48E-02 | | [somite development](http://amigo.geneontology.org/amigo/term/GO:0061053) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061053&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061053&list=upload_1&organism=Homo%20sapiens) | 5.29 | 2.65 | + | 1.89E-03 | 2.52E-02 | | [regulation of neural precursor cell proliferation](http://amigo.geneontology.org/amigo/term/GO:2000177) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000177&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000177&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.64 | + | 9.56E-04 | 1.43E-02 | | [regulation of leukocyte apoptotic process](http://amigo.geneontology.org/amigo/term/GO:2000106) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000106&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000106&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.64 | + | 9.56E-04 | 1.42E-02 | | [post-embryonic development](http://amigo.geneontology.org/amigo/term/GO:0009791) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009791&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009791&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.64 | + | 9.56E-04 | 1.42E-02 | | [positive regulation of insulin secretion](http://amigo.geneontology.org/amigo/term/GO:0032024) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032024&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032024&list=upload_1&organism=Homo%20sapiens) | 4.58 | 2.62 | + | 4.16E-03 | 4.70E-02 | | [regulation of insulin secretion](http://amigo.geneontology.org/amigo/term/GO:0050796) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050796&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050796&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.11 | + | 3.46E-03 | 4.05E-02 | | [regulation of protein secretion](http://amigo.geneontology.org/amigo/term/GO:0050708) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050708&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050708&list=upload_1&organism=Homo%20sapiens) | 16.13 | 1.86 | + | 2.28E-03 | 2.93E-02 | | [regulation of secretion by cell](http://amigo.geneontology.org/amigo/term/GO:1903530) | [566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903530&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903530&list=upload_1&organism=Homo%20sapiens) | 36.51 | 1.84 | + | 8.96E-06 | 2.53E-04 | | [regulation of secretion](http://amigo.geneontology.org/amigo/term/GO:0051046) | [623](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051046&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051046&list=upload_1&organism=Homo%20sapiens) | 40.18 | 1.79 | + | 7.70E-06 | 2.22E-04 | | [regulation of peptide hormone secretion](http://amigo.geneontology.org/amigo/term/GO:0090276) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090276&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090276&list=upload_1&organism=Homo%20sapiens) | 12.06 | 2.07 | + | 1.29E-03 | 1.84E-02 | | [regulation of hormone secretion](http://amigo.geneontology.org/amigo/term/GO:0046883) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046883&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046883&list=upload_1&organism=Homo%20sapiens) | 15.61 | 2.11 | + | 1.77E-04 | 3.55E-03 | | [regulation of peptide secretion](http://amigo.geneontology.org/amigo/term/GO:0002791) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002791&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002791&list=upload_1&organism=Homo%20sapiens) | 12.26 | 2.12 | + | 8.03E-04 | 1.24E-02 | | [regulation of peptide transport](http://amigo.geneontology.org/amigo/term/GO:0090087) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090087&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090087&list=upload_1&organism=Homo%20sapiens) | 12.38 | 2.10 | + | 8.86E-04 | 1.35E-02 | | [positive regulation of hormone secretion](http://amigo.geneontology.org/amigo/term/GO:0046887) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046887&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046887&list=upload_1&organism=Homo%20sapiens) | 8.26 | 2.30 | + | 1.55E-03 | 2.13E-02 | | [positive regulation of secretion by cell](http://amigo.geneontology.org/amigo/term/GO:1903532) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903532&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903532&list=upload_1&organism=Homo%20sapiens) | 18.32 | 1.97 | + | 3.38E-04 | 6.05E-03 | | [positive regulation of secretion](http://amigo.geneontology.org/amigo/term/GO:0051047) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051047&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051047&list=upload_1&organism=Homo%20sapiens) | 20.06 | 1.94 | + | 2.50E-04 | 4.72E-03 | | [positive regulation of peptide secretion](http://amigo.geneontology.org/amigo/term/GO:0002793) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002793&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002793&list=upload_1&organism=Homo%20sapiens) | 6.39 | 2.35 | + | 4.48E-03 | 5.00E-02 | | [regulation of ATP metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903578) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903578&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903578&list=upload_1&organism=Homo%20sapiens) | 4.58 | 2.62 | + | 4.16E-03 | 4.69E-02 | | [regulation of purine nucleotide metabolic process](http://amigo.geneontology.org/amigo/term/GO:1900542) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900542&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900542&list=upload_1&organism=Homo%20sapiens) | 5.87 | 2.56 | + | 1.80E-03 | 2.42E-02 | | [regulation of nucleotide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006140) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006140&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006140&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.56 | + | 1.28E-03 | 1.83E-02 | | [cellular response to glucose stimulus](http://amigo.geneontology.org/amigo/term/GO:0071333) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071333&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071333&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.62 | + | 2.95E-03 | 3.59E-02 | | [cellular response to hexose stimulus](http://amigo.geneontology.org/amigo/term/GO:0071331) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071331&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071331&list=upload_1&organism=Homo%20sapiens) | 5.10 | 2.75 | + | 1.39E-03 | 1.95E-02 | | [cellular response to monosaccharide stimulus](http://amigo.geneontology.org/amigo/term/GO:0071326) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071326&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071326&list=upload_1&organism=Homo%20sapiens) | 5.22 | 2.68 | + | 1.71E-03 | 2.32E-02 | | [cellular response to carbohydrate stimulus](http://amigo.geneontology.org/amigo/term/GO:0071322) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071322&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071322&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.83 | + | 3.28E-04 | 5.89E-03 | | [response to carbohydrate](http://amigo.geneontology.org/amigo/term/GO:0009743) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.74 | + | 1.86E-06 | 6.20E-05 | | [response to monosaccharide](http://amigo.geneontology.org/amigo/term/GO:0034284) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.52 | + | 9.55E-05 | 2.06E-03 | | [response to hexose](http://amigo.geneontology.org/amigo/term/GO:0009746) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&list=upload_1&organism=Homo%20sapiens) | 9.42 | 2.65 | + | 6.02E-05 | 1.39E-03 | | [response to glucose](http://amigo.geneontology.org/amigo/term/GO:0009749) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&list=upload_1&organism=Homo%20sapiens) | 9.09 | 2.53 | + | 1.80E-04 | 3.61E-03 | | [glucose homeostasis](http://amigo.geneontology.org/amigo/term/GO:0042593) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.01 | + | 1.79E-03 | 2.41E-02 | | [carbohydrate homeostasis](http://amigo.geneontology.org/amigo/term/GO:0033500) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&list=upload_1&organism=Homo%20sapiens) | 13.03 | 2.00 | + | 1.86E-03 | 2.48E-02 | | [chemical homeostasis](http://amigo.geneontology.org/amigo/term/GO:0048878) | [916](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048878&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048878&list=upload_1&organism=Homo%20sapiens) | 59.08 | 1.47 | + | 6.84E-04 | 1.09E-02 | | [cellular response to interferon-gamma](http://amigo.geneontology.org/amigo/term/GO:0071346) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071346&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071346&list=upload_1&organism=Homo%20sapiens) | 6.90 | 2.61 | + | 5.36E-04 | 8.86E-03 | | [response to interferon-gamma](http://amigo.geneontology.org/amigo/term/GO:0034341) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&list=upload_1&organism=Homo%20sapiens) | 8.39 | 2.74 | + | 4.96E-05 | 1.16E-03 | | [branching morphogenesis of an epithelial tube](http://amigo.geneontology.org/amigo/term/GO:0048754) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048754&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048754&list=upload_1&organism=Homo%20sapiens) | 8.84 | 2.60 | + | 1.44E-04 | 2.96E-03 | | [morphogenesis of a branching epithelium](http://amigo.geneontology.org/amigo/term/GO:0061138) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061138&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061138&list=upload_1&organism=Homo%20sapiens) | 10.64 | 2.35 | + | 3.03E-04 | 5.53E-03 | | [morphogenesis of a branching structure](http://amigo.geneontology.org/amigo/term/GO:0001763) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001763&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001763&list=upload_1&organism=Homo%20sapiens) | 11.29 | 2.30 | + | 2.60E-04 | 4.88E-03 | | [RNA export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0006405) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006405&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006405&list=upload_1&organism=Homo%20sapiens) | 5.42 | 2.58 | + | 2.30E-03 | 2.95E-02 | | [RNA transport](http://amigo.geneontology.org/amigo/term/GO:0050658) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050658&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050658&list=upload_1&organism=Homo%20sapiens) | 10.84 | 2.40 | + | 1.90E-04 | 3.77E-03 | | [establishment of RNA localization](http://amigo.geneontology.org/amigo/term/GO:0051236) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051236&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051236&list=upload_1&organism=Homo%20sapiens) | 10.97 | 2.37 | + | 2.04E-04 | 3.99E-03 | | [RNA localization](http://amigo.geneontology.org/amigo/term/GO:0006403) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006403&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006403&list=upload_1&organism=Homo%20sapiens) | 12.26 | 2.28 | + | 1.58E-04 | 3.22E-03 | | [nucleic acid transport](http://amigo.geneontology.org/amigo/term/GO:0050657) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050657&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050657&list=upload_1&organism=Homo%20sapiens) | 10.84 | 2.40 | + | 1.90E-04 | 3.76E-03 | | [nucleobase-containing compound transport](http://amigo.geneontology.org/amigo/term/GO:0015931) | [225](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015931&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015931&list=upload_1&organism=Homo%20sapiens) | 14.51 | 2.14 | + | 2.84E-04 | 5.27E-03 | | [glucose metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006006) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006006&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006006&list=upload_1&organism=Homo%20sapiens) | 7.35 | 2.58 | + | 6.61E-04 | 1.06E-02 | | [hexose metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019318) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019318&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019318&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.39 | + | 2.45E-04 | 4.63E-03 | | [monosaccharide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0005996) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0005996&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0005996&list=upload_1&organism=Homo%20sapiens) | 11.35 | 2.20 | + | 8.37E-04 | 1.28E-02 | | [carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0005975) | [475](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0005975&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0005975&list=upload_1&organism=Homo%20sapiens) | 30.64 | 1.60 | + | 2.83E-03 | 3.47E-02 | | [regulation of embryonic development](http://amigo.geneontology.org/amigo/term/GO:0045995) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045995&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045995&list=upload_1&organism=Homo%20sapiens) | 5.81 | 2.58 | + | 1.64E-03 | 2.23E-02 | | [G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000082) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.55 | + | 2.54E-03 | 3.20E-02 | | [mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044772) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&list=upload_1&organism=Homo%20sapiens) | 11.16 | 2.24 | + | 4.61E-04 | 7.85E-03 | | [cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044770) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&list=upload_1&organism=Homo%20sapiens) | 11.80 | 2.29 | + | 2.08E-04 | 4.04E-03 | | [positive regulation of developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048639) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048639&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048639&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.55 | + | 4.13E-05 | 9.94E-04 | | [regulation of developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048638) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048638&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048638&list=upload_1&organism=Homo%20sapiens) | 20.90 | 2.01 | + | 8.59E-05 | 1.87E-03 | | [regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0040008) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&list=upload_1&organism=Homo%20sapiens) | 40.44 | 1.88 | + | 1.08E-06 | 3.78E-05 | | [positive regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0045927) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045927&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045927&list=upload_1&organism=Homo%20sapiens) | 16.77 | 2.09 | + | 1.74E-04 | 3.51E-03 | | [cellular response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0071482) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&list=upload_1&organism=Homo%20sapiens) | 7.48 | 2.54 | + | 7.21E-04 | 1.13E-02 | | [response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0009416) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 20.45 | 2.15 | + | 1.01E-05 | 2.83E-04 | | [DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0071897) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071897&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071897&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.53 | + | 2.20E-03 | 2.84E-02 | | [nucleobase-containing compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0034654) | [1007](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 64.95 | 1.76 | + | 5.16E-08 | 2.29E-06 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 69.60 | 1.75 | + | 1.63E-08 | 7.64E-07 | | [organic cyclic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901362) | [1216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&reflist=1) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 78.43 | 1.75 | + | 2.09E-09 | 1.10E-07 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 70.24 | 1.79 | + | 2.14E-09 | 1.12E-07 | | [cellular response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097306) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097306&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097306&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.53 | + | 2.20E-03 | 2.84E-02 | | [positive regulation of I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0043123) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043123&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043123&list=upload_1&organism=Homo%20sapiens) | 12.26 | 2.53 | + | 1.22E-05 | 3.34E-04 | | [regulation of I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0043122) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043122&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043122&list=upload_1&organism=Homo%20sapiens) | 16.25 | 2.21 | + | 4.81E-05 | 1.13E-03 | | [embryonic placenta development](http://amigo.geneontology.org/amigo/term/GO:0001892) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001892&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001892&list=upload_1&organism=Homo%20sapiens) | 5.55 | 2.52 | + | 2.79E-03 | 3.45E-02 | | [embryonic organ development](http://amigo.geneontology.org/amigo/term/GO:0048568) | [454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&list=upload_1&organism=Homo%20sapiens) | 29.28 | 1.91 | + | 1.87E-05 | 4.95E-04 | | [in utero embryonic development](http://amigo.geneontology.org/amigo/term/GO:0001701) | [395](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&list=upload_1&organism=Homo%20sapiens) | 25.48 | 1.96 | + | 3.00E-05 | 7.51E-04 | | [chordate embryonic development](http://amigo.geneontology.org/amigo/term/GO:0043009) | [655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&list=upload_1&organism=Homo%20sapiens) | 42.25 | 1.78 | + | 8.21E-06 | 2.35E-04 | | [embryo development ending in birth or egg hatching](http://amigo.geneontology.org/amigo/term/GO:0009792) | [677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&list=upload_1&organism=Homo%20sapiens) | 43.67 | 1.76 | + | 7.90E-06 | 2.27E-04 | | [placenta development](http://amigo.geneontology.org/amigo/term/GO:0001890) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&list=upload_1&organism=Homo%20sapiens) | 9.74 | 2.36 | + | 5.76E-04 | 9.44E-03 | | [regulation of receptor signaling pathway via STAT](http://amigo.geneontology.org/amigo/term/GO:1904892) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904892&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904892&list=upload_1&organism=Homo%20sapiens) | 5.55 | 2.52 | + | 2.79E-03 | 3.44E-02 | | [regulation of phosphatase activity](http://amigo.geneontology.org/amigo/term/GO:0010921) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010921&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010921&list=upload_1&organism=Homo%20sapiens) | 5.55 | 2.52 | + | 2.79E-03 | 3.44E-02 | | [positive regulation of MAP kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043406) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043406&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043406&list=upload_1&organism=Homo%20sapiens) | 7.55 | 2.52 | + | 7.57E-04 | 1.18E-02 | | [positive regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071902) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071902&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071902&list=upload_1&organism=Homo%20sapiens) | 14.96 | 2.00 | + | 9.29E-04 | 1.39E-02 | | [positive regulation of protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:0045860) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045860&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045860&list=upload_1&organism=Homo%20sapiens) | 27.22 | 1.80 | + | 2.62E-04 | 4.90E-03 | | [positive regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0033674) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&list=upload_1&organism=Homo%20sapiens) | 32.19 | 1.99 | + | 1.50E-06 | 5.10E-05 | | [regulation of protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:0045859) | [668](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&list=upload_1&organism=Homo%20sapiens) | 43.09 | 1.79 | + | 4.78E-06 | 1.44E-04 | | [regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071900) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&list=upload_1&organism=Homo%20sapiens) | 25.22 | 1.94 | + | 4.28E-05 | 1.03E-03 | | [regulation of MAP kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043405) | [184](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043405&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043405&list=upload_1&organism=Homo%20sapiens) | 11.87 | 2.11 | + | 1.12E-03 | 1.64E-02 | | [positive regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043410) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043410&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043410&list=upload_1&organism=Homo%20sapiens) | 31.22 | 2.24 | + | 6.52E-09 | 3.23E-07 | | [regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043408) | [672](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&list=upload_1&organism=Homo%20sapiens) | 43.34 | 2.21 | + | 1.42E-11 | 1.00E-09 | | [cerebellum development](http://amigo.geneontology.org/amigo/term/GO:0021549) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021549&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021549&list=upload_1&organism=Homo%20sapiens) | 6.77 | 2.51 | + | 1.58E-03 | 2.16E-02 | | [metencephalon development](http://amigo.geneontology.org/amigo/term/GO:0022037) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022037&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022037&list=upload_1&organism=Homo%20sapiens) | 7.42 | 2.29 | + | 2.87E-03 | 3.50E-02 | | [hindbrain development](http://amigo.geneontology.org/amigo/term/GO:0030902) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.19 | + | 1.34E-03 | 1.90E-02 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 49.99 | 1.62 | + | 7.15E-05 | 1.60E-03 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 53.08 | 1.62 | + | 3.55E-05 | 8.79E-04 | | [positive regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045766) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.51 | + | 5.15E-05 | 1.20E-03 | | [regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045765) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&list=upload_1&organism=Homo%20sapiens) | 18.58 | 1.83 | + | 1.96E-03 | 2.61E-02 | | [regulation of vasculature development](http://amigo.geneontology.org/amigo/term/GO:1901342) | [292](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901342&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901342&list=upload_1&organism=Homo%20sapiens) | 18.83 | 1.81 | + | 2.12E-03 | 2.75E-02 | | [positive regulation of vasculature development](http://amigo.geneontology.org/amigo/term/GO:1904018) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904018&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904018&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.51 | + | 5.15E-05 | 1.20E-03 | | [cellular response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990830) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.50 | + | 3.32E-03 | 3.92E-02 | | [response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990823) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.47 | + | 3.46E-03 | 4.06E-02 | | [response to nutrient](http://amigo.geneontology.org/amigo/term/GO:0007584) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&list=upload_1&organism=Homo%20sapiens) | 9.61 | 2.50 | + | 1.45E-04 | 2.98E-03 | | [response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031667) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&list=upload_1&organism=Homo%20sapiens) | 30.32 | 2.21 | + | 2.08E-08 | 9.59E-07 | | [response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0009991) | [500](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&list=upload_1&organism=Homo%20sapiens) | 32.25 | 2.20 | + | 7.41E-09 | 3.66E-07 | | [regulation of mitotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0007088) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007088&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007088&list=upload_1&organism=Homo%20sapiens) | 7.61 | 2.50 | + | 7.99E-04 | 1.23E-02 | | [regulation of nuclear division](http://amigo.geneontology.org/amigo/term/GO:0051783) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051783&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051783&list=upload_1&organism=Homo%20sapiens) | 9.35 | 2.25 | + | 1.46E-03 | 2.03E-02 | | [negative regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0043433) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043433&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043433&list=upload_1&organism=Homo%20sapiens) | 11.22 | 2.49 | + | 3.95E-05 | 9.58E-04 | | [response to alkaloid](http://amigo.geneontology.org/amigo/term/GO:0043279) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&list=upload_1&organism=Homo%20sapiens) | 6.45 | 2.48 | + | 2.39E-03 | 3.04E-02 | | [regulation of protein dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035304) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035304&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035304&list=upload_1&organism=Homo%20sapiens) | 6.06 | 2.47 | + | 3.46E-03 | 4.06E-02 | | [response to UV](http://amigo.geneontology.org/amigo/term/GO:0009411) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&list=upload_1&organism=Homo%20sapiens) | 9.74 | 2.46 | + | 1.68E-04 | 3.39E-03 | | [regulation of sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0033045) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033045&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033045&list=upload_1&organism=Homo%20sapiens) | 6.90 | 2.46 | + | 1.74E-03 | 2.36E-02 | | [regulation of chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0051983) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&list=upload_1&organism=Homo%20sapiens) | 8.45 | 2.37 | + | 8.87E-04 | 1.35E-02 | | [organ growth](http://amigo.geneontology.org/amigo/term/GO:0035265) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035265&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035265&list=upload_1&organism=Homo%20sapiens) | 6.51 | 2.46 | + | 2.51E-03 | 3.17E-02 | | [cardiocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0035051) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035051&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035051&list=upload_1&organism=Homo%20sapiens) | 7.35 | 2.45 | + | 1.28E-03 | 1.84E-02 | | [negative regulation of response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0002832) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002832&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002832&list=upload_1&organism=Homo%20sapiens) | 7.35 | 2.45 | + | 1.28E-03 | 1.84E-02 | | [regulation of response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0002831) | [364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002831&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002831&list=upload_1&organism=Homo%20sapiens) | 23.48 | 2.00 | + | 3.61E-05 | 8.90E-04 | | [regulation of Notch signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0008593) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008593&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008593&list=upload_1&organism=Homo%20sapiens) | 6.13 | 2.45 | + | 3.62E-03 | 4.18E-02 | | [histone methylation](http://amigo.geneontology.org/amigo/term/GO:0016571) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&list=upload_1&organism=Homo%20sapiens) | 6.97 | 2.44 | + | 1.84E-03 | 2.46E-02 | | [viral entry into host cell](http://amigo.geneontology.org/amigo/term/GO:0046718) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046718&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046718&list=upload_1&organism=Homo%20sapiens) | 6.97 | 2.44 | + | 1.84E-03 | 2.46E-02 | | [viral life cycle](http://amigo.geneontology.org/amigo/term/GO:0019058) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019058&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019058&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.26 | + | 3.10E-04 | 5.64E-03 | | [viral process](http://amigo.geneontology.org/amigo/term/GO:0016032) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&list=upload_1&organism=Homo%20sapiens) | 16.19 | 2.10 | + | 1.48E-04 | 3.03E-03 | | [entry into host](http://amigo.geneontology.org/amigo/term/GO:0044409) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044409&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044409&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.54 | + | 1.04E-03 | 1.53E-02 | | [movement in host](http://amigo.geneontology.org/amigo/term/GO:0044000) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044000&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044000&list=upload_1&organism=Homo%20sapiens) | 8.97 | 2.23 | + | 2.07E-03 | 2.71E-02 | | [biological process involved in interaction with host](http://amigo.geneontology.org/amigo/term/GO:0051701) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051701&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051701&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.39 | + | 2.45E-04 | 4.62E-03 | | [regulation of cyclin-dependent protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0000079) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&list=upload_1&organism=Homo%20sapiens) | 7.42 | 2.43 | + | 1.36E-03 | 1.92E-02 | | [regulation of cyclin-dependent protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:1904029) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&list=upload_1&organism=Homo%20sapiens) | 7.61 | 2.50 | + | 7.99E-04 | 1.23E-02 | | [transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007179) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&list=upload_1&organism=Homo%20sapiens) | 6.19 | 2.42 | + | 3.80E-03 | 4.37E-02 | | [cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:0071560) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.52 | + | 9.55E-05 | 2.06E-03 | | [response to transforming growth factor beta](http://amigo.geneontology.org/amigo/term/GO:0071559) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&list=upload_1&organism=Homo%20sapiens) | 10.38 | 2.50 | + | 7.26E-05 | 1.62E-03 | | [myeloid leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002274) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002274&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002274&list=upload_1&organism=Homo%20sapiens) | 9.55 | 2.41 | + | 2.95E-04 | 5.42E-03 | | [regulation of mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0048024) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048024&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048024&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.40 | + | 2.07E-03 | 2.72E-02 | | [erythrocyte homeostasis](http://amigo.geneontology.org/amigo/term/GO:0034101) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034101&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034101&list=upload_1&organism=Homo%20sapiens) | 6.71 | 2.39 | + | 2.95E-03 | 3.59E-02 | | [myeloid cell homeostasis](http://amigo.geneontology.org/amigo/term/GO:0002262) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&list=upload_1&organism=Homo%20sapiens) | 8.51 | 2.58 | + | 2.18E-04 | 4.18E-03 | | [homeostasis of number of cells](http://amigo.geneontology.org/amigo/term/GO:0048872) | [257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&list=upload_1&organism=Homo%20sapiens) | 16.58 | 2.29 | + | 1.11E-05 | 3.09E-04 | | [regulation of glucose metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010906) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010906&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010906&list=upload_1&organism=Homo%20sapiens) | 6.71 | 2.39 | + | 2.95E-03 | 3.59E-02 | | [regulation of carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006109) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006109&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006109&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.05 | + | 2.08E-03 | 2.72E-02 | | [regulation of mitotic sister chromatid separation](http://amigo.geneontology.org/amigo/term/GO:0010965) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010965&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010965&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.37 | + | 4.23E-03 | 4.76E-02 | | [regulation of chromosome separation](http://amigo.geneontology.org/amigo/term/GO:1905818) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905818&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905818&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.37 | + | 2.20E-03 | 2.84E-02 | | [negative regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0017148) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017148&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017148&list=upload_1&organism=Homo%20sapiens) | 10.97 | 2.37 | + | 2.04E-04 | 3.98E-03 | | [negative regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034249) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034249&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034249&list=upload_1&organism=Homo%20sapiens) | 12.38 | 2.50 | + | 1.43E-05 | 3.87E-04 | | [negative regulation of cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000113) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000113&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000113&list=upload_1&organism=Homo%20sapiens) | 12.26 | 2.28 | + | 1.58E-04 | 3.22E-03 | | [mRNA transport](http://amigo.geneontology.org/amigo/term/GO:0051028) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051028&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051028&list=upload_1&organism=Homo%20sapiens) | 8.90 | 2.36 | + | 6.78E-04 | 1.08E-02 | | [positive regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070374) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&list=upload_1&organism=Homo%20sapiens) | 14.00 | 2.36 | + | 2.40E-05 | 6.19E-04 | | [regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070372) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&list=upload_1&organism=Homo%20sapiens) | 19.54 | 2.20 | + | 7.03E-06 | 2.04E-04 | | [cellular response to interleukin-1](http://amigo.geneontology.org/amigo/term/GO:0071347) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071347&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071347&list=upload_1&organism=Homo%20sapiens) | 6.39 | 2.35 | + | 4.48E-03 | 5.00E-02 | | [response to interleukin-1](http://amigo.geneontology.org/amigo/term/GO:0070555) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070555&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070555&list=upload_1&organism=Homo%20sapiens) | 8.13 | 2.46 | + | 6.31E-04 | 1.03E-02 | | [regulation of macroautophagy](http://amigo.geneontology.org/amigo/term/GO:0016241) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&list=upload_1&organism=Homo%20sapiens) | 10.32 | 2.33 | + | 4.49E-04 | 7.68E-03 | | [regulation of osteoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045667) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045667&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045667&list=upload_1&organism=Homo%20sapiens) | 8.19 | 2.32 | + | 1.44E-03 | 2.01E-02 | | [positive regulation of lipid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045834) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045834&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045834&list=upload_1&organism=Homo%20sapiens) | 9.93 | 2.32 | + | 6.39E-04 | 1.03E-02 | | [positive regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031398) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031398&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031398&list=upload_1&organism=Homo%20sapiens) | 7.80 | 2.31 | + | 2.03E-03 | 2.67E-02 | | [positive regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903322) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903322&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903322&list=upload_1&organism=Homo%20sapiens) | 9.03 | 2.55 | + | 1.69E-04 | 3.41E-03 | | [positive regulation of synaptic transmission](http://amigo.geneontology.org/amigo/term/GO:0050806) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050806&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050806&list=upload_1&organism=Homo%20sapiens) | 8.71 | 2.30 | + | 1.79E-03 | 2.41E-02 | | [modulation of chemical synaptic transmission](http://amigo.geneontology.org/amigo/term/GO:0050804) | [438](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050804&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050804&list=upload_1&organism=Homo%20sapiens) | 28.25 | 1.81 | + | 1.60E-04 | 3.26E-03 | | [regulation of trans-synaptic signaling](http://amigo.geneontology.org/amigo/term/GO:0099177) | [439](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099177&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099177&list=upload_1&organism=Homo%20sapiens) | 28.32 | 1.80 | + | 1.64E-04 | 3.33E-03 | | [maintenance of location](http://amigo.geneontology.org/amigo/term/GO:0051235) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051235&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051235&list=upload_1&organism=Homo%20sapiens) | 11.35 | 2.29 | + | 2.75E-04 | 5.13E-03 | | [negative regulation of inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0050728) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050728&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050728&list=upload_1&organism=Homo%20sapiens) | 9.61 | 2.29 | + | 9.46E-04 | 1.41E-02 | | [regulation of inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0050727) | [372](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&list=upload_1&organism=Homo%20sapiens) | 23.99 | 2.00 | + | 2.75E-05 | 7.02E-04 | | [regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031347) | [642](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&list=upload_1&organism=Homo%20sapiens) | 41.41 | 2.00 | + | 2.03E-08 | 9.42E-07 | | [regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032101) | [973](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&list=upload_1&organism=Homo%20sapiens) | 62.76 | 1.91 | + | 1.75E-10 | 1.05E-08 | | [negative regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031348) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031348&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031348&list=upload_1&organism=Homo%20sapiens) | 15.22 | 2.43 | + | 4.42E-06 | 1.35E-04 | | [negative regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032102) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&list=upload_1&organism=Homo%20sapiens) | 25.22 | 2.22 | + | 3.19E-07 | 1.22E-05 | | [tissue homeostasis](http://amigo.geneontology.org/amigo/term/GO:0001894) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&list=upload_1&organism=Homo%20sapiens) | 15.80 | 2.28 | + | 2.19E-05 | 5.69E-04 | | [multicellular organismal homeostasis](http://amigo.geneontology.org/amigo/term/GO:0048871) | [380](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&list=upload_1&organism=Homo%20sapiens) | 24.51 | 1.92 | + | 8.09E-05 | 1.78E-03 | | [regulation of cell-matrix adhesion](http://amigo.geneontology.org/amigo/term/GO:0001952) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001952&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001952&list=upload_1&organism=Homo%20sapiens) | 7.93 | 2.27 | + | 2.34E-03 | 2.99E-02 | | [regulation of cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0010810) | [219](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010810&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010810&list=upload_1&organism=Homo%20sapiens) | 14.13 | 2.34 | + | 2.76E-05 | 7.02E-04 | | [neuromuscular process](http://amigo.geneontology.org/amigo/term/GO:0050905) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050905&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050905&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.26 | + | 1.40E-03 | 1.97E-02 | | [positive regulation of inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0050729) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050729&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050729&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.26 | + | 1.40E-03 | 1.97E-02 | | [positive regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031349) | [296](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031349&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031349&list=upload_1&organism=Homo%20sapiens) | 19.09 | 2.04 | + | 1.08E-04 | 2.28E-03 | | [positive regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032103) | [455](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&list=upload_1&organism=Homo%20sapiens) | 29.35 | 1.91 | + | 1.92E-05 | 5.06E-04 | | [recombinational repair](http://amigo.geneontology.org/amigo/term/GO:0000725) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&list=upload_1&organism=Homo%20sapiens) | 7.55 | 2.25 | + | 3.29E-03 | 3.89E-02 | | [peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018105) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&list=upload_1&organism=Homo%20sapiens) | 12.00 | 2.25 | + | 2.51E-04 | 4.73E-03 | | [peptidyl-serine modification](http://amigo.geneontology.org/amigo/term/GO:0018209) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&list=upload_1&organism=Homo%20sapiens) | 13.29 | 2.03 | + | 1.25E-03 | 1.80E-02 | | [positive regulation of peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0050731) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050731&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050731&list=upload_1&organism=Homo%20sapiens) | 12.45 | 2.25 | + | 2.88E-04 | 5.34E-03 | | [regulation of peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0050730) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050730&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050730&list=upload_1&organism=Homo%20sapiens) | 16.83 | 2.02 | + | 3.07E-04 | 5.59E-03 | | [B cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030183) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030183&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030183&list=upload_1&organism=Homo%20sapiens) | 8.51 | 2.23 | + | 2.82E-03 | 3.46E-02 | | [B cell activation](http://amigo.geneontology.org/amigo/term/GO:0042113) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&list=upload_1&organism=Homo%20sapiens) | 12.32 | 2.19 | + | 4.63E-04 | 7.84E-03 | | [negative regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050777) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050777&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050777&list=upload_1&organism=Homo%20sapiens) | 12.13 | 2.23 | + | 4.19E-04 | 7.23E-03 | | [negative regulation of immune system process](http://amigo.geneontology.org/amigo/term/GO:0002683) | [434](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002683&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002683&list=upload_1&organism=Homo%20sapiens) | 27.99 | 1.86 | + | 6.83E-05 | 1.54E-03 | | [negative regulation of cell growth](http://amigo.geneontology.org/amigo/term/GO:0030308) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030308&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030308&list=upload_1&organism=Homo%20sapiens) | 12.13 | 2.23 | + | 4.19E-04 | 7.22E-03 | | [regulation of cell growth](http://amigo.geneontology.org/amigo/term/GO:0001558) | [429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&list=upload_1&organism=Homo%20sapiens) | 27.67 | 1.88 | + | 6.08E-05 | 1.40E-03 | | [negative regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0045926) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&list=upload_1&organism=Homo%20sapiens) | 15.93 | 2.01 | + | 5.37E-04 | 8.86E-03 | | [protein polyubiquitination](http://amigo.geneontology.org/amigo/term/GO:0000209) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000209&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000209&list=upload_1&organism=Homo%20sapiens) | 14.84 | 2.22 | + | 7.06E-05 | 1.58E-03 | | [mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006402) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006402&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006402&list=upload_1&organism=Homo%20sapiens) | 8.13 | 2.21 | + | 4.01E-03 | 4.53E-02 | | [RNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006401) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&list=upload_1&organism=Homo%20sapiens) | 10.45 | 2.30 | + | 4.92E-04 | 8.26E-03 | | [nucleobase-containing compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0034655) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034655&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034655&list=upload_1&organism=Homo%20sapiens) | 18.32 | 2.02 | + | 2.05E-04 | 3.99E-03 | | [cellular nitrogen compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044270) | [330](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044270&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044270&list=upload_1&organism=Homo%20sapiens) | 21.29 | 2.02 | + | 6.25E-05 | 1.43E-03 | | [heterocycle catabolic process](http://amigo.geneontology.org/amigo/term/GO:0046700) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046700&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046700&list=upload_1&organism=Homo%20sapiens) | 20.90 | 1.96 | + | 1.39E-04 | 2.88E-03 | | [aromatic compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0019439) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019439&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019439&list=upload_1&organism=Homo%20sapiens) | 22.32 | 1.84 | + | 5.10E-04 | 8.50E-03 | | [organic cyclic compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901361) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901361&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901361&list=upload_1&organism=Homo%20sapiens) | 24.12 | 1.87 | + | 1.78E-04 | 3.57E-03 | | [mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016071) | [607](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&list=upload_1&organism=Homo%20sapiens) | 39.15 | 1.71 | + | 7.25E-05 | 1.62E-03 | | [positive regulation of small molecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0062013) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062013&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062013&list=upload_1&organism=Homo%20sapiens) | 9.48 | 2.21 | + | 1.61E-03 | 2.20E-02 | | [response to xenobiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009410) | [423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 27.28 | 2.16 | + | 3.12E-07 | 1.20E-05 | | [ameboidal-type cell migration](http://amigo.geneontology.org/amigo/term/GO:0001667) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001667&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001667&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.16 | + | 3.94E-04 | 6.91E-03 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 58.24 | 1.67 | + | 4.69E-06 | 1.42E-04 | | [cell motility](http://amigo.geneontology.org/amigo/term/GO:0048870) | [1061](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&reflist=1) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&list=upload_1&organism=Homo%20sapiens) | 68.43 | 1.55 | + | 2.88E-05 | 7.27E-04 | | [negative regulation of secretion by cell](http://amigo.geneontology.org/amigo/term/GO:1903531) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903531&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903531&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.15 | + | 2.64E-03 | 3.30E-02 | | [negative regulation of secretion](http://amigo.geneontology.org/amigo/term/GO:0051048) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051048&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051048&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.14 | + | 1.80E-03 | 2.42E-02 | | [negative regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051051) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&list=upload_1&organism=Homo%20sapiens) | 28.06 | 1.75 | + | 4.66E-04 | 7.88E-03 | | [positive regulation of epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050679) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050679&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050679&list=upload_1&organism=Homo%20sapiens) | 13.48 | 2.15 | + | 3.14E-04 | 5.68E-03 | | [regulation of epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050678) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&list=upload_1&organism=Homo%20sapiens) | 23.80 | 1.93 | + | 6.92E-05 | 1.56E-03 | | [aerobic respiration](http://amigo.geneontology.org/amigo/term/GO:0009060) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009060&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009060&list=upload_1&organism=Homo%20sapiens) | 10.26 | 2.15 | + | 2.40E-03 | 3.05E-02 | | [energy derivation by oxidation of organic compounds](http://amigo.geneontology.org/amigo/term/GO:0015980) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015980&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015980&list=upload_1&organism=Homo%20sapiens) | 16.83 | 1.84 | + | 2.69E-03 | 3.35E-02 | | [generation of precursor metabolites and energy](http://amigo.geneontology.org/amigo/term/GO:0006091) | [406](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006091&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006091&list=upload_1&organism=Homo%20sapiens) | 26.19 | 1.87 | + | 9.19E-05 | 1.99E-03 | | [cellular component disassembly](http://amigo.geneontology.org/amigo/term/GO:0022411) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&list=upload_1&organism=Homo%20sapiens) | 20.51 | 2.15 | + | 1.06E-05 | 2.96E-04 | | [anterior/posterior pattern specification](http://amigo.geneontology.org/amigo/term/GO:0009952) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&list=upload_1&organism=Homo%20sapiens) | 14.06 | 2.13 | + | 3.86E-04 | 6.81E-03 | | [regulation of endothelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0001936) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001936&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001936&list=upload_1&organism=Homo%20sapiens) | 8.97 | 2.12 | + | 3.89E-03 | 4.43E-02 | | [mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0000398) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000398&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000398&list=upload_1&organism=Homo%20sapiens) | 15.67 | 2.11 | + | 1.85E-04 | 3.69E-03 | | [mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0006397) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&list=upload_1&organism=Homo%20sapiens) | 29.09 | 1.58 | + | 4.16E-03 | 4.69E-02 | | [RNA splicing, via transesterification reactions with bulged adenosine as nucleophile](http://amigo.geneontology.org/amigo/term/GO:0000377) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000377&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000377&list=upload_1&organism=Homo%20sapiens) | 15.67 | 2.11 | + | 1.85E-04 | 3.68E-03 | | [RNA splicing, via transesterification reactions](http://amigo.geneontology.org/amigo/term/GO:0000375) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000375&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000375&list=upload_1&organism=Homo%20sapiens) | 15.93 | 2.07 | + | 3.28E-04 | 5.88E-03 | | [RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0008380) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&list=upload_1&organism=Homo%20sapiens) | 23.74 | 1.81 | + | 5.03E-04 | 8.41E-03 | | [cellular response to starvation](http://amigo.geneontology.org/amigo/term/GO:0009267) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.09 | + | 1.56E-03 | 2.14E-02 | | [cellular response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031669) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&list=upload_1&organism=Homo%20sapiens) | 14.58 | 2.13 | + | 2.93E-04 | 5.40E-03 | | [cellular response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0031668) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&list=upload_1&organism=Homo%20sapiens) | 16.51 | 2.06 | + | 2.56E-04 | 4.81E-03 | | [response to starvation](http://amigo.geneontology.org/amigo/term/GO:0042594) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&list=upload_1&organism=Homo%20sapiens) | 13.87 | 2.16 | + | 2.25E-04 | 4.32E-03 | | [negative regulation of cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008285) | [713](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 45.99 | 2.09 | + | 2.39E-10 | 1.41E-08 | | [double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:0006302) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&list=upload_1&organism=Homo%20sapiens) | 13.09 | 2.06 | + | 1.13E-03 | 1.66E-02 | | [negative regulation of transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0000122) | [974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&reflist=1) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 62.82 | 2.05 | + | 4.60E-13 | 3.72E-11 | | [cell division](http://amigo.geneontology.org/amigo/term/GO:0051301) | [514](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&list=upload_1&organism=Homo%20sapiens) | 33.15 | 2.05 | + | 2.14E-07 | 8.63E-06 | | [adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains](http://amigo.geneontology.org/amigo/term/GO:0002460) | [265](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002460&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002460&list=upload_1&organism=Homo%20sapiens) | 17.09 | 2.05 | + | 2.06E-04 | 4.00E-03 | | [regulation of signaling receptor activity](http://amigo.geneontology.org/amigo/term/GO:0010469) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010469&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010469&list=upload_1&organism=Homo%20sapiens) | 11.35 | 2.03 | + | 2.60E-03 | 3.26E-02 | | [defense response to virus](http://amigo.geneontology.org/amigo/term/GO:0051607) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051607&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051607&list=upload_1&organism=Homo%20sapiens) | 16.32 | 2.02 | + | 3.90E-04 | 6.88E-03 | | [defense response to symbiont](http://amigo.geneontology.org/amigo/term/GO:0140546) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140546&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140546&list=upload_1&organism=Homo%20sapiens) | 16.38 | 2.01 | + | 4.05E-04 | 7.06E-03 | | [protein complex oligomerization](http://amigo.geneontology.org/amigo/term/GO:0051259) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051259&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051259&list=upload_1&organism=Homo%20sapiens) | 16.38 | 2.01 | + | 4.05E-04 | 7.05E-03 | | [mesenchyme development](http://amigo.geneontology.org/amigo/term/GO:0060485) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&list=upload_1&organism=Homo%20sapiens) | 15.42 | 2.01 | + | 6.93E-04 | 1.10E-02 | | [negative regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001818) | [286](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001818&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001818&list=upload_1&organism=Homo%20sapiens) | 18.45 | 2.01 | + | 2.16E-04 | 4.16E-03 | | [transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0006366) | [356](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&list=upload_1&organism=Homo%20sapiens) | 22.96 | 2.00 | + | 3.18E-05 | 7.93E-04 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 39.54 | 1.80 | + | 9.17E-06 | 2.58E-04 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 39.60 | 1.79 | + | 9.40E-06 | 2.64E-04 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 40.25 | 1.76 | + | 1.58E-05 | 4.24E-04 | | [regulation of innate immune response](http://amigo.geneontology.org/amigo/term/GO:0045088) | [240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045088&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045088&list=upload_1&organism=Homo%20sapiens) | 15.48 | 2.00 | + | 7.14E-04 | 1.13E-02 | | [regulation of synaptic plasticity](http://amigo.geneontology.org/amigo/term/GO:0048167) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048167&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048167&list=upload_1&organism=Homo%20sapiens) | 12.51 | 2.00 | + | 2.38E-03 | 3.03E-02 | | [positive regulation of cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1904064) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904064&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904064&list=upload_1&organism=Homo%20sapiens) | 11.03 | 1.99 | + | 3.76E-03 | 4.33E-02 | | [positive regulation of ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034767) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034767&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034767&list=upload_1&organism=Homo%20sapiens) | 12.00 | 2.00 | + | 3.10E-03 | 3.74E-02 | | [positive regulation of transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034764) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034764&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034764&list=upload_1&organism=Homo%20sapiens) | 15.22 | 2.04 | + | 6.42E-04 | 1.04E-02 | | [regulation of transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034762) | [593](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034762&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034762&list=upload_1&organism=Homo%20sapiens) | 38.25 | 1.59 | + | 8.19E-04 | 1.26E-02 | | [regulation of ion transport](http://amigo.geneontology.org/amigo/term/GO:0043269) | [708](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043269&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043269&list=upload_1&organism=Homo%20sapiens) | 45.67 | 1.60 | + | 2.28E-04 | 4.36E-03 | | [regulation of ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034765) | [510](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034765&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034765&list=upload_1&organism=Homo%20sapiens) | 32.90 | 1.61 | + | 1.62E-03 | 2.21E-02 | | [establishment or maintenance of cell polarity](http://amigo.geneontology.org/amigo/term/GO:0007163) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007163&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007163&list=upload_1&organism=Homo%20sapiens) | 13.55 | 1.99 | + | 1.47E-03 | 2.04E-02 | | [lymphocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002449) | [257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002449&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002449&list=upload_1&organism=Homo%20sapiens) | 16.58 | 1.99 | + | 4.58E-04 | 7.80E-03 | | [regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001020) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 20.25 | 1.98 | + | 1.69E-04 | 3.41E-03 | | [learning or memory](http://amigo.geneontology.org/amigo/term/GO:0007611) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007611&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007611&list=upload_1&organism=Homo%20sapiens) | 17.74 | 1.97 | + | 4.18E-04 | 7.23E-03 | | [cognition](http://amigo.geneontology.org/amigo/term/GO:0050890) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050890&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050890&list=upload_1&organism=Homo%20sapiens) | 20.45 | 1.96 | + | 1.84E-04 | 3.67E-03 | | [establishment of organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051656) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&list=upload_1&organism=Homo%20sapiens) | 24.45 | 1.92 | + | 7.89E-05 | 1.74E-03 | | [organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051640) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&list=upload_1&organism=Homo%20sapiens) | 33.09 | 1.72 | + | 2.34E-04 | 4.47E-03 | | [chemical synaptic transmission](http://amigo.geneontology.org/amigo/term/GO:0007268) | [414](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007268&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007268&list=upload_1&organism=Homo%20sapiens) | 26.70 | 1.91 | + | 4.53E-05 | 1.08E-03 | | [anterograde trans-synaptic signaling](http://amigo.geneontology.org/amigo/term/GO:0098916) | [414](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098916&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098916&list=upload_1&organism=Homo%20sapiens) | 26.70 | 1.91 | + | 4.53E-05 | 1.08E-03 | | [trans-synaptic signaling](http://amigo.geneontology.org/amigo/term/GO:0099537) | [431](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099537&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099537&list=upload_1&organism=Homo%20sapiens) | 27.80 | 1.83 | + | 1.00E-04 | 2.14E-03 | | [synaptic signaling](http://amigo.geneontology.org/amigo/term/GO:0099536) | [461](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099536&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099536&list=upload_1&organism=Homo%20sapiens) | 29.73 | 1.85 | + | 4.94E-05 | 1.16E-03 | | [cell-cell signaling](http://amigo.geneontology.org/amigo/term/GO:0007267) | [1083](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&reflist=1) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&list=upload_1&organism=Homo%20sapiens) | 69.85 | 1.65 | + | 7.55E-07 | 2.75E-05 | | [regulation of vesicle-mediated transport](http://amigo.geneontology.org/amigo/term/GO:0060627) | [552](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060627&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060627&list=upload_1&organism=Homo%20sapiens) | 35.60 | 1.88 | + | 4.59E-06 | 1.39E-04 | | [regulation of lymphocyte proliferation](http://amigo.geneontology.org/amigo/term/GO:0050670) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050670&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050670&list=upload_1&organism=Homo%20sapiens) | 15.61 | 1.86 | + | 2.89E-03 | 3.53E-02 | | [regulation of mononuclear cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0032944) | 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[34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001503&list=upload_1&organism=Homo%20sapiens) | 18.71 | 1.82 | + | 2.03E-03 | 2.68E-02 | | [sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0007548) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&list=upload_1&organism=Homo%20sapiens) | 18.19 | 1.81 | + | 2.63E-03 | 3.29E-02 | | [response to wounding](http://amigo.geneontology.org/amigo/term/GO:0009611) | [447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&list=upload_1&organism=Homo%20sapiens) | 28.83 | 1.77 | + | 2.68E-04 | 5.00E-03 | | [muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0060537) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&list=upload_1&organism=Homo%20sapiens) | 21.03 | 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[10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007608&list=upload_1&organism=Homo%20sapiens) | 30.32 | .33 | - | 4.18E-05 | 1.00E-03 | | Unclassified | [2725](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&list=upload_1&organism=Homo%20sapiens) | 175.76 | .19 | - | 1.58E-41 | 4.95E-38 | |

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