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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 | [696](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 1218 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [710](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [605](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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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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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) | | [fungiform papilla formation](http://amigo.geneontology.org/amigo/term/GO:0061198) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061198&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061198&list=upload_1&organism=Homo%20sapiens) | .18 | 16.90 | + | 3.06E-03 | 4.32E-02 | | [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) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&list=upload_1&organism=Homo%20sapiens) | 55.67 | 1.90 | + | 2.08E-09 | 1.27E-07 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 132.34 | 1.75 | + | 9.26E-16 | 9.68E-14 | | [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) | 304.31 | 1.59 | + | 6.60E-28 | 1.36E-25 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [527](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 335.84 | 1.57 | + | 7.39E-30 | 1.70E-27 | | [sensory organ development](http://amigo.geneontology.org/amigo/term/GO:0007423) | [582](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007423&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007423&list=upload_1&organism=Homo%20sapiens) | 34.43 | 1.77 | + | 5.28E-05 | 1.40E-03 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [337](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 192.50 | 1.75 | + | 4.01E-24 | 6.62E-22 | | [animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009887) | [1003](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&list=upload_1&organism=Homo%20sapiens) | 59.34 | 1.77 | + | 8.89E-08 | 4.22E-06 | | [regulation of muscle atrophy](http://amigo.geneontology.org/amigo/term/GO:0014735) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014735&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014735&list=upload_1&organism=Homo%20sapiens) | .18 | 16.90 | + | 3.06E-03 | 4.32E-02 | | [regulation of muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043502) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&list=upload_1&organism=Homo%20sapiens) | 4.73 | 3.38 | + | 7.84E-05 | 1.97E-03 | | [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) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 238.64 | 1.67 | + | 2.46E-25 | 4.34E-23 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [910](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 698.42 | 1.30 | + | 1.53E-34 | 4.21E-32 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [946](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 742.08 | 1.27 | + | 1.02E-33 | 2.67E-31 | | [regulation of muscle system process](http://amigo.geneontology.org/amigo/term/GO:0090257) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090257&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090257&list=upload_1&organism=Homo%20sapiens) | 13.96 | 2.01 | + | 1.06E-03 | 1.85E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044057&list=upload_1&organism=Homo%20sapiens) | 33.60 | 1.55 | + | 3.32E-03 | 4.60E-02 | | [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) | [297](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 162.68 | 1.83 | + | 1.69E-23 | 2.63E-21 | | [hair follicle placode formation](http://amigo.geneontology.org/amigo/term/GO:0060789) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060789&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060789&list=upload_1&organism=Homo%20sapiens) | .30 | 13.52 | + | 9.73E-04 | 1.74E-02 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [562](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 389.32 | 1.44 | + | 1.65E-23 | 2.59E-21 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [180](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 102.11 | 1.76 | + | 1.15E-12 | 1.00E-10 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 63.42 | 1.83 | + | 3.46E-09 | 2.01E-07 | | [negative regulation of cardiac muscle hypertrophy in response to stress](http://amigo.geneontology.org/amigo/term/GO:1903243) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903243&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903243&list=upload_1&organism=Homo%20sapiens) | .41 | 12.07 | + | 3.07E-04 | 6.48E-03 | | [regulation of cardiac muscle hypertrophy in response to stress](http://amigo.geneontology.org/amigo/term/GO:1903242) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903242&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903242&list=upload_1&organism=Homo%20sapiens) | .59 | 10.14 | + | 1.48E-04 | 3.43E-03 | | [regulation of cardiac muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0010612) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010612&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010612&list=upload_1&organism=Homo%20sapiens) | .59 | 10.14 | + | 1.48E-04 | 3.42E-03 | | [regulation of cardiac muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0010611) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010611&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010611&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.76 | + | 2.60E-04 | 5.66E-03 | | [regulation of muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014743) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014743&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014743&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.56 | + | 4.00E-04 | 7.99E-03 | | [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) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 81.22 | 2.34 | + | 2.97E-25 | 5.18E-23 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010614&list=upload_1&organism=Homo%20sapiens) | 1.66 | 5.43 | + | 1.54E-04 | 3.54E-03 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014741&list=upload_1&organism=Homo%20sapiens) | 1.77 | 5.07 | + | 2.37E-04 | 5.22E-03 | | [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) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&list=upload_1&organism=Homo%20sapiens) | 61.46 | 1.97 | + | 1.89E-11 | 1.48E-09 | | [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) | [536](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 314.36 | 1.71 | + | 2.67E-40 | 1.08E-37 | | [negative regulation of cardiac muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0010616) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010616&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010616&list=upload_1&organism=Homo%20sapiens) | .41 | 12.07 | + | 3.07E-04 | 6.48E-03 | | [negative regulation of muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0014745) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014745&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014745&list=upload_1&organism=Homo%20sapiens) | .59 | 10.14 | + | 1.48E-04 | 3.42E-03 | | [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) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 95.84 | 1.73 | + | 3.77E-11 | 2.87E-09 | | [mammary gland branching involved in pregnancy](http://amigo.geneontology.org/amigo/term/GO:0060745) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060745&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060745&list=upload_1&organism=Homo%20sapiens) | .41 | 12.07 | + | 3.07E-04 | 6.47E-03 | | [maternal process involved in female pregnancy](http://amigo.geneontology.org/amigo/term/GO:0060135) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060135&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060135&list=upload_1&organism=Homo%20sapiens) | 3.55 | 3.38 | + | 5.97E-04 | 1.13E-02 | | [multicellular organismal reproductive process](http://amigo.geneontology.org/amigo/term/GO:0048609) | [870](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048609&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048609&list=upload_1&organism=Homo%20sapiens) | 51.47 | 1.44 | + | 3.62E-03 | 4.94E-02 | | [reproductive process](http://amigo.geneontology.org/amigo/term/GO:0022414) | [1437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&list=upload_1&organism=Homo%20sapiens) | 85.01 | 1.41 | + | 2.97E-04 | 6.31E-03 | | [reproduction](http://amigo.geneontology.org/amigo/term/GO:0000003) | [1447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&list=upload_1&organism=Homo%20sapiens) | 85.60 | 1.41 | + | 2.51E-04 | 5.48E-03 | | [multicellular organism reproduction](http://amigo.geneontology.org/amigo/term/GO:0032504) | [908](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032504&reflist=1) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032504&list=upload_1&organism=Homo%20sapiens) | 53.72 | 1.45 | + | 1.76E-03 | 2.78E-02 | | [mammary gland duct morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060603) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060603&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060603&list=upload_1&organism=Homo%20sapiens) | 1.95 | 4.61 | + | 4.30E-04 | 8.51E-03 | | [epithelial tube morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060562) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060562&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060562&list=upload_1&organism=Homo%20sapiens) | 18.81 | 1.81 | + | 2.09E-03 | 3.24E-02 | | [morphogenesis of an epithelium](http://amigo.geneontology.org/amigo/term/GO:0002009) | [459](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002009&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002009&list=upload_1&organism=Homo%20sapiens) | 27.15 | 1.77 | + | 3.78E-04 | 7.66E-03 | | [tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048729) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&list=upload_1&organism=Homo%20sapiens) | 33.60 | 1.93 | + | 2.41E-06 | 9.13E-05 | | [tube morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0035239) | [673](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&list=upload_1&organism=Homo%20sapiens) | 39.81 | 1.76 | + | 2.00E-05 | 5.93E-04 | | [tube development](http://amigo.geneontology.org/amigo/term/GO:0035295) | [885](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&list=upload_1&organism=Homo%20sapiens) | 52.35 | 1.76 | + | 1.01E-06 | 4.09E-05 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 250.12 | 1.70 | + | 5.64E-29 | 1.24E-26 | | [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) | 3.73 | 4.02 | + | 2.32E-05 | 6.82E-04 | | [mammary gland development](http://amigo.geneontology.org/amigo/term/GO:0030879) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030879&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030879&list=upload_1&organism=Homo%20sapiens) | 7.75 | 2.97 | + | 1.54E-05 | 4.75E-04 | | [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) | 24.96 | 2.68 | + | 9.86E-12 | 7.97E-10 | | [mammary gland morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060443) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060443&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060443&list=upload_1&organism=Homo%20sapiens) | 2.84 | 4.23 | + | 1.01E-04 | 2.47E-03 | | [gland morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0022612) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022612&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022612&list=upload_1&organism=Homo%20sapiens) | 6.27 | 2.71 | + | 4.89E-04 | 9.47E-03 | | [developmental process involved in reproduction](http://amigo.geneontology.org/amigo/term/GO:0003006) | [947](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&list=upload_1&organism=Homo%20sapiens) | 56.02 | 1.59 | + | 5.27E-05 | 1.40E-03 | | [histone H4 deacetylation](http://amigo.geneontology.org/amigo/term/GO:0070933) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&list=upload_1&organism=Homo%20sapiens) | .47 | 10.56 | + | 4.76E-04 | 9.30E-03 | | [histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0016575) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&list=upload_1&organism=Homo%20sapiens) | 3.55 | 5.63 | + | 1.07E-08 | 5.90E-07 | | [histone modification](http://amigo.geneontology.org/amigo/term/GO:0016570) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&list=upload_1&organism=Homo%20sapiens) | 21.59 | 5.14 | + | 2.62E-39 | 9.78E-37 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 157.24 | 1.81 | + | 1.13E-21 | 1.59E-19 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [295](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 170.55 | 1.73 | + | 5.18E-20 | 6.66E-18 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [600](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 351.46 | 1.71 | + | 1.14E-47 | 5.77E-45 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [681](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 455.34 | 1.50 | + | 5.35E-37 | 1.61E-34 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [707](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 481.01 | 1.47 | + | 1.08E-36 | 3.15E-34 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 231.90 | 1.65 | + | 1.76E-23 | 2.70E-21 | | [organonitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901564) | [5013](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&reflist=1) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 296.56 | 1.51 | + | 4.51E-21 | 6.10E-19 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 396.95 | 1.59 | + | 1.77E-41 | 7.69E-39 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [649](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 427.59 | 1.52 | + | 3.57E-36 | 1.02E-33 | | [protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0006476) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&list=upload_1&organism=Homo%20sapiens) | 3.79 | 5.28 | + | 2.61E-08 | 1.37E-06 | | [protein deacylation](http://amigo.geneontology.org/amigo/term/GO:0035601) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&list=upload_1&organism=Homo%20sapiens) | 4.44 | 4.73 | + | 5.77E-08 | 2.86E-06 | | [macromolecule deacylation](http://amigo.geneontology.org/amigo/term/GO:0098732) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&list=upload_1&organism=Homo%20sapiens) | 4.67 | 4.71 | + | 3.05E-08 | 1.58E-06 | | [regulation of transcription from RNA polymerase II promoter in response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0043619) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043619&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043619&list=upload_1&organism=Homo%20sapiens) | .47 | 10.56 | + | 4.76E-04 | 9.29E-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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043618&list=upload_1&organism=Homo%20sapiens) | 2.43 | 4.54 | + | 1.15E-04 | 2.77E-03 | | [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) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 154.17 | 2.39 | + | 3.22E-54 | 1.68E-51 | | [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) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&list=upload_1&organism=Homo%20sapiens) | 204.33 | 2.25 | + | 5.97E-64 | 4.93E-61 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 287.21 | 1.93 | + | 3.23E-59 | 1.95E-56 | | [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) | [664](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 367.61 | 1.81 | + | 3.55E-65 | 3.48E-62 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [691](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 399.55 | 1.73 | + | 9.97E-62 | 6.25E-59 | | [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) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&list=upload_1&organism=Homo%20sapiens) | 204.45 | 2.25 | + | 6.81E-64 | 5.34E-61 | | [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) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 204.98 | 2.24 | + | 1.61E-63 | 1.20E-60 | | [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) | [497](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 232.96 | 2.13 | + | 2.41E-63 | 1.72E-60 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [512](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 246.27 | 2.08 | + | 2.07E-62 | 1.35E-59 | | [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) | [486](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 221.96 | 2.19 | + | 7.21E-65 | 6.65E-62 | | [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) | [518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 240.59 | 2.15 | + | 2.26E-68 | 2.96E-65 | | [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) | [638](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 337.73 | 1.89 | + | 1.11E-68 | 1.58E-65 | | [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) | [620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 334.06 | 1.86 | + | 6.08E-63 | 4.15E-60 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [879](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 661.80 | 1.33 | + | 2.72E-35 | 7.61E-33 | | [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) | [643](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 347.37 | 1.85 | + | 3.39E-66 | 3.54E-63 | | [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) | [511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 242.67 | 2.11 | + | 3.80E-64 | 3.31E-61 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043620&list=upload_1&organism=Homo%20sapiens) | 2.78 | 4.32 | + | 8.49E-05 | 2.11E-03 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 94.59 | 2.15 | + | 8.11E-23 | 1.20E-20 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 388.61 | 1.36 | + | 5.87E-16 | 6.22E-14 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [1086](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 889.97 | 1.22 | + | 1.63E-41 | 7.53E-39 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [645](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 485.63 | 1.33 | + | 4.21E-19 | 5.12E-17 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [343](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 205.04 | 1.67 | + | 1.68E-21 | 2.31E-19 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&list=upload_1&organism=Homo%20sapiens) | 13.13 | 2.59 | + | 2.88E-06 | 1.08E-04 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&list=upload_1&organism=Homo%20sapiens) | 16.15 | 2.48 | + | 1.19E-06 | 4.77E-05 | | [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) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 154.76 | 1.81 | + | 1.54E-21 | 2.14E-19 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 240.18 | 1.56 | + | 1.18E-18 | 1.36E-16 | | [response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0006979) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 21.71 | 2.26 | + | 7.77E-07 | 3.21E-05 | | [monoubiquitinated histone H2A deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0035522) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035522&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035522&list=upload_1&organism=Homo%20sapiens) | 1.72 | 9.91 | + | 1.68E-10 | 1.19E-08 | | [monoubiquitinated histone deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0035521) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035521&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035521&list=upload_1&organism=Homo%20sapiens) | 1.72 | 9.91 | + | 1.68E-10 | 1.18E-08 | | [monoubiquitinated protein deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0035520) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035520&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035520&list=upload_1&organism=Homo%20sapiens) | 2.01 | 8.95 | + | 1.72E-10 | 1.20E-08 | | [protein deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016579) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016579&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016579&list=upload_1&organism=Homo%20sapiens) | 8.93 | 2.69 | + | 4.28E-05 | 1.18E-03 | | [protein modification by small protein removal](http://amigo.geneontology.org/amigo/term/GO:0070646) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070646&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070646&list=upload_1&organism=Homo%20sapiens) | 10.00 | 3.10 | + | 2.39E-07 | 1.08E-05 | | [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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070647&list=upload_1&organism=Homo%20sapiens) | 53.12 | 1.47 | + | 1.63E-03 | 2.60E-02 | | [proteolysis](http://amigo.geneontology.org/amigo/term/GO:0006508) | [1266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&list=upload_1&organism=Homo%20sapiens) | 74.89 | 1.66 | + | 1.75E-07 | 8.05E-06 | | [histone deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016578) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016578&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016578&list=upload_1&organism=Homo%20sapiens) | 2.60 | 8.07 | + | 2.36E-11 | 1.82E-09 | | [positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1902255) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902255&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902255&list=upload_1&organism=Homo%20sapiens) | .41 | 9.66 | + | 2.33E-03 | 3.52E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 6.15 | 3.74 | + | 5.25E-07 | 2.22E-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) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 101.81 | 1.62 | + | 4.63E-09 | 2.66E-07 | | [regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009966) | [2989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&reflist=1) | [285](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 176.82 | 1.61 | + | 1.99E-15 | 2.07E-13 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 199.30 | 1.63 | + | 1.40E-18 | 1.59E-16 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 200.01 | 1.62 | + | 2.23E-18 | 2.48E-16 | | [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) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 59.10 | 1.44 | + | 1.73E-03 | 2.75E-02 | | [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) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 90.39 | 1.59 | + | 1.60E-07 | 7.45E-06 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 100.63 | 1.54 | + | 3.42E-07 | 1.50E-05 | | [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) | [643](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 372.93 | 1.72 | + | 1.54E-54 | 8.35E-52 | | [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) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 100.33 | 1.53 | + | 4.36E-07 | 1.88E-05 | | [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) | [606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 335.42 | 1.81 | + | 1.04E-56 | 6.05E-54 | | [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) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 131.51 | 1.63 | + | 8.32E-12 | 6.79E-10 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001244&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.05 | + | 2.07E-03 | 3.21E-02 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&list=upload_1&organism=Homo%20sapiens) | 21.53 | 2.23 | + | 1.97E-06 | 7.61E-05 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 86.84 | 2.10 | + | 1.86E-19 | 2.33E-17 | | [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) | [184](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 88.62 | 2.08 | + | 2.56E-19 | 3.18E-17 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [196](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 97.85 | 2.00 | + | 5.03E-19 | 6.02E-17 | | [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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&list=upload_1&organism=Homo%20sapiens) | 29.76 | 1.85 | + | 4.89E-05 | 1.32E-03 | | [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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&list=upload_1&organism=Homo%20sapiens) | 30.53 | 1.83 | + | 4.26E-05 | 1.18E-03 | | [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) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 34.49 | 1.83 | + | 1.69E-05 | 5.14E-04 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&list=upload_1&organism=Homo%20sapiens) | 9.88 | 2.63 | + | 4.31E-05 | 1.19E-03 | | [regulation of intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1902253) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902253&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902253&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.75 | + | 3.55E-04 | 7.27E-03 | | [DNA methylation-dependent heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0006346) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006346&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006346&list=upload_1&organism=Homo%20sapiens) | .41 | 9.66 | + | 2.33E-03 | 3.51E-02 | | [facultative heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0140718) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&list=upload_1&organism=Homo%20sapiens) | .77 | 7.80 | + | 4.33E-04 | 8.55E-03 | | [heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0031507) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031507&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031507&list=upload_1&organism=Homo%20sapiens) | 3.08 | 4.55 | + | 1.34E-05 | 4.22E-04 | | [heterochromatin organization](http://amigo.geneontology.org/amigo/term/GO:0070828) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070828&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070828&list=upload_1&organism=Homo%20sapiens) | 3.67 | 4.36 | + | 5.25E-06 | 1.84E-04 | | [chromatin remodeling](http://amigo.geneontology.org/amigo/term/GO:0006338) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&list=upload_1&organism=Homo%20sapiens) | 19.11 | 4.66 | + | 5.40E-29 | 1.21E-26 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006325) | [585](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&reflist=1) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&list=upload_1&organism=Homo%20sapiens) | 34.61 | 4.13 | + | 2.87E-41 | 1.22E-38 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [530](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 326.73 | 1.62 | + | 8.39E-34 | 2.27E-31 | | [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) | [539](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 338.80 | 1.59 | + | 2.11E-32 | 5.26E-30 | | [negative regulation of gene expression, epigenetic](http://amigo.geneontology.org/amigo/term/GO:0045814) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045814&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045814&list=upload_1&organism=Homo%20sapiens) | 3.90 | 4.61 | + | 6.98E-07 | 2.91E-05 | | [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) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 53.36 | 2.17 | + | 2.16E-13 | 1.97E-11 | | [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) | [352](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 163.51 | 2.15 | + | 4.49E-42 | 2.13E-39 | | [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) | [370](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 176.76 | 2.09 | + | 3.57E-42 | 1.75E-39 | | [epigenetic regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0040029) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040029&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040029&list=upload_1&organism=Homo%20sapiens) | 6.98 | 4.15 | + | 2.36E-09 | 1.43E-07 | | [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) | .41 | 9.66 | + | 2.33E-03 | 3.51E-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) | .47 | 8.45 | + | 3.34E-03 | 4.61E-02 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [349](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 208.18 | 1.68 | + | 4.34E-22 | 6.19E-20 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [351](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 209.54 | 1.68 | + | 3.72E-22 | 5.34E-20 | | [mRNA transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0042789) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042789&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042789&list=upload_1&organism=Homo%20sapiens) | 2.66 | 8.64 | + | 8.84E-13 | 7.79E-11 | | [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) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&list=upload_1&organism=Homo%20sapiens) | 21.06 | 4.32 | + | 1.35E-27 | 2.68E-25 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 36.26 | 3.83 | + | 4.88E-37 | 1.50E-34 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 36.32 | 3.85 | + | 1.56E-37 | 5.33E-35 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 36.91 | 3.79 | + | 7.13E-37 | 2.11E-34 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 87.97 | 2.35 | + | 5.70E-28 | 1.19E-25 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 149.91 | 1.74 | + | 8.09E-18 | 8.75E-16 | | [biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009058) | [2603](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&reflist=1) | [269](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&list=upload_1&organism=Homo%20sapiens) | 153.99 | 1.75 | + | 1.26E-18 | 1.45E-16 | | [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) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 59.57 | 2.72 | + | 1.04E-27 | 2.12E-25 | | [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) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 93.94 | 2.27 | + | 1.03E-26 | 1.94E-24 | | [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) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 211.37 | 1.77 | + | 3.50E-28 | 7.62E-26 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 390.80 | 1.51 | + | 2.22E-30 | 5.20E-28 | | [cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044249) | [2464](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&reflist=1) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&list=upload_1&organism=Homo%20sapiens) | 145.76 | 1.77 | + | 1.55E-18 | 1.75E-16 | | [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) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 167.12 | 1.88 | + | 6.83E-27 | 1.32E-24 | | [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) | [349](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 194.75 | 1.79 | + | 7.45E-27 | 1.42E-24 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 177.41 | 1.83 | + | 5.13E-26 | 9.36E-24 | | [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) | [328](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 180.43 | 1.82 | + | 6.55E-26 | 1.18E-23 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 63.83 | 2.66 | + | 3.57E-28 | 7.67E-26 | | [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) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 71.94 | 2.49 | + | 2.17E-26 | 4.06E-24 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 64.42 | 2.64 | + | 1.20E-27 | 2.41E-25 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 96.72 | 2.22 | + | 4.88E-26 | 9.00E-24 | | [nucleic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090304) | [2276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&reflist=1) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 134.64 | 2.15 | + | 8.74E-34 | 2.32E-31 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [285](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 136.89 | 2.08 | + | 7.32E-31 | 1.74E-28 | | [mRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0009299) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009299&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009299&list=upload_1&organism=Homo%20sapiens) | 3.02 | 8.29 | + | 1.87E-13 | 1.72E-11 | | [mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016071) | [607](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&list=upload_1&organism=Homo%20sapiens) | 35.91 | 2.37 | + | 9.48E-12 | 7.70E-10 | | [foregut morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0007440) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007440&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007440&list=upload_1&organism=Homo%20sapiens) | .59 | 8.45 | + | 1.01E-03 | 1.78E-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) | 2.84 | 3.87 | + | 3.71E-04 | 7.55E-03 | | [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) | 7.81 | 2.43 | + | 9.37E-04 | 1.68E-02 | | [digestive system development](http://amigo.geneontology.org/amigo/term/GO:0055123) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&list=upload_1&organism=Homo%20sapiens) | 8.46 | 2.36 | + | 8.67E-04 | 1.57E-02 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 227.05 | 1.72 | + | 1.77E-27 | 3.48E-25 | | [regulation of nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:2000819) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000819&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000819&list=upload_1&organism=Homo%20sapiens) | 1.66 | 8.45 | + | 3.23E-08 | 1.67E-06 | | [regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006282) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&list=upload_1&organism=Homo%20sapiens) | 12.54 | 4.94 | + | 1.25E-21 | 1.75E-19 | | [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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 32.00 | 3.56 | + | 5.29E-28 | 1.12E-25 | | [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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 18.58 | 4.25 | + | 1.03E-23 | 1.65E-21 | | [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) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 41.94 | 3.05 | + | 7.10E-26 | 1.27E-23 | | [positive regulation of telomere maintenance in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:1904507) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904507&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904507&list=upload_1&organism=Homo%20sapiens) | .71 | 8.45 | + | 3.11E-04 | 6.54E-03 | | [regulation of telomere maintenance in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:1904505) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904505&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904505&list=upload_1&organism=Homo%20sapiens) | .95 | 7.40 | + | 1.85E-04 | 4.17E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&list=upload_1&organism=Homo%20sapiens) | 5.97 | 3.18 | + | 3.64E-05 | 1.04E-03 | | [regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0033044) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 14.91 | 4.36 | + | 3.45E-20 | 4.51E-18 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 70.34 | 2.22 | + | 1.09E-18 | 1.27E-16 | | [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) | [263](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 139.85 | 1.88 | + | 3.45E-22 | 5.00E-20 | | [positive regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001022) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&list=upload_1&organism=Homo%20sapiens) | 9.94 | 3.92 | + | 1.88E-11 | 1.49E-09 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&list=upload_1&organism=Homo%20sapiens) | 3.90 | 3.07 | + | 1.24E-03 | 2.08E-02 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 6.27 | 3.99 | + | 5.87E-08 | 2.90E-06 | | [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) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&list=upload_1&organism=Homo%20sapiens) | 30.05 | 2.23 | + | 1.10E-08 | 6.07E-07 | | [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) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 62.35 | 1.96 | + | 2.42E-11 | 1.86E-09 | | [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) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 18.04 | 3.44 | + | 4.54E-15 | 4.68E-13 | | [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) | [362](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 121.75 | 2.97 | + | 2.53E-75 | 7.92E-72 | | [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) | [454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 187.77 | 2.42 | + | 1.15E-71 | 2.01E-68 | | [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) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 228.23 | 2.19 | + | 5.24E-67 | 5.87E-64 | | [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) | [441](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 184.69 | 2.39 | + | 1.33E-67 | 1.60E-64 | | [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) | [483](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 209.54 | 2.31 | + | 4.41E-71 | 6.92E-68 | | [regulation of epithelial cell proliferation involved in prostate gland development](http://amigo.geneontology.org/amigo/term/GO:0060768) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060768&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060768&list=upload_1&organism=Homo%20sapiens) | .59 | 8.45 | + | 1.01E-03 | 1.78E-02 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&list=upload_1&organism=Homo%20sapiens) | 21.83 | 2.20 | + | 2.30E-06 | 8.80E-05 | | [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) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 99.03 | 2.01 | + | 1.82E-19 | 2.33E-17 | | [nucleotide-excision repair, DNA incision](http://amigo.geneontology.org/amigo/term/GO:0033683) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033683&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033683&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.63E-02 | | [nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006289) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&list=upload_1&organism=Homo%20sapiens) | 3.31 | 4.83 | + | 1.72E-06 | 6.72E-05 | | [DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006281) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&list=upload_1&organism=Homo%20sapiens) | 30.05 | 2.26 | + | 5.69E-09 | 3.25E-07 | | [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) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 44.72 | 2.53 | + | 2.63E-17 | 2.82E-15 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 46.97 | 2.15 | + | 1.61E-11 | 1.27E-09 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [241](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 148.96 | 1.62 | + | 4.61E-13 | 4.11E-11 | | [negative regulation by host of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0044828) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044828&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044828&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.62E-02 | | [negative regulation by host of viral process](http://amigo.geneontology.org/amigo/term/GO:0044793) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044793&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044793&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.71E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044788&list=upload_1&organism=Homo%20sapiens) | 2.66 | 3.38 | + | 2.81E-03 | 4.05E-02 | | [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) | 4.91 | 4.68 | + | 1.61E-08 | 8.75E-07 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 6.68 | 3.89 | + | 4.92E-08 | 2.45E-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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 15.44 | 2.33 | + | 1.66E-05 | 5.08E-04 | | [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) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&list=upload_1&organism=Homo%20sapiens) | 94.77 | 1.50 | + | 4.52E-06 | 1.61E-04 | | [intracellular transport of virus](http://amigo.geneontology.org/amigo/term/GO:0075733) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0075733&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0075733&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.62E-02 | | [viral process](http://amigo.geneontology.org/amigo/term/GO:0016032) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&list=upload_1&organism=Homo%20sapiens) | 14.85 | 2.02 | + | 6.07E-04 | 1.15E-02 | | [histone H4-K12 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043983) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043983&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043983&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.62E-02 | | [histone H4 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043967) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&list=upload_1&organism=Homo%20sapiens) | 3.61 | 6.65 | + | 2.28E-11 | 1.77E-09 | | [histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0016573) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&list=upload_1&organism=Homo%20sapiens) | 7.45 | 7.11 | + | 1.60E-24 | 2.67E-22 | | [internal peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:0018393) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018393&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018393&list=upload_1&organism=Homo%20sapiens) | 7.81 | 6.79 | + | 9.08E-24 | 1.47E-21 | | [peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:0018394) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&list=upload_1&organism=Homo%20sapiens) | 7.99 | 6.64 | + | 2.10E-23 | 3.19E-21 | | [protein acetylation](http://amigo.geneontology.org/amigo/term/GO:0006473) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&list=upload_1&organism=Homo%20sapiens) | 9.17 | 6.11 | + | 3.08E-23 | 4.64E-21 | | [protein acylation](http://amigo.geneontology.org/amigo/term/GO:0043543) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&list=upload_1&organism=Homo%20sapiens) | 11.54 | 5.11 | + | 3.03E-21 | 4.14E-19 | | [peptidyl-lysine modification](http://amigo.geneontology.org/amigo/term/GO:0018205) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&list=upload_1&organism=Homo%20sapiens) | 18.40 | 4.40 | + | 4.10E-25 | 6.98E-23 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 52.18 | 2.57 | + | 5.89E-21 | 7.89E-19 | | [internal protein amino acid acetylation](http://amigo.geneontology.org/amigo/term/GO:0006475) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006475&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006475&list=upload_1&organism=Homo%20sapiens) | 7.93 | 6.69 | + | 1.59E-23 | 2.52E-21 | | [histone H3-K4 demethylation](http://amigo.geneontology.org/amigo/term/GO:0034720) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034720&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034720&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.61E-02 | | [histone lysine demethylation](http://amigo.geneontology.org/amigo/term/GO:0070076) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.23 | + | 2.83E-03 | 4.05E-02 | | [histone demethylation](http://amigo.geneontology.org/amigo/term/GO:0016577) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&list=upload_1&organism=Homo%20sapiens) | 1.72 | 4.08 | + | 3.34E-03 | 4.60E-02 | | [regulation of RNA polymerase II transcription preinitiation complex assembly](http://amigo.geneontology.org/amigo/term/GO:0045898) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045898&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045898&list=upload_1&organism=Homo%20sapiens) | .47 | 8.45 | + | 3.34E-03 | 4.60E-02 | | [regulation of transcription initiation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0060260) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060260&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060260&list=upload_1&organism=Homo%20sapiens) | 3.96 | 6.81 | + | 8.21E-13 | 7.27E-11 | | [regulation of DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:2000142) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000142&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000142&list=upload_1&organism=Homo%20sapiens) | 4.56 | 6.81 | + | 1.71E-14 | 1.73E-12 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&list=upload_1&organism=Homo%20sapiens) | 24.37 | 1.89 | + | 1.20E-04 | 2.88E-03 | | [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) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 56.26 | 1.83 | + | 2.74E-08 | 1.43E-06 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&list=upload_1&organism=Homo%20sapiens) | 1.01 | 7.95 | + | 4.26E-05 | 1.18E-03 | | [histone H3-K14 acetylation](http://amigo.geneontology.org/amigo/term/GO:0044154) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044154&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044154&list=upload_1&organism=Homo%20sapiens) | 1.01 | 7.95 | + | 4.26E-05 | 1.18E-03 | | [histone H3 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043966) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043966&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043966&list=upload_1&organism=Homo%20sapiens) | 3.67 | 9.00 | + | 3.89E-18 | 4.26E-16 | | [negative regulation of autophagosome assembly](http://amigo.geneontology.org/amigo/term/GO:1902902) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902902&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902902&list=upload_1&organism=Homo%20sapiens) | .89 | 7.89 | + | 1.35E-04 | 3.19E-03 | | [regulation of autophagosome assembly](http://amigo.geneontology.org/amigo/term/GO:2000785) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000785&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000785&list=upload_1&organism=Homo%20sapiens) | 2.66 | 3.38 | + | 2.81E-03 | 4.06E-02 | | [regulation of organelle assembly](http://amigo.geneontology.org/amigo/term/GO:1902115) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902115&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902115&list=upload_1&organism=Homo%20sapiens) | 12.36 | 2.18 | + | 4.69E-04 | 9.18E-03 | | [regulation of vacuole organization](http://amigo.geneontology.org/amigo/term/GO:0044088) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044088&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044088&list=upload_1&organism=Homo%20sapiens) | 3.02 | 3.31 | + | 1.90E-03 | 2.97E-02 | | [negative regulation of macroautophagy](http://amigo.geneontology.org/amigo/term/GO:0016242) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016242&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016242&list=upload_1&organism=Homo%20sapiens) | 2.07 | 5.31 | + | 3.45E-05 | 9.84E-04 | | [negative regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010507) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010507&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010507&list=upload_1&organism=Homo%20sapiens) | 5.09 | 2.95 | + | 4.76E-04 | 9.28E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 14.32 | 2.44 | + | 7.52E-06 | 2.57E-04 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&list=upload_1&organism=Homo%20sapiens) | 19.29 | 2.44 | + | 1.70E-07 | 7.84E-06 | | [regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009894) | [987](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&reflist=1) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&list=upload_1&organism=Homo%20sapiens) | 58.39 | 1.92 | + | 5.34E-10 | 3.55E-08 | | [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) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 133.93 | 2.30 | + | 3.45E-41 | 1.43E-38 | | [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) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 279.93 | 1.76 | + | 1.88E-39 | 7.20E-37 | | [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) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&list=upload_1&organism=Homo%20sapiens) | 46.50 | 2.00 | + | 2.98E-09 | 1.77E-07 | | [regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010506) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&list=upload_1&organism=Homo%20sapiens) | 20.41 | 2.11 | + | 1.75E-05 | 5.30E-04 | | [regulation of macroautophagy](http://amigo.geneontology.org/amigo/term/GO:0016241) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&list=upload_1&organism=Homo%20sapiens) | 9.47 | 2.22 | + | 1.56E-03 | 2.50E-02 | | [negative regulation of organelle assembly](http://amigo.geneontology.org/amigo/term/GO:1902116) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902116&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902116&list=upload_1&organism=Homo%20sapiens) | 2.60 | 4.61 | + | 4.95E-05 | 1.33E-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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&list=upload_1&organism=Homo%20sapiens) | 20.41 | 2.60 | + | 6.25E-09 | 3.57E-07 | | [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) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 40.82 | 2.20 | + | 5.48E-11 | 4.09E-09 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&list=upload_1&organism=Homo%20sapiens) | 2.78 | 7.55 | + | 6.21E-11 | 4.61E-09 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&list=upload_1&organism=Homo%20sapiens) | 3.14 | 7.34 | + | 1.22E-11 | 9.78E-10 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 4.38 | 6.62 | + | 2.07E-13 | 1.90E-11 | | [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) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 109.32 | 3.10 | + | 6.12E-74 | 1.60E-70 | | [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) | [329](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 101.46 | 3.24 | + | 9.42E-76 | 7.39E-72 | | [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) | [329](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 101.46 | 3.24 | + | 9.42E-76 | 1.48E-71 | | [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) | [329](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 101.81 | 3.23 | + | 2.05E-75 | 1.07E-71 | | [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) | [358](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 121.16 | 2.95 | + | 1.03E-73 | 2.30E-70 | | [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) | [360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 123.46 | 2.92 | + | 8.13E-73 | 1.59E-69 | | [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) | [351](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 114.94 | 3.05 | + | 2.20E-75 | 8.64E-72 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 3.73 | 6.98 | + | 1.41E-12 | 1.22E-10 | | [positive regulation of gluconeogenesis](http://amigo.geneontology.org/amigo/term/GO:0045722) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045722&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045722&list=upload_1&organism=Homo%20sapiens) | .95 | 7.40 | + | 1.85E-04 | 4.18E-03 | | [positive regulation of glucose metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010907) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010907&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010907&list=upload_1&organism=Homo%20sapiens) | 2.31 | 3.90 | + | 1.20E-03 | 2.03E-02 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062013&list=upload_1&organism=Homo%20sapiens) | 8.70 | 2.53 | + | 2.48E-04 | 5.43E-03 | | [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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062012&list=upload_1&organism=Homo%20sapiens) | 19.70 | 2.13 | + | 1.92E-05 | 5.72E-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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010906&list=upload_1&organism=Homo%20sapiens) | 6.15 | 2.93 | + | 1.47E-04 | 3.42E-03 | | [regulation of cellular carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010675) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010675&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010675&list=upload_1&organism=Homo%20sapiens) | 9.35 | 2.46 | + | 2.26E-04 | 5.01E-03 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006109&list=upload_1&organism=Homo%20sapiens) | 11.18 | 2.41 | + | 8.01E-05 | 2.01E-03 | | [positive regulation of cellular carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010676) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010676&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010676&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.19 | + | 2.44E-03 | 3.64E-02 | | [positive regulation of carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045913) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045913&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045913&list=upload_1&organism=Homo%20sapiens) | 4.44 | 3.16 | + | 4.00E-04 | 7.99E-03 | | [regulation of gluconeogenesis](http://amigo.geneontology.org/amigo/term/GO:0006111) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006111&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006111&list=upload_1&organism=Homo%20sapiens) | 3.02 | 3.65 | + | 5.79E-04 | 1.10E-02 | | [regulation of carbohydrate biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0043255) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043255&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043255&list=upload_1&organism=Homo%20sapiens) | 5.86 | 2.56 | + | 1.70E-03 | 2.69E-02 | | [negative regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060253) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060253&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060253&list=upload_1&organism=Homo%20sapiens) | .95 | 7.40 | + | 1.85E-04 | 4.17E-03 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 2.07 | 5.80 | + | 7.37E-06 | 2.52E-04 | | [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) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 42.18 | 2.25 | + | 7.03E-12 | 5.77E-10 | | [negative regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014014) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&list=upload_1&organism=Homo%20sapiens) | 2.43 | 3.71 | + | 1.62E-03 | 2.58E-02 | | [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) | 5.97 | 3.35 | + | 1.20E-05 | 3.80E-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) | 22.07 | 2.22 | + | 1.50E-06 | 5.90E-05 | | [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) | 26.74 | 1.98 | + | 1.20E-05 | 3.81E-04 | | [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) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 81.82 | 2.13 | + | 4.36E-19 | 5.26E-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) | [294](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 147.24 | 2.00 | + | 4.51E-29 | 1.02E-26 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 30.35 | 2.11 | + | 1.68E-07 | 7.79E-06 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 93.53 | 2.19 | + | 5.12E-24 | 8.36E-22 | | [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) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&list=upload_1&organism=Homo%20sapiens) | 54.60 | 2.22 | + | 1.53E-14 | 1.56E-12 | | [negative regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0010721) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010721&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010721&list=upload_1&organism=Homo%20sapiens) | 10.83 | 2.12 | + | 1.84E-03 | 2.89E-02 | | [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) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 39.99 | 2.28 | + | 1.10E-11 | 8.81E-10 | | [histone H2A acetylation](http://amigo.geneontology.org/amigo/term/GO:0043968) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043968&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043968&list=upload_1&organism=Homo%20sapiens) | 1.36 | 7.35 | + | 8.09E-06 | 2.71E-04 | | [regulation of histone H4 acetylation](http://amigo.geneontology.org/amigo/term/GO:0090239) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090239&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090239&list=upload_1&organism=Homo%20sapiens) | .83 | 7.24 | + | 5.90E-04 | 1.12E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&list=upload_1&organism=Homo%20sapiens) | 4.02 | 5.47 | + | 3.12E-09 | 1.83E-07 | | [regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031056) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&list=upload_1&organism=Homo%20sapiens) | 10.71 | 4.86 | + | 4.54E-18 | 4.95E-16 | | [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) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 92.46 | 2.10 | + | 7.50E-21 | 9.88E-19 | | [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) | [289](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&list=upload_1&organism=Homo%20sapiens) | 153.04 | 1.89 | + | 7.27E-25 | 1.23E-22 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000756&list=upload_1&organism=Homo%20sapiens) | 4.56 | 5.27 | + | 1.13E-09 | 7.30E-08 | | [regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901983) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&list=upload_1&organism=Homo%20sapiens) | 5.27 | 5.13 | + | 1.72E-10 | 1.20E-08 | | [histone exchange](http://amigo.geneontology.org/amigo/term/GO:0043486) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043486&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043486&list=upload_1&organism=Homo%20sapiens) | .83 | 7.24 | + | 5.90E-04 | 1.12E-02 | | [nucleosome organization](http://amigo.geneontology.org/amigo/term/GO:0034728) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&list=upload_1&organism=Homo%20sapiens) | 7.39 | 3.38 | + | 8.70E-07 | 3.57E-05 | | [protein-DNA complex subunit organization](http://amigo.geneontology.org/amigo/term/GO:0071824) | [233](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&list=upload_1&organism=Homo%20sapiens) | 13.78 | 3.85 | + | 9.27E-15 | 9.50E-13 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 84.18 | 1.92 | + | 3.06E-14 | 3.02E-12 | | [positive regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:1902459) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902459&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902459&list=upload_1&organism=Homo%20sapiens) | 2.78 | 7.19 | + | 3.50E-10 | 2.35E-08 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&list=upload_1&organism=Homo%20sapiens) | 4.14 | 5.80 | + | 2.29E-10 | 1.56E-08 | | [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) | 79.21 | 2.28 | + | 4.66E-23 | 6.96E-21 | | [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) | [177](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 89.62 | 1.97 | + | 1.34E-16 | 1.43E-14 | | [positive regulation of transcription initiation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0060261) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060261&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060261&list=upload_1&organism=Homo%20sapiens) | 3.49 | 7.16 | + | 2.39E-12 | 2.03E-10 | | [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) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&list=upload_1&organism=Homo%20sapiens) | 74.48 | 3.26 | + | 1.20E-54 | 6.70E-52 | | [positive regulation of DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:2000144) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000144&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000144&list=upload_1&organism=Homo%20sapiens) | 3.90 | 7.43 | + | 2.02E-14 | 2.03E-12 | | [regulation of cell fate specification](http://amigo.geneontology.org/amigo/term/GO:0042659) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042659&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042659&list=upload_1&organism=Homo%20sapiens) | 1.54 | 7.15 | + | 3.51E-06 | 1.30E-04 | | [regulation of cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0010453) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010453&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010453&list=upload_1&organism=Homo%20sapiens) | 2.37 | 5.49 | + | 5.01E-06 | 1.77E-04 | | [nucleosome disassembly](http://amigo.geneontology.org/amigo/term/GO:0006337) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006337&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006337&list=upload_1&organism=Homo%20sapiens) | 1.12 | 7.12 | + | 7.91E-05 | 1.99E-03 | | [protein-DNA complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032986) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&list=upload_1&organism=Homo%20sapiens) | 1.24 | 7.24 | + | 2.53E-05 | 7.35E-04 | | [protein-containing complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032984) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&list=upload_1&organism=Homo%20sapiens) | 7.93 | 2.78 | + | 5.75E-05 | 1.51E-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) | 18.81 | 2.34 | + | 1.27E-06 | 5.06E-05 | | [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) | .71 | 7.04 | + | 1.90E-03 | 2.97E-02 | | [regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0050790) | [2373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&reflist=1) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 140.38 | 1.49 | + | 1.76E-08 | 9.57E-07 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [294](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 183.03 | 1.61 | + | 9.24E-16 | 9.72E-14 | | [regulation of ATP-dependent activity](http://amigo.geneontology.org/amigo/term/GO:0043462) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043462&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043462&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.01 | + | 9.37E-04 | 1.68E-02 | | [positive regulation of chromatin organization](http://amigo.geneontology.org/amigo/term/GO:1905269) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905269&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905269&list=upload_1&organism=Homo%20sapiens) | 1.01 | 6.96 | + | 2.49E-04 | 5.44E-03 | | [regulation of chromatin organization](http://amigo.geneontology.org/amigo/term/GO:1902275) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902275&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902275&list=upload_1&organism=Homo%20sapiens) | 2.60 | 5.38 | + | 2.68E-06 | 1.01E-04 | | [regulation of G0 to G1 transition](http://amigo.geneontology.org/amigo/term/GO:0070316) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070316&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070316&list=upload_1&organism=Homo%20sapiens) | 2.19 | 6.85 | + | 9.35E-08 | 4.43E-06 | | [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) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 42.30 | 2.67 | + | 6.64E-19 | 7.89E-17 | | [regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051726) | [1122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&reflist=1) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 66.38 | 2.74 | + | 1.45E-31 | 3.56E-29 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060965&list=upload_1&organism=Homo%20sapiens) | 1.18 | 6.76 | + | 1.05E-04 | 2.56E-03 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&list=upload_1&organism=Homo%20sapiens) | 2.48 | 3.62 | + | 1.87E-03 | 2.93E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.46E-03 | 3.67E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&list=upload_1&organism=Homo%20sapiens) | 2.66 | 3.38 | + | 2.81E-03 | 4.05E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&list=upload_1&organism=Homo%20sapiens) | 2.72 | 3.31 | + | 3.20E-03 | 4.47E-02 | | [negative regulation of post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:1900369) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900369&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900369&list=upload_1&organism=Homo%20sapiens) | 1.24 | 6.44 | + | 1.38E-04 | 3.24E-03 | | [negative regulation of post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060149) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060149&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060149&list=upload_1&organism=Homo%20sapiens) | 1.24 | 6.44 | + | 1.38E-04 | 3.24E-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) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 68.09 | 2.26 | + | 3.32E-19 | 4.10E-17 | | [negative regulation of gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0060967) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060967&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060967&list=upload_1&organism=Homo%20sapiens) | 1.24 | 6.44 | + | 1.38E-04 | 3.23E-03 | | [regulation of DNA methylation](http://amigo.geneontology.org/amigo/term/GO:0044030) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&list=upload_1&organism=Homo%20sapiens) | 1.48 | 6.76 | + | 1.45E-05 | 4.51E-04 | | [DNA catabolic process, endonucleolytic](http://amigo.geneontology.org/amigo/term/GO:0000737) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000737&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000737&list=upload_1&organism=Homo%20sapiens) | 1.06 | 6.57 | + | 3.29E-04 | 6.81E-03 | | [DNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006308) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006308&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006308&list=upload_1&organism=Homo%20sapiens) | 1.30 | 5.38 | + | 8.79E-04 | 1.59E-02 | | [cellular macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044265) | [785](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&list=upload_1&organism=Homo%20sapiens) | 46.44 | 1.66 | + | 5.35E-05 | 1.42E-03 | | [macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009057) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&list=upload_1&organism=Homo%20sapiens) | 58.51 | 1.57 | + | 5.58E-05 | 1.47E-03 | | [organic substance catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901575) | [1679](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&list=upload_1&organism=Homo%20sapiens) | 99.33 | 1.39 | + | 1.82E-04 | 4.11E-03 | | [catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009056) | [1974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&reflist=1) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&list=upload_1&organism=Homo%20sapiens) | 116.78 | 1.36 | + | 1.55E-04 | 3.57E-03 | | [cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044248) | [1625](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&reflist=1) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&list=upload_1&organism=Homo%20sapiens) | 96.13 | 1.40 | + | 1.45E-04 | 3.37E-03 | | [negative regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035067) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035067&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035067&list=upload_1&organism=Homo%20sapiens) | 1.06 | 6.57 | + | 3.29E-04 | 6.80E-03 | | [negative regulation of peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:2000757) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000757&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000757&list=upload_1&organism=Homo%20sapiens) | 1.24 | 6.44 | + | 1.38E-04 | 3.25E-03 | | [negative regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901984) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901984&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901984&list=upload_1&organism=Homo%20sapiens) | 1.42 | 5.63 | + | 2.92E-04 | 6.22E-03 | | [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) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 29.76 | 2.32 | + | 1.58E-09 | 9.96E-08 | | [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) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 61.64 | 1.95 | + | 4.72E-11 | 3.56E-09 | | [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) | [321](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 142.51 | 2.25 | + | 1.71E-41 | 7.66E-39 | | [negative regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031057) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031057&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031057&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.83 | + | 7.59E-06 | 2.57E-04 | | [positive regulation of transcription regulatory region DNA binding](http://amigo.geneontology.org/amigo/term/GO:2000679) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000679&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000679&list=upload_1&organism=Homo%20sapiens) | 1.54 | 6.50 | + | 1.91E-05 | 5.71E-04 | | [regulation of transcription regulatory region DNA binding](http://amigo.geneontology.org/amigo/term/GO:2000677) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000677&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000677&list=upload_1&organism=Homo%20sapiens) | 3.25 | 5.53 | + | 7.24E-08 | 3.51E-06 | | [regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0051101) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 7.34 | 4.09 | + | 1.72E-09 | 1.07E-07 | | [regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051098) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&list=upload_1&organism=Homo%20sapiens) | 22.13 | 2.89 | + | 1.59E-12 | 1.37E-10 | | [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) | 3.43 | 3.79 | + | 1.36E-04 | 3.19E-03 | | [positive regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051099) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.52 | + | 4.55E-05 | 1.25E-03 | | [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) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 94.06 | 1.64 | + | 9.15E-09 | 5.14E-07 | | [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) | .77 | 6.50 | + | 2.51E-03 | 3.72E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&list=upload_1&organism=Homo%20sapiens) | 16.27 | 2.27 | + | 1.60E-05 | 4.89E-04 | | [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) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043086&list=upload_1&organism=Homo%20sapiens) | 46.20 | 1.58 | + | 3.26E-04 | 6.75E-03 | | [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) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 68.03 | 1.84 | + | 5.12E-10 | 3.42E-08 | | [regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051338) | [915](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 54.13 | 1.59 | + | 7.23E-05 | 1.85E-03 | | [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) | 2.37 | 4.65 | + | 9.52E-05 | 2.35E-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) | [235](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 90.69 | 2.59 | + | 9.37E-38 | 3.34E-35 | | [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) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 96.07 | 2.53 | + | 1.27E-37 | 4.42E-35 | | [negative regulation of DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051053) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051053&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051053&list=upload_1&organism=Homo%20sapiens) | 8.76 | 2.40 | + | 5.55E-04 | 1.06E-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) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 92.40 | 2.62 | + | 1.10E-39 | 4.33E-37 | | [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) | [240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 94.30 | 2.55 | + | 2.39E-37 | 7.96E-35 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&list=upload_1&organism=Homo%20sapiens) | 7.39 | 3.11 | + | 7.92E-06 | 2.67E-04 | | [regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051972) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&list=upload_1&organism=Homo%20sapiens) | 2.96 | 4.06 | + | 1.40E-04 | 3.27E-03 | | [positive regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033145) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033145&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033145&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.71E-02 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.94 | + | 8.69E-06 | 2.88E-04 | | [histone H3 deacetylation](http://amigo.geneontology.org/amigo/term/GO:0070932) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070932&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070932&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.71E-02 | | [negative regulation of histone H3-K9 methylation](http://amigo.geneontology.org/amigo/term/GO:0051573) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051573&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051573&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.70E-02 | | [regulation of histone H3-K9 methylation](http://amigo.geneontology.org/amigo/term/GO:0051570) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051570&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051570&list=upload_1&organism=Homo%20sapiens) | 1.60 | 5.63 | + | 1.23E-04 | 2.94E-03 | | [regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031060) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&list=upload_1&organism=Homo%20sapiens) | 4.97 | 4.43 | + | 7.65E-08 | 3.69E-06 | | [negative regulation of macrophage derived foam cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0010745) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010745&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010745&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.70E-02 | | [regulation of macrophage derived foam cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0010743) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010743&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010743&list=upload_1&organism=Homo%20sapiens) | 1.83 | 4.36 | + | 1.21E-03 | 2.04E-02 | | [eyelid development in camera-type eye](http://amigo.geneontology.org/amigo/term/GO:0061029) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061029&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061029&list=upload_1&organism=Homo%20sapiens) | .77 | 6.50 | + | 2.51E-03 | 3.70E-02 | | [camera-type eye development](http://amigo.geneontology.org/amigo/term/GO:0043010) | [334](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043010&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043010&list=upload_1&organism=Homo%20sapiens) | 19.76 | 1.87 | + | 8.13E-04 | 1.48E-02 | | [eye development](http://amigo.geneontology.org/amigo/term/GO:0001654) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001654&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001654&list=upload_1&organism=Homo%20sapiens) | 22.72 | 1.72 | + | 2.51E-03 | 3.70E-02 | | [visual system development](http://amigo.geneontology.org/amigo/term/GO:0150063) | [388](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0150063&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0150063&list=upload_1&organism=Homo%20sapiens) | 22.95 | 1.70 | + | 2.66E-03 | 3.87E-02 | | [sensory system development](http://amigo.geneontology.org/amigo/term/GO:0048880) | [394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048880&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048880&list=upload_1&organism=Homo%20sapiens) | 23.31 | 1.72 | + | 2.01E-03 | 3.13E-02 | | [negative regulation of transcription regulatory region DNA binding](http://amigo.geneontology.org/amigo/term/GO:2000678) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000678&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000678&list=upload_1&organism=Homo%20sapiens) | 1.24 | 6.44 | + | 1.38E-04 | 3.25E-03 | | [negative regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0043392) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043392&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043392&list=upload_1&organism=Homo%20sapiens) | 3.19 | 4.38 | + | 1.93E-05 | 5.73E-04 | | [negative regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051100) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 9.64 | 3.32 | + | 3.92E-08 | 2.00E-06 | | [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) | 1.24 | 6.44 | + | 1.38E-04 | 3.23E-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) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 78.27 | 2.73 | + | 2.94E-37 | 9.59E-35 | | [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) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 78.38 | 2.73 | + | 3.53E-37 | 1.13E-34 | | [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) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 78.50 | 2.73 | + | 4.26E-37 | 1.34E-34 | | [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) | [227](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 84.89 | 2.67 | + | 3.78E-38 | 1.38E-35 | | [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) | 1.30 | 6.15 | + | 1.80E-04 | 4.08E-03 | | [histone H4-K8 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043982) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043982&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043982&list=upload_1&organism=Homo%20sapiens) | .95 | 6.34 | + | 1.03E-03 | 1.81E-02 | | [histone H4-K5 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043981) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043981&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043981&list=upload_1&organism=Homo%20sapiens) | .95 | 6.34 | + | 1.03E-03 | 1.81E-02 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051571&list=upload_1&organism=Homo%20sapiens) | 1.60 | 6.26 | + | 2.48E-05 | 7.23E-04 | | [regulation of histone H3-K4 methylation](http://amigo.geneontology.org/amigo/term/GO:0051569) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051569&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051569&list=upload_1&organism=Homo%20sapiens) | 2.31 | 5.20 | + | 1.82E-05 | 5.49E-04 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031062&list=upload_1&organism=Homo%20sapiens) | 3.08 | 5.20 | + | 7.60E-07 | 3.15E-05 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 6.33 | 5.06 | + | 4.92E-12 | 4.10E-10 | | [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) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 60.28 | 1.92 | + | 1.85E-10 | 1.27E-08 | | [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) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 89.62 | 1.86 | + | 1.57E-13 | 1.48E-11 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902176&list=upload_1&organism=Homo%20sapiens) | 1.12 | 6.23 | + | 4.29E-04 | 8.50E-03 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902175&list=upload_1&organism=Homo%20sapiens) | 1.72 | 4.08 | + | 3.34E-03 | 4.60E-02 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903201&list=upload_1&organism=Homo%20sapiens) | 4.32 | 2.78 | + | 2.63E-03 | 3.84E-02 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900407&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.82 | + | 1.07E-03 | 1.87E-02 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902882&list=upload_1&organism=Homo%20sapiens) | 5.56 | 2.70 | + | 1.07E-03 | 1.87E-02 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001243&list=upload_1&organism=Homo%20sapiens) | 5.86 | 2.56 | + | 1.70E-03 | 2.70E-02 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&list=upload_1&organism=Homo%20sapiens) | 13.55 | 2.58 | + | 2.10E-06 | 8.08E-05 | | [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) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 53.12 | 2.22 | + | 2.36E-14 | 2.34E-12 | | [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) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 54.31 | 2.17 | + | 1.17E-13 | 1.11E-11 | | [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) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&list=upload_1&organism=Homo%20sapiens) | 60.46 | 2.05 | + | 1.10E-12 | 9.65E-11 | | [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) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 74.36 | 1.84 | + | 7.00E-11 | 5.15E-09 | | [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) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 80.28 | 1.86 | + | 4.21E-12 | 3.53E-10 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 80.63 | 1.85 | + | 6.59E-12 | 5.44E-10 | | [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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&list=upload_1&organism=Homo%20sapiens) | 30.64 | 1.93 | + | 7.96E-06 | 2.67E-04 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903202&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.60 | + | 1.11E-03 | 1.92E-02 | | [RNA polymerase II preinitiation complex assembly](http://amigo.geneontology.org/amigo/term/GO:0051123) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051123&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051123&list=upload_1&organism=Homo%20sapiens) | 3.37 | 6.23 | + | 1.06E-09 | 6.91E-08 | | [transcription initiation at RNA polymerase II promoter](http://amigo.geneontology.org/amigo/term/GO:0006367) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006367&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006367&list=upload_1&organism=Homo%20sapiens) | 4.67 | 6.42 | + | 1.54E-13 | 1.46E-11 | | [DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:0006352) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006352&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006352&list=upload_1&organism=Homo%20sapiens) | 6.74 | 5.34 | + | 5.94E-14 | 5.68E-12 | | [transcription preinitiation complex assembly](http://amigo.geneontology.org/amigo/term/GO:0070897) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070897&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070897&list=upload_1&organism=Homo%20sapiens) | 4.20 | 5.71 | + | 2.91E-10 | 1.97E-08 | | [protein-DNA complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065004) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&list=upload_1&organism=Homo%20sapiens) | 11.83 | 3.30 | + | 1.56E-09 | 9.84E-08 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 75.13 | 1.82 | + | 1.29E-10 | 9.21E-09 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 141.62 | 1.57 | + | 9.01E-11 | 6.54E-09 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 155.76 | 1.52 | + | 2.10E-10 | 1.44E-08 | | [liver regeneration](http://amigo.geneontology.org/amigo/term/GO:0097421) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097421&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097421&list=upload_1&organism=Homo%20sapiens) | 1.77 | 6.20 | + | 1.06E-05 | 3.40E-04 | | [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) | 7.75 | 3.35 | + | 6.00E-07 | 2.52E-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) | 7.93 | 3.28 | + | 8.73E-07 | 3.58E-05 | | [animal organ regeneration](http://amigo.geneontology.org/amigo/term/GO:0031100) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&list=upload_1&organism=Homo%20sapiens) | 3.96 | 4.29 | + | 3.26E-06 | 1.22E-04 | | [regeneration](http://amigo.geneontology.org/amigo/term/GO:0031099) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&list=upload_1&organism=Homo%20sapiens) | 9.11 | 3.62 | + | 3.76E-09 | 2.17E-07 | | [histone H3-K4 trimethylation](http://amigo.geneontology.org/amigo/term/GO:0080182) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080182&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080182&list=upload_1&organism=Homo%20sapiens) | 1.30 | 6.15 | + | 1.80E-04 | 4.07E-03 | | [peptidyl-lysine trimethylation](http://amigo.geneontology.org/amigo/term/GO:0018023) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018023&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018023&list=upload_1&organism=Homo%20sapiens) | 2.48 | 3.62 | + | 1.87E-03 | 2.93E-02 | | [peptidyl-lysine methylation](http://amigo.geneontology.org/amigo/term/GO:0018022) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018022&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018022&list=upload_1&organism=Homo%20sapiens) | 5.38 | 4.09 | + | 2.51E-07 | 1.13E-05 | | [protein methylation](http://amigo.geneontology.org/amigo/term/GO:0006479) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006479&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006479&list=upload_1&organism=Homo%20sapiens) | 8.81 | 3.40 | + | 6.37E-08 | 3.12E-06 | | [protein alkylation](http://amigo.geneontology.org/amigo/term/GO:0008213) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008213&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008213&list=upload_1&organism=Homo%20sapiens) | 8.81 | 3.40 | + | 6.37E-08 | 3.11E-06 | | [macromolecule methylation](http://amigo.geneontology.org/amigo/term/GO:0043414) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&list=upload_1&organism=Homo%20sapiens) | 16.56 | 2.29 | + | 1.05E-05 | 3.41E-04 | | [methylation](http://amigo.geneontology.org/amigo/term/GO:0032259) | [329](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032259&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032259&list=upload_1&organism=Homo%20sapiens) | 19.46 | 2.06 | + | 7.70E-05 | 1.94E-03 | | [histone H3-K4 methylation](http://amigo.geneontology.org/amigo/term/GO:0051568) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051568&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051568&list=upload_1&organism=Homo%20sapiens) | 2.72 | 6.25 | + | 3.94E-08 | 2.00E-06 | | [histone lysine methylation](http://amigo.geneontology.org/amigo/term/GO:0034968) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034968&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034968&list=upload_1&organism=Homo%20sapiens) | 4.56 | 4.83 | + | 2.07E-08 | 1.10E-06 | | [histone methylation](http://amigo.geneontology.org/amigo/term/GO:0016571) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&list=upload_1&organism=Homo%20sapiens) | 6.39 | 4.38 | + | 1.62E-09 | 1.01E-07 | | [negative regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:1902455) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902455&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902455&list=upload_1&organism=Homo%20sapiens) | 1.48 | 6.09 | + | 7.56E-05 | 1.91E-03 | | [regulation of vascular associated smooth muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:1905063) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905063&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905063&list=upload_1&organism=Homo%20sapiens) | .83 | 6.04 | + | 3.25E-03 | 4.52E-02 | | [regulation of smooth muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051150) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051150&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051150&list=upload_1&organism=Homo%20sapiens) | 1.77 | 5.07 | + | 2.37E-04 | 5.23E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051147&list=upload_1&organism=Homo%20sapiens) | 8.05 | 2.86 | + | 2.61E-05 | 7.57E-04 | | [regulation of DNA strand elongation](http://amigo.geneontology.org/amigo/term/GO:0060382) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060382&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060382&list=upload_1&organism=Homo%20sapiens) | 1.01 | 5.97 | + | 1.33E-03 | 2.21E-02 | | [histone H2A monoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0035518) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035518&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035518&list=upload_1&organism=Homo%20sapiens) | 1.36 | 5.88 | + | 2.30E-04 | 5.09E-03 | | [histone H2A ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0033522) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033522&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033522&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.83 | + | 6.89E-04 | 1.28E-02 | | [histone ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016574) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016574&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016574&list=upload_1&organism=Homo%20sapiens) | 2.72 | 4.78 | + | 1.76E-05 | 5.33E-04 | | [histone monoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0010390) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010390&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010390&list=upload_1&organism=Homo%20sapiens) | 2.07 | 5.31 | + | 3.45E-05 | 9.82E-04 | | [protein monoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0006513) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006513&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006513&list=upload_1&organism=Homo%20sapiens) | 4.61 | 3.47 | + | 6.04E-05 | 1.58E-03 | | [regulation of heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0031445) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031445&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031445&list=upload_1&organism=Homo%20sapiens) | 1.72 | 5.83 | + | 4.09E-05 | 1.14E-03 | | [regulation of heterochromatin organization](http://amigo.geneontology.org/amigo/term/GO:0120261) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120261&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120261&list=upload_1&organism=Homo%20sapiens) | 1.72 | 5.83 | + | 4.09E-05 | 1.14E-03 | | [response to hyperoxia](http://amigo.geneontology.org/amigo/term/GO:0055093) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055093&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055093&list=upload_1&organism=Homo%20sapiens) | 1.24 | 5.63 | + | 7.00E-04 | 1.30E-02 | | [response to increased oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0036296) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036296&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036296&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.23 | + | 2.83E-03 | 4.05E-02 | | [response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0070482) | [319](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 18.87 | 2.76 | + | 1.36E-09 | 8.71E-08 | | [response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009628) | [1121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&reflist=1) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&list=upload_1&organism=Homo%20sapiens) | 66.32 | 2.28 | + | 4.20E-19 | 5.14E-17 | | [intracellular estrogen receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030520) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030520&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030520&list=upload_1&organism=Homo%20sapiens) | 1.24 | 5.63 | + | 7.00E-04 | 1.30E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&list=upload_1&organism=Homo%20sapiens) | 3.31 | 4.83 | + | 1.72E-06 | 6.71E-05 | | [intracellular receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030522) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&list=upload_1&organism=Homo%20sapiens) | 8.76 | 3.77 | + | 1.60E-09 | 1.00E-07 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [370](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 289.10 | 1.28 | + | 2.67E-07 | 1.19E-05 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 309.45 | 1.29 | + | 3.73E-08 | 1.92E-06 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 316.02 | 1.29 | + | 1.44E-08 | 7.87E-07 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&list=upload_1&organism=Homo%20sapiens) | 4.56 | 4.17 | + | 1.25E-06 | 5.00E-05 | | [hormone-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0009755) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&list=upload_1&organism=Homo%20sapiens) | 7.75 | 3.35 | + | 6.00E-07 | 2.52E-05 | | [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) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 28.93 | 2.59 | + | 2.56E-12 | 2.17E-10 | | [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) | [237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 119.85 | 1.98 | + | 2.41E-22 | 3.53E-20 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [299](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 159.96 | 1.87 | + | 3.51E-25 | 6.04E-23 | | [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) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 65.49 | 2.28 | + | 8.10E-19 | 9.56E-17 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 81.11 | 2.15 | + | 1.83E-19 | 2.32E-17 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 45.37 | 2.29 | + | 1.59E-13 | 1.48E-11 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 8.99 | 3.45 | + | 2.99E-08 | 1.55E-06 | | [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) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 30.41 | 2.63 | + | 2.51E-13 | 2.28E-11 | | [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) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 52.00 | 2.46 | + | 1.17E-18 | 1.36E-16 | | [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) | 30.70 | 2.70 | + | 2.08E-14 | 2.08E-12 | | [response to lipid](http://amigo.geneontology.org/amigo/term/GO:0033993) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&list=upload_1&organism=Homo%20sapiens) | 49.87 | 2.49 | + | 1.95E-18 | 2.18E-16 | | [response to steroid hormone](http://amigo.geneontology.org/amigo/term/GO:0048545) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 16.80 | 2.62 | + | 7.13E-08 | 3.46E-06 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045648&list=upload_1&organism=Homo%20sapiens) | 1.83 | 5.45 | + | 6.51E-05 | 1.68E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 5.92 | 3.38 | + | 1.05E-05 | 3.40E-04 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 11.83 | 2.96 | + | 1.12E-07 | 5.30E-06 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 23.54 | 2.97 | + | 4.35E-14 | 4.24E-12 | | [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) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 89.92 | 1.66 | + | 8.72E-09 | 4.92E-07 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 52.30 | 2.56 | + | 6.89E-21 | 9.15E-19 | | [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) | 2.66 | 5.26 | + | 3.33E-06 | 1.23E-04 | | [positive regulation of histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0031065) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031065&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031065&list=upload_1&organism=Homo%20sapiens) | 1.48 | 5.41 | + | 3.67E-04 | 7.47E-03 | | [positive regulation of protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0090312) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090312&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090312&list=upload_1&organism=Homo%20sapiens) | 1.83 | 4.91 | + | 2.91E-04 | 6.21E-03 | | [regulation of protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0090311) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090311&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090311&list=upload_1&organism=Homo%20sapiens) | 3.67 | 4.91 | + | 3.22E-07 | 1.42E-05 | | [regulation of histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0031063) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031063&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031063&list=upload_1&organism=Homo%20sapiens) | 2.66 | 6.01 | + | 1.52E-07 | 7.08E-06 | | [trachea development](http://amigo.geneontology.org/amigo/term/GO:0060438) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060438&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060438&list=upload_1&organism=Homo%20sapiens) | 1.12 | 5.34 | + | 2.12E-03 | 3.28E-02 | | [respiratory system development](http://amigo.geneontology.org/amigo/term/GO:0060541) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.38 | + | 7.23E-05 | 1.85E-03 | | [regulation of fibroblast apoptotic process](http://amigo.geneontology.org/amigo/term/GO:2000269) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000269&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000269&list=upload_1&organism=Homo%20sapiens) | 1.12 | 5.34 | + | 2.12E-03 | 3.28E-02 | | [regulation of tubulin deacetylation](http://amigo.geneontology.org/amigo/term/GO:0090043) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090043&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090043&list=upload_1&organism=Homo%20sapiens) | 1.12 | 5.34 | + | 2.12E-03 | 3.27E-02 | | [retina vasculature development in camera-type eye](http://amigo.geneontology.org/amigo/term/GO:0061298) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061298&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061298&list=upload_1&organism=Homo%20sapiens) | 1.12 | 5.34 | + | 2.12E-03 | 3.27E-02 | | [vasculature development](http://amigo.geneontology.org/amigo/term/GO:0001944) | [532](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001944&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001944&list=upload_1&organism=Homo%20sapiens) | 31.47 | 1.68 | + | 4.95E-04 | 9.57E-03 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 53.77 | 1.99 | + | 1.82E-10 | 1.26E-08 | | [positive regulation of transcription by RNA polymerase III](http://amigo.geneontology.org/amigo/term/GO:0045945) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045945&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045945&list=upload_1&organism=Homo%20sapiens) | 1.12 | 5.34 | + | 2.12E-03 | 3.27E-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) | 1.54 | 5.20 | + | 4.56E-04 | 8.96E-03 | | [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) | 4.02 | 3.73 | + | 4.98E-05 | 1.34E-03 | | [protein localization to centrosome](http://amigo.geneontology.org/amigo/term/GO:0071539) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071539&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071539&list=upload_1&organism=Homo%20sapiens) | 1.36 | 5.14 | + | 1.09E-03 | 1.89E-02 | | [protein localization to microtubule organizing center](http://amigo.geneontology.org/amigo/term/GO:1905508) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905508&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905508&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.34E-03 | 2.22E-02 | | [protein localization to microtubule cytoskeleton](http://amigo.geneontology.org/amigo/term/GO:0072698) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072698&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072698&list=upload_1&organism=Homo%20sapiens) | 2.31 | 3.90 | + | 1.20E-03 | 2.03E-02 | | [protein localization to cytoskeleton](http://amigo.geneontology.org/amigo/term/GO:0044380) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044380&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044380&list=upload_1&organism=Homo%20sapiens) | 2.54 | 3.54 | + | 2.15E-03 | 3.30E-02 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 41.06 | 1.83 | + | 2.79E-06 | 1.05E-04 | | [protein localization](http://amigo.geneontology.org/amigo/term/GO:0008104) | [1919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&reflist=1) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&list=upload_1&organism=Homo%20sapiens) | 113.52 | 1.44 | + | 5.86E-06 | 2.04E-04 | | [cellular macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0070727) | [1925](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&list=upload_1&organism=Homo%20sapiens) | 113.88 | 1.45 | + | 3.82E-06 | 1.39E-04 | | [cellular localization](http://amigo.geneontology.org/amigo/term/GO:0051641) | [2655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&reflist=1) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&list=upload_1&organism=Homo%20sapiens) | 157.06 | 1.42 | + | 2.00E-07 | 9.13E-06 | | [localization](http://amigo.geneontology.org/amigo/term/GO:0051179) | [4566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&reflist=1) | [336](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&list=upload_1&organism=Homo%20sapiens) | 270.11 | 1.24 | + | 1.86E-05 | 5.61E-04 | | [macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0033036) | [2345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&reflist=1) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&list=upload_1&organism=Homo%20sapiens) | 138.73 | 1.38 | + | 9.53E-06 | 3.13E-04 | | [response to immobilization stress](http://amigo.geneontology.org/amigo/term/GO:0035902) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035902&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035902&list=upload_1&organism=Homo%20sapiens) | 1.36 | 5.14 | + | 1.09E-03 | 1.89E-02 | | [cellular response to estradiol stimulus](http://amigo.geneontology.org/amigo/term/GO:0071392) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071392&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071392&list=upload_1&organism=Homo%20sapiens) | 2.37 | 5.07 | + | 2.25E-05 | 6.61E-04 | | [response to estradiol](http://amigo.geneontology.org/amigo/term/GO:0032355) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&list=upload_1&organism=Homo%20sapiens) | 7.28 | 3.71 | + | 6.31E-08 | 3.10E-06 | | [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) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 91.75 | 2.08 | + | 4.02E-20 | 5.21E-18 | | [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) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&list=upload_1&organism=Homo%20sapiens) | 62.65 | 2.09 | + | 5.27E-14 | 5.07E-12 | | [cellular senescence](http://amigo.geneontology.org/amigo/term/GO:0090398) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&list=upload_1&organism=Homo%20sapiens) | 3.55 | 5.07 | + | 2.15E-07 | 9.76E-06 | | [positive regulation of chondrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0032332) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032332&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032332&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.07 | + | 2.63E-03 | 3.84E-02 | | [regulation of cartilage development](http://amigo.geneontology.org/amigo/term/GO:0061035) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061035&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061035&list=upload_1&organism=Homo%20sapiens) | 4.32 | 2.78 | + | 2.63E-03 | 3.83E-02 | | [negative regulation of calcium-mediated signaling](http://amigo.geneontology.org/amigo/term/GO:0050849) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050849&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050849&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.07 | + | 2.63E-03 | 3.84E-02 | | [positive regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035066) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&list=upload_1&organism=Homo%20sapiens) | 2.19 | 5.03 | + | 5.27E-05 | 1.40E-03 | | [positive regulation of peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:2000758) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&list=upload_1&organism=Homo%20sapiens) | 2.54 | 4.72 | + | 4.09E-05 | 1.14E-03 | | [positive regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901985) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&list=upload_1&organism=Homo%20sapiens) | 3.14 | 4.78 | + | 3.99E-06 | 1.44E-04 | | [regulation of DNA damage checkpoint](http://amigo.geneontology.org/amigo/term/GO:2000001) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000001&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000001&list=upload_1&organism=Homo%20sapiens) | 1.60 | 5.01 | + | 5.63E-04 | 1.08E-02 | | [regulation of cell cycle checkpoint](http://amigo.geneontology.org/amigo/term/GO:1901976) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901976&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901976&list=upload_1&organism=Homo%20sapiens) | 2.90 | 3.45 | + | 1.46E-03 | 2.39E-02 | | [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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&list=upload_1&organism=Homo%20sapiens) | 25.50 | 2.82 | + | 1.77E-13 | 1.64E-11 | | [positive regulation of transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0045943) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&list=upload_1&organism=Homo%20sapiens) | 2.01 | 4.97 | + | 1.24E-04 | 2.95E-03 | | [regulation of transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0006356) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&list=upload_1&organism=Homo%20sapiens) | 2.60 | 4.23 | + | 1.95E-04 | 4.37E-03 | | [regulation of toll-like receptor 4 signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0034143) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034143&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034143&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.34E-03 | 2.23E-02 | | [synaptic transmission, GABAergic](http://amigo.geneontology.org/amigo/term/GO:0051932) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051932&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051932&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.34E-03 | 2.23E-02 | | [cell-cell signaling](http://amigo.geneontology.org/amigo/term/GO:0007267) | [1083](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&list=upload_1&organism=Homo%20sapiens) | 64.07 | 1.56 | + | 3.74E-05 | 1.06E-03 | | [negative regulation of cardiac muscle tissue growth](http://amigo.geneontology.org/amigo/term/GO:0055022) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055022&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055022&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.34E-03 | 2.22E-02 | | [negative regulation of heart growth](http://amigo.geneontology.org/amigo/term/GO:0061117) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061117&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061117&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.93 | + | 1.34E-03 | 2.22E-02 | | [negative regulation of organ growth](http://amigo.geneontology.org/amigo/term/GO:0046621) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046621&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046621&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.44E-03 | 2.36E-02 | | [regulation of developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048638) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048638&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048638&list=upload_1&organism=Homo%20sapiens) | 19.17 | 2.24 | + | 4.88E-06 | 1.73E-04 | | [regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0040008) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&list=upload_1&organism=Homo%20sapiens) | 37.09 | 2.00 | + | 1.46E-07 | 6.85E-06 | | [negative regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0045926) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&list=upload_1&organism=Homo%20sapiens) | 14.61 | 2.26 | + | 5.74E-05 | 1.51E-03 | | [regulation of organ growth](http://amigo.geneontology.org/amigo/term/GO:0046620) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046620&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046620&list=upload_1&organism=Homo%20sapiens) | 5.27 | 2.85 | + | 6.53E-04 | 1.22E-02 | | [regulation of heart growth](http://amigo.geneontology.org/amigo/term/GO:0060420) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060420&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060420&list=upload_1&organism=Homo%20sapiens) | 3.67 | 3.00 | + | 2.32E-03 | 3.51E-02 | | [regulation of cardiac muscle tissue growth](http://amigo.geneontology.org/amigo/term/GO:0055021) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055021&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055021&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.38 | + | 9.98E-04 | 1.77E-02 | | [negative regulation of JNK cascade](http://amigo.geneontology.org/amigo/term/GO:0046329) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046329&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046329&list=upload_1&organism=Homo%20sapiens) | 2.25 | 4.89 | + | 6.45E-05 | 1.67E-03 | | [regulation of stress-activated MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0032872) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032872&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032872&list=upload_1&organism=Homo%20sapiens) | 11.24 | 2.14 | + | 1.33E-03 | 2.21E-02 | | [regulation of stress-activated protein kinase signaling cascade](http://amigo.geneontology.org/amigo/term/GO:0070302) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070302&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070302&list=upload_1&organism=Homo%20sapiens) | 11.42 | 2.19 | + | 8.58E-04 | 1.56E-02 | | [negative regulation of stress-activated MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0032873) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032873&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032873&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.83 | + | 7.59E-06 | 2.59E-04 | | [negative regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043409) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.39 | + | 2.32E-04 | 5.12E-03 | | [negative regulation of stress-activated protein kinase signaling cascade](http://amigo.geneontology.org/amigo/term/GO:0070303) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070303&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070303&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.83 | + | 7.59E-06 | 2.58E-04 | | [positive regulation of myoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045663) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045663&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045663&list=upload_1&organism=Homo%20sapiens) | 2.66 | 4.88 | + | 1.45E-05 | 4.51E-04 | | [regulation of myoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045661) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045661&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045661&list=upload_1&organism=Homo%20sapiens) | 4.56 | 3.95 | + | 4.55E-06 | 1.62E-04 | | [regulation of sister chromatid cohesion](http://amigo.geneontology.org/amigo/term/GO:0007063) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007063&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007063&list=upload_1&organism=Homo%20sapiens) | 1.24 | 4.83 | + | 3.22E-03 | 4.49E-02 | | [positive regulation of neuroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0002052) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002052&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002052&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.83 | + | 6.89E-04 | 1.28E-02 | | [positive regulation of neural precursor cell proliferation](http://amigo.geneontology.org/amigo/term/GO:2000179) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000179&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000179&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.86 | + | 1.17E-04 | 2.81E-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) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 56.14 | 1.87 | + | 7.84E-09 | 4.44E-07 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000177&list=upload_1&organism=Homo%20sapiens) | 5.56 | 3.24 | + | 4.73E-05 | 1.29E-03 | | [regulation of neuroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:1902692) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902692&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902692&list=upload_1&organism=Homo%20sapiens) | 2.37 | 4.23 | + | 3.78E-04 | 7.65E-03 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 13.67 | 2.27 | + | 1.04E-04 | 2.53E-03 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&list=upload_1&organism=Homo%20sapiens) | 16.51 | 1.94 | + | 1.03E-03 | 1.81E-02 | | [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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 18.22 | 2.09 | + | 7.45E-05 | 1.89E-03 | | [transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0006360) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006360&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006360&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.83 | + | 6.89E-04 | 1.28E-02 | | [prostate gland development](http://amigo.geneontology.org/amigo/term/GO:0030850) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030850&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030850&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.83 | + | 7.59E-06 | 2.58E-04 | | [reproductive structure development](http://amigo.geneontology.org/amigo/term/GO:0048608) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&list=upload_1&organism=Homo%20sapiens) | 17.75 | 2.25 | + | 1.18E-05 | 3.76E-04 | | [reproductive system development](http://amigo.geneontology.org/amigo/term/GO:0061458) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&list=upload_1&organism=Homo%20sapiens) | 17.98 | 2.22 | + | 1.33E-05 | 4.20E-04 | | [urogenital system development](http://amigo.geneontology.org/amigo/term/GO:0001655) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&list=upload_1&organism=Homo%20sapiens) | 20.71 | 2.03 | + | 5.16E-05 | 1.38E-03 | | [regulation of transcription involved in G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000083) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000083&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000083&list=upload_1&organism=Homo%20sapiens) | 1.24 | 4.83 | + | 3.22E-03 | 4.49E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&list=upload_1&organism=Homo%20sapiens) | 5.03 | 3.78 | + | 4.38E-06 | 1.57E-04 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&list=upload_1&organism=Homo%20sapiens) | 10.23 | 3.03 | + | 3.74E-07 | 1.63E-05 | | [mitotic cell cycle process](http://amigo.geneontology.org/amigo/term/GO:1903047) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&list=upload_1&organism=Homo%20sapiens) | 31.53 | 2.38 | + | 1.25E-10 | 8.99E-09 | | [mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000278) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&list=upload_1&organism=Homo%20sapiens) | 37.09 | 2.32 | + | 1.31E-11 | 1.04E-09 | | [cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007049) | [1249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&reflist=1) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&list=upload_1&organism=Homo%20sapiens) | 73.89 | 2.17 | + | 2.46E-18 | 2.72E-16 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 49.75 | 2.05 | + | 1.49E-10 | 1.06E-08 | | [cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044770) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&list=upload_1&organism=Homo%20sapiens) | 10.83 | 2.96 | + | 3.94E-07 | 1.71E-05 | | [cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:0044843) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&list=upload_1&organism=Homo%20sapiens) | 5.15 | 3.89 | + | 1.71E-06 | 6.69E-05 | | [positive regulation of transcription elongation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0032968) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032968&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032968&list=upload_1&organism=Homo%20sapiens) | 2.96 | 4.73 | + | 9.22E-06 | 3.03E-04 | | [positive regulation of DNA-templated transcription, elongation](http://amigo.geneontology.org/amigo/term/GO:0032786) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032786&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032786&list=upload_1&organism=Homo%20sapiens) | 3.55 | 4.51 | + | 3.67E-06 | 1.35E-04 | | [regulation of DNA-templated transcription elongation](http://amigo.geneontology.org/amigo/term/GO:0032784) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032784&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032784&list=upload_1&organism=Homo%20sapiens) | 6.09 | 3.28 | + | 1.54E-05 | 4.75E-04 | | [regulation of transcription elongation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0034243) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034243&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034243&list=upload_1&organism=Homo%20sapiens) | 5.09 | 3.54 | + | 1.69E-05 | 5.13E-04 | | [cellular response to gamma radiation](http://amigo.geneontology.org/amigo/term/GO:0071480) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071480&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071480&list=upload_1&organism=Homo%20sapiens) | 1.72 | 4.66 | + | 8.36E-04 | 1.53E-02 | | [response to gamma radiation](http://amigo.geneontology.org/amigo/term/GO:0010332) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&list=upload_1&organism=Homo%20sapiens) | 3.31 | 4.53 | + | 7.02E-06 | 2.41E-04 | | [response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0010212) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&list=upload_1&organism=Homo%20sapiens) | 8.52 | 2.93 | + | 7.96E-06 | 2.68E-04 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 26.56 | 2.48 | + | 3.01E-10 | 2.02E-08 | | [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) | 4.44 | 3.61 | + | 4.01E-05 | 1.12E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 10.77 | 3.07 | + | 1.25E-07 | 5.87E-06 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 19.29 | 2.39 | + | 4.92E-07 | 2.10E-05 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&list=upload_1&organism=Homo%20sapiens) | 19.29 | 2.39 | + | 4.92E-07 | 2.10E-05 | | [positive regulation of mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0048026) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048026&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048026&list=upload_1&organism=Homo%20sapiens) | 1.54 | 4.55 | + | 1.98E-03 | 3.08E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033120&list=upload_1&organism=Homo%20sapiens) | 2.37 | 3.80 | + | 1.39E-03 | 2.30E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&list=upload_1&organism=Homo%20sapiens) | 10.71 | 3.46 | + | 1.34E-09 | 8.58E-08 | | [positive regulation of mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0050685) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050685&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050685&list=upload_1&organism=Homo%20sapiens) | 2.07 | 3.86 | + | 2.33E-03 | 3.52E-02 | | [regulation of mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0050684) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050684&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050684&list=upload_1&organism=Homo%20sapiens) | 8.28 | 2.78 | + | 3.90E-05 | 1.10E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&list=upload_1&organism=Homo%20sapiens) | 17.81 | 2.08 | + | 1.02E-04 | 2.48E-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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048024&list=upload_1&organism=Homo%20sapiens) | 6.51 | 2.77 | + | 2.72E-04 | 5.85E-03 | | [negative regulation of cyclin-dependent protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0045736) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045736&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045736&list=upload_1&organism=Homo%20sapiens) | 1.77 | 4.51 | + | 1.01E-03 | 1.78E-02 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&list=upload_1&organism=Homo%20sapiens) | 6.80 | 2.79 | + | 1.67E-04 | 3.80E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&list=upload_1&organism=Homo%20sapiens) | 6.98 | 2.87 | + | 8.35E-05 | 2.08E-03 | | [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) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&list=upload_1&organism=Homo%20sapiens) | 39.52 | 1.62 | + | 3.97E-04 | 7.99E-03 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 46.32 | 1.51 | + | 1.33E-03 | 2.21E-02 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 73.83 | 1.61 | + | 1.33E-06 | 5.25E-05 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 83.06 | 1.61 | + | 2.50E-07 | 1.13E-05 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 83.12 | 1.61 | + | 2.52E-07 | 1.13E-05 | | [regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001932) | [1105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 65.37 | 1.59 | + | 1.05E-05 | 3.40E-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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&list=upload_1&organism=Homo%20sapiens) | 23.13 | 1.82 | + | 6.26E-04 | 1.18E-02 | | [negative regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045786) | [359](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045786&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045786&list=upload_1&organism=Homo%20sapiens) | 21.24 | 2.40 | + | 8.83E-08 | 4.22E-06 | | [negative regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071901) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071901&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071901&list=upload_1&organism=Homo%20sapiens) | 6.74 | 2.82 | + | 1.51E-04 | 3.48E-03 | | [negative regulation of protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:0006469) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006469&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006469&list=upload_1&organism=Homo%20sapiens) | 12.25 | 2.29 | + | 1.50E-04 | 3.46E-03 | | [negative regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001933) | [322](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001933&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001933&list=upload_1&organism=Homo%20sapiens) | 19.05 | 2.10 | + | 4.01E-05 | 1.12E-03 | | [negative regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042326) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&list=upload_1&organism=Homo%20sapiens) | 21.59 | 2.08 | + | 1.66E-05 | 5.07E-04 | | [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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&list=upload_1&organism=Homo%20sapiens) | 24.96 | 2.08 | + | 3.70E-06 | 1.36E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&list=upload_1&organism=Homo%20sapiens) | 25.02 | 2.08 | + | 3.82E-06 | 1.39E-04 | | [negative regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0033673) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033673&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033673&list=upload_1&organism=Homo%20sapiens) | 13.67 | 2.20 | + | 1.86E-04 | 4.17E-03 | | [negative regulation of cyclin-dependent protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:1904030) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904030&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904030&list=upload_1&organism=Homo%20sapiens) | 1.77 | 4.51 | + | 1.01E-03 | 1.78E-02 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071276&list=upload_1&organism=Homo%20sapiens) | 2.25 | 4.45 | + | 2.66E-04 | 5.76E-03 | | [response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0046686) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.88 | + | 6.08E-05 | 1.59E-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) | 21.47 | 2.19 | + | 3.28E-06 | 1.22E-04 | | [response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0010035) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 31.53 | 2.28 | + | 1.37E-09 | 8.76E-08 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071248&list=upload_1&organism=Homo%20sapiens) | 11.83 | 2.20 | + | 6.14E-04 | 1.16E-02 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&list=upload_1&organism=Homo%20sapiens) | 13.61 | 2.50 | + | 5.22E-06 | 1.83E-04 | | [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) | 2.25 | 4.45 | + | 2.66E-04 | 5.75E-03 | | [regulation of monooxygenase activity](http://amigo.geneontology.org/amigo/term/GO:0032768) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032768&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032768&list=upload_1&organism=Homo%20sapiens) | 3.02 | 3.98 | + | 1.65E-04 | 3.77E-03 | | [regulation of oxidoreductase activity](http://amigo.geneontology.org/amigo/term/GO:0051341) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&list=upload_1&organism=Homo%20sapiens) | 5.97 | 2.68 | + | 7.95E-04 | 1.46E-02 | | [positive regulation of transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030511) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030511&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030511&list=upload_1&organism=Homo%20sapiens) | 1.83 | 4.36 | + | 1.21E-03 | 2.05E-02 | | [positive regulation of cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:1903846) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903846&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903846&list=upload_1&organism=Homo%20sapiens) | 1.83 | 4.36 | + | 1.21E-03 | 2.04E-02 | | [regulation of cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:1903844) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903844&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903844&list=upload_1&organism=Homo%20sapiens) | 8.40 | 3.57 | + | 2.51E-08 | 1.33E-06 | | [regulation of cellular response to growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0090287) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090287&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090287&list=upload_1&organism=Homo%20sapiens) | 18.58 | 2.31 | + | 2.06E-06 | 7.95E-05 | | [regulation of transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0017015) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017015&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017015&list=upload_1&organism=Homo%20sapiens) | 8.22 | 3.53 | + | 5.41E-08 | 2.69E-06 | | [regulation of transmembrane receptor protein serine/threonine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0090092) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090092&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090092&list=upload_1&organism=Homo%20sapiens) | 16.27 | 2.34 | + | 8.50E-06 | 2.82E-04 | | [positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0090100) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090100&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090100&list=upload_1&organism=Homo%20sapiens) | 6.98 | 2.72 | + | 2.24E-04 | 4.97E-03 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043537&list=upload_1&organism=Homo%20sapiens) | 2.07 | 4.35 | + | 6.18E-04 | 1.16E-02 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&list=upload_1&organism=Homo%20sapiens) | 5.38 | 3.16 | + | 9.92E-05 | 2.44E-03 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&list=upload_1&organism=Homo%20sapiens) | 13.55 | 1.99 | + | 1.44E-03 | 2.36E-02 | | [regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030334) | [929](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 54.96 | 1.71 | + | 1.79E-06 | 6.94E-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) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&list=upload_1&organism=Homo%20sapiens) | 58.51 | 1.69 | + | 1.78E-06 | 6.90E-05 | | [regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040012) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&list=upload_1&organism=Homo%20sapiens) | 61.17 | 1.70 | + | 7.63E-07 | 3.16E-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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010596&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.19 | + | 2.44E-03 | 3.64E-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) | 4.02 | 2.98 | + | 1.55E-03 | 2.50E-02 | | [negative regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030336) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030336&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030336&list=upload_1&organism=Homo%20sapiens) | 17.04 | 2.17 | + | 4.21E-05 | 1.17E-03 | | [negative regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000146) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000146&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000146&list=upload_1&organism=Homo%20sapiens) | 17.92 | 2.12 | + | 6.42E-05 | 1.67E-03 | | [negative regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040013) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&list=upload_1&organism=Homo%20sapiens) | 20.05 | 2.09 | + | 2.48E-05 | 7.24E-04 | | [positive regulation of double-strand break repair via homologous recombination](http://amigo.geneontology.org/amigo/term/GO:1905168) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905168&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905168&list=upload_1&organism=Homo%20sapiens) | 2.31 | 4.33 | + | 3.18E-04 | 6.63E-03 | | [positive regulation of DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0045911) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045911&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045911&list=upload_1&organism=Homo%20sapiens) | 4.26 | 2.82 | + | 2.38E-03 | 3.57E-02 | | [regulation of DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0000018) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000018&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000018&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.41 | + | 9.93E-04 | 1.76E-02 | | [positive regulation of double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:2000781) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000781&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000781&list=upload_1&organism=Homo%20sapiens) | 5.27 | 4.56 | + | 1.23E-08 | 6.74E-07 | | [regulation of double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:2000779) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000779&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000779&list=upload_1&organism=Homo%20sapiens) | 7.99 | 3.88 | + | 2.72E-09 | 1.63E-07 | | [positive regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0045739) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&list=upload_1&organism=Homo%20sapiens) | 7.69 | 4.29 | + | 9.21E-11 | 6.66E-09 | | [regulation of double-strand break repair via homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0010569) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010569&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010569&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.05 | + | 8.37E-04 | 1.52E-02 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032922&list=upload_1&organism=Homo%20sapiens) | 4.20 | 4.29 | + | 1.71E-06 | 6.68E-05 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 8.16 | 3.06 | + | 4.13E-06 | 1.49E-04 | | [rhythmic process](http://amigo.geneontology.org/amigo/term/GO:0048511) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 16.09 | 3.11 | + | 4.97E-11 | 3.73E-09 | | [cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001816) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001816&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001816&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.23 | + | 2.83E-03 | 4.06E-02 | | [response to electrical stimulus](http://amigo.geneontology.org/amigo/term/GO:0051602) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051602&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051602&list=upload_1&organism=Homo%20sapiens) | 2.60 | 4.23 | + | 1.95E-04 | 4.36E-03 | | [positive regulation of chromosome separation](http://amigo.geneontology.org/amigo/term/GO:1905820) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905820&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905820&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.23 | + | 2.83E-03 | 4.05E-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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905818&list=upload_1&organism=Homo%20sapiens) | 6.57 | 4.11 | + | 1.01E-08 | 5.61E-07 | | [regulation of chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0051983) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&list=upload_1&organism=Homo%20sapiens) | 7.75 | 4.00 | + | 1.46E-09 | 9.28E-08 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&list=upload_1&organism=Homo%20sapiens) | 14.85 | 2.42 | + | 6.00E-06 | 2.08E-04 | | [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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 20.88 | 2.44 | + | 6.65E-08 | 3.24E-06 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&list=upload_1&organism=Homo%20sapiens) | 3.31 | 4.23 | + | 2.72E-05 | 7.86E-04 | | [stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0019827) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&list=upload_1&organism=Homo%20sapiens) | 6.74 | 3.11 | + | 1.91E-05 | 5.71E-04 | | [maintenance of cell number](http://amigo.geneontology.org/amigo/term/GO:0098727) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&list=upload_1&organism=Homo%20sapiens) | 6.98 | 3.15 | + | 1.03E-05 | 3.37E-04 | | [regulation of androgen receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0060765) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060765&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060765&list=upload_1&organism=Homo%20sapiens) | 1.66 | 4.23 | + | 2.83E-03 | 4.04E-02 | | [positive regulation of epithelial to mesenchymal transition](http://amigo.geneontology.org/amigo/term/GO:0010718) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010718&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010718&list=upload_1&organism=Homo%20sapiens) | 3.08 | 4.23 | + | 5.23E-05 | 1.40E-03 | | [regulation of epithelial to mesenchymal transition](http://amigo.geneontology.org/amigo/term/GO:0010717) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010717&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010717&list=upload_1&organism=Homo%20sapiens) | 5.74 | 2.61 | + | 1.42E-03 | 2.33E-02 | | [erythrocyte development](http://amigo.geneontology.org/amigo/term/GO:0048821) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048821&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048821&list=upload_1&organism=Homo%20sapiens) | 2.19 | 4.11 | + | 8.69E-04 | 1.57E-02 | | [myeloid cell development](http://amigo.geneontology.org/amigo/term/GO:0061515) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061515&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061515&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.01 | + | 9.37E-04 | 1.68E-02 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 102.05 | 1.78 | + | 3.49E-13 | 3.13E-11 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 15.62 | 2.56 | + | 4.53E-07 | 1.95E-05 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 39.04 | 2.23 | + | 6.72E-11 | 4.97E-09 | | [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) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 42.00 | 2.21 | + | 2.01E-11 | 1.57E-09 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 44.78 | 2.17 | + | 2.69E-11 | 2.06E-09 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 143.69 | 1.38 | + | 5.59E-06 | 1.95E-04 | | [erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0030218) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030218&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030218&list=upload_1&organism=Homo%20sapiens) | 5.62 | 4.45 | + | 9.30E-09 | 5.21E-07 | | [erythrocyte homeostasis](http://amigo.geneontology.org/amigo/term/GO:0034101) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034101&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034101&list=upload_1&organism=Homo%20sapiens) | 6.15 | 4.39 | + | 3.07E-09 | 1.81E-07 | | [myeloid cell homeostasis](http://amigo.geneontology.org/amigo/term/GO:0002262) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&list=upload_1&organism=Homo%20sapiens) | 7.81 | 4.23 | + | 1.29E-10 | 9.22E-09 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&list=upload_1&organism=Homo%20sapiens) | 15.20 | 3.16 | + | 7.53E-11 | 5.49E-09 | | [homeostatic process](http://amigo.geneontology.org/amigo/term/GO:0042592) | [1424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&reflist=1) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&list=upload_1&organism=Homo%20sapiens) | 84.24 | 1.73 | + | 7.47E-10 | 4.92E-08 | | [regulation of biological quality](http://amigo.geneontology.org/amigo/term/GO:0065008) | [3677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&reflist=1) | [328](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 217.52 | 1.51 | + | 3.44E-14 | 3.37E-12 | | [cellular response to heat](http://amigo.geneontology.org/amigo/term/GO:0034605) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&list=upload_1&organism=Homo%20sapiens) | 3.19 | 4.07 | + | 7.29E-05 | 1.86E-03 | | [response to heat](http://amigo.geneontology.org/amigo/term/GO:0009408) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&list=upload_1&organism=Homo%20sapiens) | 6.09 | 3.28 | + | 1.54E-05 | 4.73E-04 | | [response to temperature stimulus](http://amigo.geneontology.org/amigo/term/GO:0009266) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&list=upload_1&organism=Homo%20sapiens) | 10.53 | 2.66 | + | 1.89E-05 | 5.69E-04 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990090&list=upload_1&organism=Homo%20sapiens) | 2.72 | 4.04 | + | 2.71E-04 | 5.83E-03 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990089&list=upload_1&organism=Homo%20sapiens) | 2.84 | 4.23 | + | 1.01E-04 | 2.47E-03 | | [response to growth factor](http://amigo.geneontology.org/amigo/term/GO:0070848) | [507](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 29.99 | 2.47 | + | 4.26E-11 | 3.23E-09 | | [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) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 28.22 | 2.37 | + | 1.11E-09 | 7.21E-08 | | [regulation of mitotic metaphase/anaphase transition](http://amigo.geneontology.org/amigo/term/GO:0030071) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030071&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030071&list=upload_1&organism=Homo%20sapiens) | 5.44 | 4.04 | + | 2.95E-07 | 1.31E-05 | | [regulation of metaphase/anaphase transition of cell cycle](http://amigo.geneontology.org/amigo/term/GO:1902099) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902099&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902099&list=upload_1&organism=Homo%20sapiens) | 5.62 | 3.91 | + | 4.72E-07 | 2.02E-05 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033045&list=upload_1&organism=Homo%20sapiens) | 6.33 | 4.11 | + | 1.91E-08 | 1.03E-06 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010965&list=upload_1&organism=Homo%20sapiens) | 5.80 | 3.97 | + | 2.12E-07 | 9.68E-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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&list=upload_1&organism=Homo%20sapiens) | 19.64 | 2.80 | + | 1.75E-10 | 1.21E-08 | | [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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 29.16 | 2.67 | + | 3.35E-13 | 3.02E-11 | | [regulation of DNA damage response, signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0043516) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043516&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043516&list=upload_1&organism=Homo%20sapiens) | 2.25 | 4.00 | + | 1.02E-03 | 1.80E-02 | | [intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0072332) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072332&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072332&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.92 | + | 1.00E-04 | 2.46E-03 | | [signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0072331) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072331&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072331&list=upload_1&organism=Homo%20sapiens) | 5.44 | 3.49 | + | 1.17E-05 | 3.74E-04 | | [intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:0035556) | [1511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&reflist=1) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&list=upload_1&organism=Homo%20sapiens) | 89.39 | 1.82 | + | 1.74E-12 | 1.49E-10 | | [intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097193) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&list=upload_1&organism=Homo%20sapiens) | 9.64 | 2.39 | + | 3.17E-04 | 6.63E-03 | | [apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097190) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&list=upload_1&organism=Homo%20sapiens) | 18.69 | 2.51 | + | 8.72E-08 | 4.18E-06 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 61.11 | 1.88 | + | 8.19E-10 | 5.37E-08 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 63.54 | 1.83 | + | 3.60E-09 | 2.09E-07 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 65.55 | 1.83 | + | 1.83E-09 | 1.13E-07 | | [response to cocaine](http://amigo.geneontology.org/amigo/term/GO:0042220) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042220&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042220&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.87 | + | 3.71E-04 | 7.54E-03 | | [response to alkaloid](http://amigo.geneontology.org/amigo/term/GO:0043279) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&list=upload_1&organism=Homo%20sapiens) | 5.92 | 2.87 | + | 2.69E-04 | 5.79E-03 | | [response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0010243) | [968](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&reflist=1) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 57.26 | 2.04 | + | 5.70E-12 | 4.73E-10 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 62.83 | 1.93 | + | 7.08E-11 | 5.19E-09 | | [myoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045445) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045445&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045445&list=upload_1&organism=Homo%20sapiens) | 2.37 | 3.80 | + | 1.39E-03 | 2.30E-02 | | [muscle structure development](http://amigo.geneontology.org/amigo/term/GO:0061061) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&list=upload_1&organism=Homo%20sapiens) | 29.52 | 2.34 | + | 1.28E-09 | 8.29E-08 | | [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) | 2.90 | 3.79 | + | 4.32E-04 | 8.53E-03 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903146&list=upload_1&organism=Homo%20sapiens) | 2.13 | 3.76 | + | 2.72E-03 | 3.94E-02 | | [regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010821) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&list=upload_1&organism=Homo%20sapiens) | 8.99 | 2.34 | + | 7.24E-04 | 1.34E-02 | | [mesenchyme morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0072132) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072132&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072132&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.76 | + | 2.60E-04 | 5.67E-03 | | [mesenchyme development](http://amigo.geneontology.org/amigo/term/GO:0060485) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&list=upload_1&organism=Homo%20sapiens) | 14.14 | 1.91 | + | 2.75E-03 | 3.97E-02 | | [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) | 2.13 | 3.76 | + | 2.72E-03 | 3.93E-02 | | [cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008283) | [718](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&list=upload_1&organism=Homo%20sapiens) | 42.48 | 1.86 | + | 8.36E-07 | 3.44E-05 | | [negative regulation of insulin secretion](http://amigo.geneontology.org/amigo/term/GO:0046676) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046676&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046676&list=upload_1&organism=Homo%20sapiens) | 2.13 | 3.76 | + | 2.72E-03 | 3.93E-02 | | [regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051049) | [1766](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&reflist=1) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&list=upload_1&organism=Homo%20sapiens) | 104.47 | 1.52 | + | 4.11E-07 | 1.78E-05 | | [regulation of localization](http://amigo.geneontology.org/amigo/term/GO:0032879) | [2104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&reflist=1) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&list=upload_1&organism=Homo%20sapiens) | 124.47 | 1.53 | + | 1.21E-08 | 6.63E-07 | | [negative regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051051) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&list=upload_1&organism=Homo%20sapiens) | 25.73 | 1.83 | + | 2.62E-04 | 5.68E-03 | | [regulation of protein transport](http://amigo.geneontology.org/amigo/term/GO:0051223) | [502](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&list=upload_1&organism=Homo%20sapiens) | 29.70 | 1.82 | + | 7.43E-05 | 1.89E-03 | | [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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&list=upload_1&organism=Homo%20sapiens) | 31.18 | 1.80 | + | 7.43E-05 | 1.89E-03 | | [regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:0032880) | [850](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&list=upload_1&organism=Homo%20sapiens) | 50.28 | 1.85 | + | 8.88E-08 | 4.23E-06 | | [regulation of cellular localization](http://amigo.geneontology.org/amigo/term/GO:0060341) | [962](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&reflist=1) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&list=upload_1&organism=Homo%20sapiens) | 56.91 | 1.86 | + | 6.68E-09 | 3.80E-07 | | [embryonic digit morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0042733) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042733&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042733&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.72 | + | 1.57E-04 | 3.60E-03 | | [embryonic morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048598) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&list=upload_1&organism=Homo%20sapiens) | 34.96 | 1.86 | + | 8.47E-06 | 2.81E-04 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 62.65 | 1.85 | + | 1.87E-09 | 1.15E-07 | | [embryonic limb morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0030326) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030326&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030326&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.51 | + | 1.08E-03 | 1.87E-02 | | [limb development](http://amigo.geneontology.org/amigo/term/GO:0060173) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060173&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060173&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.24 | + | 5.93E-04 | 1.13E-02 | | [appendage development](http://amigo.geneontology.org/amigo/term/GO:0048736) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048736&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048736&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.24 | + | 5.93E-04 | 1.12E-02 | | [embryonic appendage morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0035113) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035113&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035113&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.51 | + | 1.08E-03 | 1.87E-02 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&list=upload_1&organism=Homo%20sapiens) | 4.85 | 3.71 | + | 9.64E-06 | 3.15E-04 | | [negative regulation of cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0010812) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010812&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010812&list=upload_1&organism=Homo%20sapiens) | 3.55 | 3.66 | + | 1.82E-04 | 4.11E-03 | | [negative regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0007162) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007162&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007162&list=upload_1&organism=Homo%20sapiens) | 17.16 | 1.92 | + | 8.42E-04 | 1.53E-02 | | [regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0030155) | [789](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 46.68 | 1.76 | + | 3.60E-06 | 1.33E-04 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010810&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.01 | + | 1.76E-03 | 2.78E-02 | | [transcription elongation by RNA polymerase II promoter](http://amigo.geneontology.org/amigo/term/GO:0006368) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006368&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006368&list=upload_1&organism=Homo%20sapiens) | 2.19 | 3.65 | + | 3.14E-03 | 4.41E-02 | | [DNA-templated transcription elongation](http://amigo.geneontology.org/amigo/term/GO:0006354) | [185](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006354&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006354&list=upload_1&organism=Homo%20sapiens) | 10.94 | 3.47 | + | 7.13E-10 | 4.72E-08 | | [regulation of cardiac muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0010665) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010665&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010665&list=upload_1&organism=Homo%20sapiens) | 2.19 | 3.65 | + | 3.14E-03 | 4.40E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045995&list=upload_1&organism=Homo%20sapiens) | 5.32 | 3.57 | + | 8.94E-06 | 2.95E-04 | | [positive regulation of fatty acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045923) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045923&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045923&list=upload_1&organism=Homo%20sapiens) | 2.25 | 3.56 | + | 3.62E-03 | 4.94E-02 | | [regulation of fatty acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019217) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019217&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019217&list=upload_1&organism=Homo%20sapiens) | 5.62 | 2.67 | + | 1.18E-03 | 2.01E-02 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019216&list=upload_1&organism=Homo%20sapiens) | 20.47 | 1.76 | + | 2.20E-03 | 3.35E-02 | | [regulation of cellular ketone metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010565) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010565&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010565&list=upload_1&organism=Homo%20sapiens) | 7.99 | 2.38 | + | 1.12E-03 | 1.93E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045834&list=upload_1&organism=Homo%20sapiens) | 9.11 | 2.20 | + | 2.26E-03 | 3.42E-02 | | [central nervous system neuron axonogenesis](http://amigo.geneontology.org/amigo/term/GO:0021955) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021955&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021955&list=upload_1&organism=Homo%20sapiens) | 2.25 | 3.56 | + | 3.62E-03 | 4.94E-02 | | [neuron development](http://amigo.geneontology.org/amigo/term/GO:0048666) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&list=upload_1&organism=Homo%20sapiens) | 49.87 | 1.74 | + | 2.46E-06 | 9.32E-05 | | [neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0030182) | [1065](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&list=upload_1&organism=Homo%20sapiens) | 63.00 | 1.67 | + | 1.50E-06 | 5.90E-05 | | [generation of neurons](http://amigo.geneontology.org/amigo/term/GO:0048699) | [1134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&list=upload_1&organism=Homo%20sapiens) | 67.08 | 1.68 | + | 3.10E-07 | 1.37E-05 | | [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) | 76.31 | 1.74 | + | 3.59E-09 | 2.09E-07 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [221](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 129.61 | 1.71 | + | 4.70E-14 | 4.55E-12 | | [central nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007417) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 61.17 | 1.86 | + | 1.86E-09 | 1.14E-07 | | [axonogenesis](http://amigo.geneontology.org/amigo/term/GO:0007409) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007409&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007409&list=upload_1&organism=Homo%20sapiens) | 21.59 | 1.85 | + | 4.35E-04 | 8.58E-03 | | [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) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048667&list=upload_1&organism=Homo%20sapiens) | 26.03 | 1.88 | + | 8.43E-05 | 2.10E-03 | | [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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000904&list=upload_1&organism=Homo%20sapiens) | 32.89 | 1.70 | + | 3.17E-04 | 6.63E-03 | | [cell morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0000902) | [713](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&list=upload_1&organism=Homo%20sapiens) | 42.18 | 1.80 | + | 3.75E-06 | 1.37E-04 | | [neuron projection morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048812) | [479](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048812&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048812&list=upload_1&organism=Homo%20sapiens) | 28.34 | 1.94 | + | 1.36E-05 | 4.25E-04 | | [neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0031175) | [677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&list=upload_1&organism=Homo%20sapiens) | 40.05 | 1.90 | + | 6.18E-07 | 2.59E-05 | | [plasma membrane bounded cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0120036) | [1115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120036&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120036&list=upload_1&organism=Homo%20sapiens) | 65.96 | 1.46 | + | 4.89E-04 | 9.46E-03 | | [cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0030030) | [1161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030030&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030030&list=upload_1&organism=Homo%20sapiens) | 68.68 | 1.44 | + | 6.14E-04 | 1.16E-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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120039&list=upload_1&organism=Homo%20sapiens) | 28.63 | 1.96 | + | 9.63E-06 | 3.15E-04 | | [cell projection morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048858) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048858&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048858&list=upload_1&organism=Homo%20sapiens) | 28.93 | 1.94 | + | 1.10E-05 | 3.52E-04 | | [cell part morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032990) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032990&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032990&list=upload_1&organism=Homo%20sapiens) | 30.05 | 1.90 | + | 1.58E-05 | 4.86E-04 | | [cellular component morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032989) | [604](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&list=upload_1&organism=Homo%20sapiens) | 35.73 | 1.99 | + | 3.49E-07 | 1.52E-05 | | [axon development](http://amigo.geneontology.org/amigo/term/GO:0061564) | [404](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061564&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061564&list=upload_1&organism=Homo%20sapiens) | 23.90 | 1.84 | + | 3.50E-04 | 7.19E-03 | | [myofibril assembly](http://amigo.geneontology.org/amigo/term/GO:0030239) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030239&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030239&list=upload_1&organism=Homo%20sapiens) | 3.67 | 3.54 | + | 2.40E-04 | 5.28E-03 | | [cellular component assembly involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0010927) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010927&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010927&list=upload_1&organism=Homo%20sapiens) | 6.39 | 2.50 | + | 2.28E-03 | 3.45E-02 | | [striated muscle cell development](http://amigo.geneontology.org/amigo/term/GO:0055002) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055002&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055002&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.49 | + | 2.75E-04 | 5.89E-03 | | [muscle cell development](http://amigo.geneontology.org/amigo/term/GO:0055001) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055001&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055001&list=upload_1&organism=Homo%20sapiens) | 9.47 | 2.64 | + | 6.15E-05 | 1.61E-03 | | [muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0042692) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&list=upload_1&organism=Homo%20sapiens) | 15.85 | 2.33 | + | 1.19E-05 | 3.78E-04 | | [striated muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051146) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051146&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051146&list=upload_1&organism=Homo%20sapiens) | 12.07 | 2.32 | + | 1.27E-04 | 3.04E-03 | | [actomyosin structure organization](http://amigo.geneontology.org/amigo/term/GO:0031032) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&list=upload_1&organism=Homo%20sapiens) | 6.74 | 2.52 | + | 1.54E-03 | 2.47E-02 | | [actin cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0030036) | [549](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030036&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030036&list=upload_1&organism=Homo%20sapiens) | 32.48 | 1.57 | + | 2.81E-03 | 4.04E-02 | | [cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0007010) | [1240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&list=upload_1&organism=Homo%20sapiens) | 73.36 | 1.43 | + | 4.60E-04 | 9.01E-03 | | [organelle organization](http://amigo.geneontology.org/amigo/term/GO:0006996) | [3026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&reflist=1) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&list=upload_1&organism=Homo%20sapiens) | 179.01 | 1.35 | + | 2.34E-06 | 8.92E-05 | | [actin filament-based process](http://amigo.geneontology.org/amigo/term/GO:0030029) | [611](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030029&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030029&list=upload_1&organism=Homo%20sapiens) | 36.15 | 1.55 | + | 2.58E-03 | 3.79E-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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&list=upload_1&organism=Homo%20sapiens) | 18.69 | 1.82 | + | 2.02E-03 | 3.14E-02 | | [supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:0097435) | [580](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097435&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097435&list=upload_1&organism=Homo%20sapiens) | 34.31 | 1.60 | + | 1.48E-03 | 2.41E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045429&list=upload_1&organism=Homo%20sapiens) | 2.54 | 3.54 | + | 2.15E-03 | 3.30E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904407&list=upload_1&organism=Homo%20sapiens) | 2.66 | 3.38 | + | 2.81E-03 | 4.04E-02 | | [regulation of nitric oxide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0080164) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080164&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080164&list=upload_1&organism=Homo%20sapiens) | 3.79 | 2.91 | + | 2.88E-03 | 4.11E-02 | | [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) | 3.49 | 3.15 | + | 1.64E-03 | 2.62E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071364&list=upload_1&organism=Homo%20sapiens) | 2.54 | 3.54 | + | 2.15E-03 | 3.30E-02 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070849&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.96 | + | 3.18E-04 | 6.63E-03 | | [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) | 2.54 | 3.54 | + | 2.15E-03 | 3.29E-02 | | [regulation of glycoprotein biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010559) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010559&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010559&list=upload_1&organism=Homo%20sapiens) | 2.54 | 3.54 | + | 2.15E-03 | 3.29E-02 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&list=upload_1&organism=Homo%20sapiens) | 29.16 | 1.61 | + | 3.05E-03 | 4.32E-02 | | [regulation of stem cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0072091) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072091&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072091&list=upload_1&organism=Homo%20sapiens) | 4.85 | 3.50 | + | 3.19E-05 | 9.17E-04 | | [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) | 2.60 | 3.46 | + | 2.46E-03 | 3.68E-02 | | [regulation of oligodendrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0048713) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048713&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048713&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.46E-03 | 3.67E-02 | | [endodermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0035987) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.46E-03 | 3.67E-02 | | [endoderm formation](http://amigo.geneontology.org/amigo/term/GO:0001706) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.76 | + | 2.60E-04 | 5.66E-03 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 4.79 | 3.76 | + | 8.34E-06 | 2.78E-04 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.68 | + | 2.70E-04 | 5.83E-03 | | [gastrulation](http://amigo.geneontology.org/amigo/term/GO:0007369) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&list=upload_1&organism=Homo%20sapiens) | 10.00 | 2.20 | + | 1.24E-03 | 2.09E-02 | | [DNA damage response, signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0030330) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030330&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030330&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.46E-03 | 3.66E-02 | | [signal transduction in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:0042770) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042770&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042770&list=upload_1&organism=Homo%20sapiens) | 7.99 | 3.01 | + | 8.46E-06 | 2.82E-04 | | [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) | 2.90 | 3.45 | + | 1.46E-03 | 2.38E-02 | | [skeletal muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0035914) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035914&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035914&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.44 | + | 8.75E-04 | 1.58E-02 | | [skeletal muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0007519) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007519&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007519&list=upload_1&organism=Homo%20sapiens) | 7.93 | 2.65 | + | 1.50E-04 | 3.46E-03 | | [muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0060537) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&list=upload_1&organism=Homo%20sapiens) | 19.29 | 2.33 | + | 9.83E-07 | 4.01E-05 | | [skeletal muscle organ development](http://amigo.geneontology.org/amigo/term/GO:0060538) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060538&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060538&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.43 | + | 4.88E-04 | 9.47E-03 | | [muscle organ development](http://amigo.geneontology.org/amigo/term/GO:0007517) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007517&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007517&list=upload_1&organism=Homo%20sapiens) | 17.98 | 2.39 | + | 1.29E-06 | 5.10E-05 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051148&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.44 | + | 5.24E-04 | 1.01E-02 | | [telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0000723) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&list=upload_1&organism=Homo%20sapiens) | 5.56 | 3.42 | + | 1.53E-05 | 4.73E-04 | | [telomere organization](http://amigo.geneontology.org/amigo/term/GO:0032200) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&list=upload_1&organism=Homo%20sapiens) | 6.09 | 3.28 | + | 1.54E-05 | 4.74E-04 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 26.27 | 2.40 | + | 3.05E-09 | 1.80E-07 | | [positive regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043525) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043525&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043525&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.38 | + | 9.98E-04 | 1.77E-02 | | [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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043523&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.33 | + | 6.74E-05 | 1.73E-03 | | [regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901214) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&list=upload_1&organism=Homo%20sapiens) | 19.23 | 2.08 | + | 4.54E-05 | 1.25E-03 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&list=upload_1&organism=Homo%20sapiens) | 5.50 | 2.54 | + | 2.51E-03 | 3.70E-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) | 6.80 | 3.38 | + | 2.35E-06 | 8.96E-05 | | [protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:0034504) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&list=upload_1&organism=Homo%20sapiens) | 11.48 | 3.14 | + | 2.02E-08 | 1.08E-06 | | [intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0006886) | [682](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&list=upload_1&organism=Homo%20sapiens) | 40.35 | 1.69 | + | 9.08E-05 | 2.25E-03 | | [intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0046907) | [1360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&list=upload_1&organism=Homo%20sapiens) | 80.45 | 1.52 | + | 1.34E-05 | 4.22E-04 | | [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) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&list=upload_1&organism=Homo%20sapiens) | 103.64 | 1.54 | + | 1.62E-07 | 7.52E-06 | | [establishment of localization](http://amigo.geneontology.org/amigo/term/GO:0051234) | [3997](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&reflist=1) | [289](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&list=upload_1&organism=Homo%20sapiens) | 236.45 | 1.22 | + | 3.15E-04 | 6.60E-03 | | [transport](http://amigo.geneontology.org/amigo/term/GO:0006810) | [3840](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&reflist=1) | [271](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&list=upload_1&organism=Homo%20sapiens) | 227.17 | 1.19 | + | 2.24E-03 | 3.41E-02 | | [protein transport](http://amigo.geneontology.org/amigo/term/GO:0015031) | [1179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&list=upload_1&organism=Homo%20sapiens) | 69.75 | 1.51 | + | 7.50E-05 | 1.90E-03 | | [establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:0045184) | [1267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&list=upload_1&organism=Homo%20sapiens) | 74.95 | 1.51 | + | 3.59E-05 | 1.02E-03 | | [nitrogen compound transport](http://amigo.geneontology.org/amigo/term/GO:0071705) | [1589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&list=upload_1&organism=Homo%20sapiens) | 94.00 | 1.41 | + | 1.23E-04 | 2.95E-03 | | [import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0051170) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&list=upload_1&organism=Homo%20sapiens) | 7.04 | 3.27 | + | 3.89E-06 | 1.41E-04 | | [nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0006913) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&list=upload_1&organism=Homo%20sapiens) | 14.67 | 2.45 | + | 5.15E-06 | 1.82E-04 | | [nuclear transport](http://amigo.geneontology.org/amigo/term/GO:0051169) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&list=upload_1&organism=Homo%20sapiens) | 14.67 | 2.45 | + | 5.15E-06 | 1.81E-04 | | [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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&list=upload_1&organism=Homo%20sapiens) | 19.76 | 2.18 | + | 1.15E-05 | 3.69E-04 | | [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) | 3.85 | 3.38 | + | 3.58E-04 | 7.32E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&list=upload_1&organism=Homo%20sapiens) | 6.21 | 2.74 | + | 4.44E-04 | 8.72E-03 | | [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) | 36.68 | 1.91 | + | 1.25E-06 | 4.99E-05 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&list=upload_1&organism=Homo%20sapiens) | 6.92 | 3.32 | + | 3.03E-06 | 1.14E-04 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 7.75 | 3.35 | + | 6.00E-07 | 2.53E-05 | | [regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045619) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 12.42 | 2.90 | + | 1.17E-07 | 5.49E-06 | | [regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902105) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 18.69 | 2.73 | + | 2.35E-09 | 1.43E-07 | | [regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051249) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&list=upload_1&organism=Homo%20sapiens) | 34.96 | 1.72 | + | 1.72E-04 | 3.91E-03 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 40.46 | 1.71 | + | 4.89E-05 | 1.32E-03 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 43.84 | 1.67 | + | 6.51E-05 | 1.68E-03 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&list=upload_1&organism=Homo%20sapiens) | 10.83 | 3.14 | + | 4.84E-08 | 2.43E-06 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 10.83 | 3.14 | + | 4.84E-08 | 2.42E-06 | | [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) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 57.21 | 1.47 | + | 9.13E-04 | 1.64E-02 | | [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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 14.97 | 2.20 | + | 7.59E-05 | 1.91E-03 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 16.33 | 2.20 | + | 4.93E-05 | 1.33E-03 | | [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) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&list=upload_1&organism=Homo%20sapiens) | 21.83 | 2.02 | + | 4.78E-05 | 1.30E-03 | | [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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&list=upload_1&organism=Homo%20sapiens) | 28.63 | 1.85 | + | 5.55E-05 | 1.47E-03 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 19.17 | 2.09 | + | 4.35E-05 | 1.20E-03 | | [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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 28.87 | 1.77 | + | 2.68E-04 | 5.79E-03 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&list=upload_1&organism=Homo%20sapiens) | 22.30 | 2.06 | + | 1.49E-05 | 4.62E-04 | | [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) | 10.59 | 3.02 | + | 2.55E-07 | 1.14E-05 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071385&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.32 | + | 1.13E-03 | 1.94E-02 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071384&list=upload_1&organism=Homo%20sapiens) | 3.85 | 2.86 | + | 3.20E-03 | 4.47E-02 | | [ventricular cardiac muscle tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0055010) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055010&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055010&list=upload_1&organism=Homo%20sapiens) | 2.72 | 3.31 | + | 3.20E-03 | 4.47E-02 | | [ventricular cardiac muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0003229) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003229&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003229&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.07 | + | 3.09E-03 | 4.34E-02 | | [cardiac muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0048738) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048738&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048738&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.14 | + | 1.79E-03 | 2.82E-02 | | [striated muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0014706) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&list=upload_1&organism=Homo%20sapiens) | 11.12 | 2.16 | + | 1.25E-03 | 2.10E-02 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 32.83 | 2.31 | + | 2.89E-10 | 1.96E-08 | | [cardiac ventricle morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003208) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003208&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003208&list=upload_1&organism=Homo%20sapiens) | 4.14 | 2.90 | + | 1.93E-03 | 3.01E-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) | 14.73 | 2.04 | + | 5.57E-04 | 1.07E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001251&list=upload_1&organism=Homo%20sapiens) | 4.85 | 3.30 | + | 1.01E-04 | 2.47E-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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000045&list=upload_1&organism=Homo%20sapiens) | 9.70 | 3.30 | + | 4.44E-08 | 2.24E-06 | | [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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 11.36 | 3.35 | + | 1.76E-09 | 1.09E-07 | | [response to estrogen](http://amigo.geneontology.org/amigo/term/GO:0043627) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043627&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043627&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.29 | + | 2.78E-04 | 5.94E-03 | | [face development](http://amigo.geneontology.org/amigo/term/GO:0060324) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060324&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060324&list=upload_1&organism=Homo%20sapiens) | 3.08 | 3.25 | + | 2.16E-03 | 3.29E-02 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 48.69 | 1.89 | + | 3.82E-08 | 1.96E-06 | | [Fc receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038093) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&list=upload_1&organism=Homo%20sapiens) | 3.08 | 3.25 | + | 2.16E-03 | 3.29E-02 | | [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) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 128.61 | 1.34 | + | 1.66E-04 | 3.78E-03 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905953&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.24 | + | 3.63E-03 | 4.93E-02 | | [regulation of glycolytic process](http://amigo.geneontology.org/amigo/term/GO:0006110) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006110&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006110&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.24 | + | 3.63E-03 | 4.93E-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) | 4.20 | 2.86 | + | 2.14E-03 | 3.30E-02 | | [regulation of carbohydrate catabolic process](http://amigo.geneontology.org/amigo/term/GO:0043470) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043470&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043470&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.07 | + | 3.09E-03 | 4.34E-02 | | [negative regulation of cold-induced thermogenesis](http://amigo.geneontology.org/amigo/term/GO:0120163) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120163&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120163&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.24 | + | 3.63E-03 | 4.93E-02 | | [regulation of cold-induced thermogenesis](http://amigo.geneontology.org/amigo/term/GO:0120161) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120161&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120161&list=upload_1&organism=Homo%20sapiens) | 8.70 | 2.18 | + | 3.13E-03 | 4.39E-02 | | [negative regulation of transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030512) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030512&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030512&list=upload_1&organism=Homo%20sapiens) | 5.56 | 3.24 | + | 4.73E-05 | 1.29E-03 | | [negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0090101) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090101&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090101&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.20 | + | 3.01E-03 | 4.26E-02 | | [extracellular matrix disassembly](http://amigo.geneontology.org/amigo/term/GO:0022617) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022617&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022617&list=upload_1&organism=Homo%20sapiens) | 2.78 | 3.24 | + | 3.63E-03 | 4.92E-02 | | [SMAD protein signal transduction](http://amigo.geneontology.org/amigo/term/GO:0060395) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060395&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060395&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.22 | + | 8.71E-04 | 1.58E-02 | | [transmembrane receptor protein serine/threonine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007178) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007178&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007178&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.13 | + | 7.49E-04 | 1.38E-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) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&list=upload_1&organism=Homo%20sapiens) | 37.86 | 1.58 | + | 1.03E-03 | 1.81E-02 | | [apoptotic mitochondrial changes](http://amigo.geneontology.org/amigo/term/GO:0008637) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008637&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008637&list=upload_1&organism=Homo%20sapiens) | 3.43 | 3.21 | + | 1.45E-03 | 2.37E-02 | | [negative regulation of epithelial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1904036) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904036&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904036&list=upload_1&organism=Homo%20sapiens) | 3.43 | 3.21 | + | 1.45E-03 | 2.37E-02 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&list=upload_1&organism=Homo%20sapiens) | 4.38 | 3.20 | + | 3.55E-04 | 7.26E-03 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.19 | + | 2.44E-03 | 3.65E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&list=upload_1&organism=Homo%20sapiens) | 7.99 | 2.75 | + | 6.34E-05 | 1.65E-03 | | [response to cold](http://amigo.geneontology.org/amigo/term/GO:0009409) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009409&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009409&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.19 | + | 2.44E-03 | 3.65E-02 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&list=upload_1&organism=Homo%20sapiens) | 6.92 | 3.18 | + | 9.18E-06 | 3.02E-04 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&list=upload_1&organism=Homo%20sapiens) | 9.88 | 2.83 | + | 4.20E-06 | 1.51E-04 | | [Rho protein signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007266) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007266&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007266&list=upload_1&organism=Homo%20sapiens) | 3.79 | 3.17 | + | 9.82E-04 | 1.75E-02 | | [Ras protein signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007265) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.27 | + | 2.98E-04 | 6.32E-03 | | [small GTPase mediated signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007264) | [270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007264&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007264&list=upload_1&organism=Homo%20sapiens) | 15.97 | 2.13 | + | 1.22E-04 | 2.92E-03 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046824&list=upload_1&organism=Homo%20sapiens) | 3.79 | 3.17 | + | 9.82E-04 | 1.75E-02 | | [regulation of intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0032386) | [342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&list=upload_1&organism=Homo%20sapiens) | 20.23 | 1.98 | + | 1.66E-04 | 3.79E-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) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&list=upload_1&organism=Homo%20sapiens) | 54.37 | 1.56 | + | 1.34E-04 | 3.16E-03 | | [regulation of nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0046822) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&list=upload_1&organism=Homo%20sapiens) | 6.63 | 2.72 | + | 3.30E-04 | 6.82E-03 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048524&list=upload_1&organism=Homo%20sapiens) | 3.85 | 3.12 | + | 1.11E-03 | 1.91E-02 | | [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) | 9.70 | 2.58 | + | 7.33E-05 | 1.87E-03 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 8.05 | 3.11 | + | 3.30E-06 | 1.22E-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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&list=upload_1&organism=Homo%20sapiens) | 5.80 | 3.10 | + | 7.59E-05 | 1.92E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&list=upload_1&organism=Homo%20sapiens) | 9.11 | 2.20 | + | 2.26E-03 | 3.42E-02 | | [axonal transport](http://amigo.geneontology.org/amigo/term/GO:0098930) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098930&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098930&list=upload_1&organism=Homo%20sapiens) | 3.55 | 3.10 | + | 1.84E-03 | 2.90E-02 | | [axo-dendritic transport](http://amigo.geneontology.org/amigo/term/GO:0008088) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008088&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008088&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.24 | + | 3.14E-04 | 6.60E-03 | | [transport along microtubule](http://amigo.geneontology.org/amigo/term/GO:0010970) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&list=upload_1&organism=Homo%20sapiens) | 9.52 | 2.52 | + | 1.28E-04 | 3.04E-03 | | [microtubule-based process](http://amigo.geneontology.org/amigo/term/GO:0007017) | [809](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&list=upload_1&organism=Homo%20sapiens) | 47.86 | 1.50 | + | 1.22E-03 | 2.06E-02 | | [cytoskeleton-dependent intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0030705) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&list=upload_1&organism=Homo%20sapiens) | 11.77 | 2.29 | + | 1.95E-04 | 4.36E-03 | | [microtubule-based transport](http://amigo.geneontology.org/amigo/term/GO:0099111) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099111&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099111&list=upload_1&organism=Homo%20sapiens) | 12.01 | 2.00 | + | 3.10E-03 | 4.35E-02 | | [regulation of circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0042752) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&list=upload_1&organism=Homo%20sapiens) | 7.10 | 3.10 | + | 1.30E-05 | 4.11E-04 | | [positive regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014015) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&list=upload_1&organism=Homo%20sapiens) | 3.90 | 3.07 | + | 1.24E-03 | 2.08E-02 | | [regulation of fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048145) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&list=upload_1&organism=Homo%20sapiens) | 5.27 | 3.04 | + | 2.31E-04 | 5.11E-03 | | [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) | 4.97 | 3.02 | + | 3.82E-04 | 7.73E-03 | | [cellular response to UV](http://amigo.geneontology.org/amigo/term/GO:0034644) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034644&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034644&list=upload_1&organism=Homo%20sapiens) | 5.32 | 3.01 | + | 2.59E-04 | 5.64E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&list=upload_1&organism=Homo%20sapiens) | 6.86 | 2.91 | + | 6.78E-05 | 1.74E-03 | | [response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0009416) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 18.75 | 2.72 | + | 2.49E-09 | 1.50E-07 | | [response to UV](http://amigo.geneontology.org/amigo/term/GO:0009411) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&list=upload_1&organism=Homo%20sapiens) | 8.93 | 3.36 | + | 8.23E-08 | 3.96E-06 | | [tissue regeneration](http://amigo.geneontology.org/amigo/term/GO:0042246) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042246&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042246&list=upload_1&organism=Homo%20sapiens) | 3.67 | 3.00 | + | 2.32E-03 | 3.50E-02 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 24.43 | 2.46 | + | 2.95E-09 | 1.76E-07 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 24.43 | 2.46 | + | 2.95E-09 | 1.77E-07 | | [mitotic sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0000070) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000070&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000070&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.96 | + | 3.72E-05 | 1.05E-03 | | [mitotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0140014) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&list=upload_1&organism=Homo%20sapiens) | 10.23 | 2.35 | + | 4.22E-04 | 8.38E-03 | | [nuclear division](http://amigo.geneontology.org/amigo/term/GO:0000280) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000280&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000280&list=upload_1&organism=Homo%20sapiens) | 19.11 | 1.83 | + | 1.52E-03 | 2.45E-02 | | [organelle fission](http://amigo.geneontology.org/amigo/term/GO:0048285) | [349](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048285&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048285&list=upload_1&organism=Homo%20sapiens) | 20.65 | 1.74 | + | 2.36E-03 | 3.54E-02 | | [sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0000819) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000819&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000819&list=upload_1&organism=Homo%20sapiens) | 8.76 | 2.74 | + | 3.22E-05 | 9.23E-04 | | [nuclear chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0098813) | [234](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098813&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098813&list=upload_1&organism=Homo%20sapiens) | 13.84 | 2.02 | + | 9.83E-04 | 1.75E-02 | | [chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0007059) | [291](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007059&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007059&list=upload_1&organism=Homo%20sapiens) | 17.21 | 1.98 | + | 5.39E-04 | 1.04E-02 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 5.44 | 2.94 | + | 3.22E-04 | 6.69E-03 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 5.80 | 2.93 | + | 2.18E-04 | 4.84E-03 | | [DNA conformation change](http://amigo.geneontology.org/amigo/term/GO:0071103) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&list=upload_1&organism=Homo%20sapiens) | 6.33 | 2.84 | + | 2.01E-04 | 4.50E-03 | | [somitogenesis](http://amigo.geneontology.org/amigo/term/GO:0001756) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001756&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001756&list=upload_1&organism=Homo%20sapiens) | 3.79 | 2.91 | + | 2.88E-03 | 4.11E-02 | | [chordate embryonic development](http://amigo.geneontology.org/amigo/term/GO:0043009) | [655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&list=upload_1&organism=Homo%20sapiens) | 38.75 | 2.04 | + | 2.65E-08 | 1.39E-06 | | [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) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&list=upload_1&organism=Homo%20sapiens) | 40.05 | 2.00 | + | 4.37E-08 | 2.21E-06 | | [regionalization](http://amigo.geneontology.org/amigo/term/GO:0003002) | [342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003002&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003002&list=upload_1&organism=Homo%20sapiens) | 20.23 | 1.78 | + | 2.04E-03 | 3.17E-02 | | [pattern specification process](http://amigo.geneontology.org/amigo/term/GO:0007389) | [457](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007389&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007389&list=upload_1&organism=Homo%20sapiens) | 27.04 | 1.63 | + | 2.98E-03 | 4.24E-02 | | [anterior/posterior pattern specification](http://amigo.geneontology.org/amigo/term/GO:0009952) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.02 | + | 1.70E-03 | 2.70E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&list=upload_1&organism=Homo%20sapiens) | 7.57 | 2.91 | + | 3.13E-05 | 8.99E-04 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 16.39 | 2.69 | + | 4.31E-08 | 2.19E-06 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 17.16 | 2.62 | + | 4.85E-08 | 2.42E-06 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&list=upload_1&organism=Homo%20sapiens) | 8.05 | 2.86 | + | 2.61E-05 | 7.56E-04 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&list=upload_1&organism=Homo%20sapiens) | 9.05 | 2.76 | + | 1.99E-05 | 5.90E-04 | | [regulation of osteoclast differentiation](http://amigo.geneontology.org/amigo/term/GO:0045670) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045670&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045670&list=upload_1&organism=Homo%20sapiens) | 4.14 | 2.90 | + | 1.93E-03 | 3.02E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002761&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.63 | + | 3.26E-04 | 6.75E-03 | | [negative regulation of epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050680) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050680&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050680&list=upload_1&organism=Homo%20sapiens) | 8.28 | 2.90 | + | 1.44E-05 | 4.51E-04 | | [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) | 4.50 | 2.89 | + | 1.30E-03 | 2.16E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031098&list=upload_1&organism=Homo%20sapiens) | 4.73 | 2.96 | + | 7.05E-04 | 1.30E-02 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 13.01 | 2.69 | + | 1.22E-06 | 4.90E-05 | | [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) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 57.62 | 2.88 | + | 5.58E-31 | 1.35E-28 | | [neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0051402) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&list=upload_1&organism=Homo%20sapiens) | 5.56 | 2.88 | + | 3.97E-04 | 7.99E-03 | | [neuron death](http://amigo.geneontology.org/amigo/term/GO:0070997) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070997&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070997&list=upload_1&organism=Homo%20sapiens) | 6.21 | 2.58 | + | 1.15E-03 | 1.96E-02 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&list=upload_1&organism=Homo%20sapiens) | 5.56 | 2.88 | + | 3.97E-04 | 7.98E-03 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 11.89 | 2.44 | + | 3.76E-05 | 1.06E-03 | | [endocrine system development](http://amigo.geneontology.org/amigo/term/GO:0035270) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&list=upload_1&organism=Homo%20sapiens) | 7.69 | 2.86 | + | 3.85E-05 | 1.08E-03 | | [protein autoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0051865) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&list=upload_1&organism=Homo%20sapiens) | 4.56 | 2.85 | + | 1.44E-03 | 2.36E-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) | 4.56 | 2.85 | + | 1.44E-03 | 2.35E-02 | | [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) | 7.75 | 2.71 | + | 1.13E-04 | 2.73E-03 | | [negative regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001021) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001021&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001021&list=upload_1&organism=Homo%20sapiens) | 4.91 | 2.85 | + | 9.69E-04 | 1.73E-02 | | [positive regulation of protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:1900182) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900182&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900182&list=upload_1&organism=Homo%20sapiens) | 5.27 | 2.85 | + | 6.53E-04 | 1.22E-02 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903829&list=upload_1&organism=Homo%20sapiens) | 27.33 | 1.68 | + | 1.19E-03 | 2.03E-02 | | [regulation of protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:1900180) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900180&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900180&list=upload_1&organism=Homo%20sapiens) | 8.34 | 2.40 | + | 7.63E-04 | 1.40E-02 | | [cellular glucose homeostasis](http://amigo.geneontology.org/amigo/term/GO:0001678) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001678&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001678&list=upload_1&organism=Homo%20sapiens) | 5.97 | 2.85 | + | 2.98E-04 | 6.32E-03 | | [glucose homeostasis](http://amigo.geneontology.org/amigo/term/GO:0042593) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&list=upload_1&organism=Homo%20sapiens) | 11.89 | 2.10 | + | 1.11E-03 | 1.92E-02 | | [carbohydrate homeostasis](http://amigo.geneontology.org/amigo/term/GO:0033500) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&list=upload_1&organism=Homo%20sapiens) | 11.95 | 2.09 | + | 1.16E-03 | 1.98E-02 | | [chemical homeostasis](http://amigo.geneontology.org/amigo/term/GO:0048878) | [916](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048878&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048878&list=upload_1&organism=Homo%20sapiens) | 54.19 | 1.49 | + | 6.74E-04 | 1.26E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&list=upload_1&organism=Homo%20sapiens) | 5.68 | 2.82 | + | 4.88E-04 | 9.48E-03 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&list=upload_1&organism=Homo%20sapiens) | 9.11 | 2.96 | + | 2.98E-06 | 1.12E-04 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&list=upload_1&organism=Homo%20sapiens) | 9.52 | 2.94 | + | 2.26E-06 | 8.66E-05 | | [stem cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0072089) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072089&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072089&list=upload_1&organism=Homo%20sapiens) | 4.61 | 2.82 | + | 1.60E-03 | 2.56E-02 | | [oligodendrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0048709) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048709&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048709&list=upload_1&organism=Homo%20sapiens) | 4.67 | 2.78 | + | 1.77E-03 | 2.78E-02 | | [glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0010001) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010001&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010001&list=upload_1&organism=Homo%20sapiens) | 11.06 | 2.17 | + | 1.23E-03 | 2.07E-02 | | [gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0042063) | [246](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&list=upload_1&organism=Homo%20sapiens) | 14.55 | 1.99 | + | 1.26E-03 | 2.11E-02 | | [spliceosomal complex assembly](http://amigo.geneontology.org/amigo/term/GO:0000245) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000245&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000245&list=upload_1&organism=Homo%20sapiens) | 4.32 | 2.78 | + | 2.63E-03 | 3.84E-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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000398&list=upload_1&organism=Homo%20sapiens) | 14.38 | 2.64 | + | 5.02E-07 | 2.13E-05 | | [mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0006397) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&list=upload_1&organism=Homo%20sapiens) | 26.68 | 2.10 | + | 1.12E-06 | 4.51E-05 | | [RNA processing](http://amigo.geneontology.org/amigo/term/GO:0006396) | [868](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&list=upload_1&organism=Homo%20sapiens) | 51.35 | 1.56 | + | 2.14E-04 | 4.77E-03 | | [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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000377&list=upload_1&organism=Homo%20sapiens) | 14.38 | 2.64 | + | 5.02E-07 | 2.13E-05 | | [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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000375&list=upload_1&organism=Homo%20sapiens) | 14.61 | 2.67 | + | 3.01E-07 | 1.33E-05 | | [RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0008380) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&list=upload_1&organism=Homo%20sapiens) | 21.77 | 2.34 | + | 2.28E-07 | 1.03E-05 | | [ribonucleoprotein complex assembly](http://amigo.geneontology.org/amigo/term/GO:0022618) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&list=upload_1&organism=Homo%20sapiens) | 11.89 | 2.78 | + | 9.14E-07 | 3.73E-05 | | [ribonucleoprotein complex biogenesis](http://amigo.geneontology.org/amigo/term/GO:0022613) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&list=upload_1&organism=Homo%20sapiens) | 26.56 | 1.81 | + | 2.24E-04 | 4.98E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071826&list=upload_1&organism=Homo%20sapiens) | 12.36 | 2.83 | + | 2.85E-07 | 1.27E-05 | | [positive regulation of neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0045666) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045666&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045666&list=upload_1&organism=Homo%20sapiens) | 5.44 | 2.76 | + | 8.83E-04 | 1.59E-02 | | [regulation of neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0045664) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045664&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045664&list=upload_1&organism=Homo%20sapiens) | 11.54 | 2.43 | + | 5.49E-05 | 1.45E-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) | 5.09 | 2.75 | + | 1.31E-03 | 2.18E-02 | | [embryonic organ development](http://amigo.geneontology.org/amigo/term/GO:0048568) | [454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&list=upload_1&organism=Homo%20sapiens) | 26.86 | 1.94 | + | 2.11E-05 | 6.24E-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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&list=upload_1&organism=Homo%20sapiens) | 23.37 | 2.40 | + | 1.95E-08 | 1.05E-06 | | [placenta development](http://amigo.geneontology.org/amigo/term/GO:0001890) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&list=upload_1&organism=Homo%20sapiens) | 8.93 | 2.91 | + | 6.02E-06 | 2.08E-04 | | [organelle transport along microtubule](http://amigo.geneontology.org/amigo/term/GO:0072384) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072384&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072384&list=upload_1&organism=Homo%20sapiens) | 4.79 | 2.71 | + | 2.15E-03 | 3.29E-02 | | [establishment of organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051656) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&list=upload_1&organism=Homo%20sapiens) | 22.42 | 1.96 | + | 9.48E-05 | 2.34E-03 | | [organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051640) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&list=upload_1&organism=Homo%20sapiens) | 30.35 | 1.85 | + | 3.93E-05 | 1.11E-03 | | [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) | 5.97 | 2.68 | + | 7.95E-04 | 1.45E-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) | 6.74 | 2.67 | + | 3.99E-04 | 8.01E-03 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&list=upload_1&organism=Homo%20sapiens) | 4.91 | 2.65 | + | 2.60E-03 | 3.81E-02 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043280&list=upload_1&organism=Homo%20sapiens) | 7.63 | 2.36 | + | 1.64E-03 | 2.62E-02 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&list=upload_1&organism=Homo%20sapiens) | 12.30 | 1.95 | + | 3.57E-03 | 4.88E-02 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 43.95 | 1.75 | + | 8.31E-06 | 2.78E-04 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&list=upload_1&organism=Homo%20sapiens) | 11.42 | 2.10 | + | 1.47E-03 | 2.39E-02 | | [positive regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0045862) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&list=upload_1&organism=Homo%20sapiens) | 22.07 | 1.95 | + | 1.30E-04 | 3.10E-03 | | [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) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 70.63 | 1.40 | + | 1.40E-03 | 2.31E-02 | | [odontogenesis of dentin-containing tooth](http://amigo.geneontology.org/amigo/term/GO:0042475) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042475&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042475&list=upload_1&organism=Homo%20sapiens) | 4.91 | 2.65 | + | 2.60E-03 | 3.81E-02 | | [odontogenesis](http://amigo.geneontology.org/amigo/term/GO:0042476) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042476&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042476&list=upload_1&organism=Homo%20sapiens) | 7.45 | 2.28 | + | 2.90E-03 | 4.12E-02 | | [negative regulation of cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:1902807) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902807&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902807&list=upload_1&organism=Homo%20sapiens) | 4.97 | 2.62 | + | 2.85E-03 | 4.07E-02 | | [negative regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901988) | [224](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901988&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901988&list=upload_1&organism=Homo%20sapiens) | 13.25 | 2.34 | + | 4.64E-05 | 1.27E-03 | | [negative regulation of cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0010948) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010948&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010948&list=upload_1&organism=Homo%20sapiens) | 16.09 | 2.36 | + | 7.75E-06 | 2.62E-04 | | [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) | 11.48 | 2.61 | + | 1.05E-05 | 3.41E-04 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 18.52 | 2.27 | + | 5.90E-06 | 2.05E-04 | | [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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&list=upload_1&organism=Homo%20sapiens) | 19.58 | 2.14 | + | 1.79E-05 | 5.40E-04 | | [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) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&list=upload_1&organism=Homo%20sapiens) | 84.71 | 1.36 | + | 1.55E-03 | 2.49E-02 | | [response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009607) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&list=upload_1&organism=Homo%20sapiens) | 87.44 | 1.38 | + | 5.48E-04 | 1.05E-02 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 146.06 | 1.41 | + | 1.12E-06 | 4.52E-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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&list=upload_1&organism=Homo%20sapiens) | 84.54 | 1.35 | + | 2.25E-03 | 3.42E-02 | | [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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&list=upload_1&organism=Homo%20sapiens) | 12.07 | 2.49 | + | 2.06E-05 | 6.08E-04 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&list=upload_1&organism=Homo%20sapiens) | 13.67 | 2.63 | + | 1.09E-06 | 4.41E-05 | | [BMP signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030509) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030509&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030509&list=upload_1&organism=Homo%20sapiens) | 5.38 | 2.60 | + | 2.10E-03 | 3.25E-02 | | [cell fate specification](http://amigo.geneontology.org/amigo/term/GO:0001708) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001708&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001708&list=upload_1&organism=Homo%20sapiens) | 5.03 | 2.59 | + | 3.12E-03 | 4.38E-02 | | [cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0045165) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&list=upload_1&organism=Homo%20sapiens) | 14.79 | 2.10 | + | 3.24E-04 | 6.72E-03 | | [DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000077) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&list=upload_1&organism=Homo%20sapiens) | 6.21 | 2.58 | + | 1.15E-03 | 1.96E-02 | | [DNA integrity checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0031570) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031570&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031570&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.54 | + | 1.48E-03 | 2.41E-02 | | [cell cycle checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000075) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&list=upload_1&organism=Homo%20sapiens) | 9.29 | 2.15 | + | 2.58E-03 | 3.79E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&list=upload_1&organism=Homo%20sapiens) | 8.99 | 2.56 | + | 1.60E-04 | 3.66E-03 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071322&list=upload_1&organism=Homo%20sapiens) | 5.50 | 2.54 | + | 2.51E-03 | 3.70E-02 | | [response to carbohydrate](http://amigo.geneontology.org/amigo/term/GO:0009743) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.71 | + | 6.24E-06 | 2.16E-04 | | [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) | 7.51 | 2.53 | + | 7.28E-04 | 1.34E-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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043433&list=upload_1&organism=Homo%20sapiens) | 10.29 | 2.53 | + | 6.27E-05 | 1.63E-03 | | [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) | 25.91 | 2.70 | + | 2.58E-12 | 2.18E-10 | | [post-embryonic development](http://amigo.geneontology.org/amigo/term/GO:0009791) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009791&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009791&list=upload_1&organism=Homo%20sapiens) | 5.56 | 2.52 | + | 2.74E-03 | 3.97E-02 | | [cartilage development](http://amigo.geneontology.org/amigo/term/GO:0051216) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051216&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051216&list=upload_1&organism=Homo%20sapiens) | 9.94 | 2.52 | + | 9.23E-05 | 2.28E-03 | | [connective tissue development](http://amigo.geneontology.org/amigo/term/GO:0061448) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061448&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061448&list=upload_1&organism=Homo%20sapiens) | 13.19 | 2.20 | + | 2.45E-04 | 5.38E-03 | | [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) | 7.16 | 2.51 | + | 1.08E-03 | 1.87E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903322&list=upload_1&organism=Homo%20sapiens) | 8.28 | 2.54 | + | 3.48E-04 | 7.17E-03 | | [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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&list=upload_1&organism=Homo%20sapiens) | 14.97 | 2.61 | + | 4.52E-07 | 1.95E-05 | | [regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031396) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&list=upload_1&organism=Homo%20sapiens) | 12.48 | 2.40 | + | 4.76E-05 | 1.29E-03 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.51 | + | 1.08E-03 | 1.87E-02 | | [lung development](http://amigo.geneontology.org/amigo/term/GO:0030324) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.51 | + | 4.87E-05 | 1.32E-03 | | [respiratory tube development](http://amigo.geneontology.org/amigo/term/GO:0030323) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&list=upload_1&organism=Homo%20sapiens) | 11.00 | 2.45 | + | 6.44E-05 | 1.67E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&list=upload_1&organism=Homo%20sapiens) | 8.40 | 2.50 | + | 3.86E-04 | 7.80E-03 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&list=upload_1&organism=Homo%20sapiens) | 10.18 | 2.56 | + | 5.55E-05 | 1.47E-03 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&list=upload_1&organism=Homo%20sapiens) | 13.49 | 2.15 | + | 3.05E-04 | 6.46E-03 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061136&list=upload_1&organism=Homo%20sapiens) | 11.48 | 2.09 | + | 1.52E-03 | 2.46E-02 | | [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) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&list=upload_1&organism=Homo%20sapiens) | 21.71 | 1.89 | + | 2.81E-04 | 6.00E-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) | 8.40 | 2.50 | + | 3.86E-04 | 7.79E-03 | | [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) | 6.80 | 2.50 | + | 1.60E-03 | 2.55E-02 | | [hindbrain development](http://amigo.geneontology.org/amigo/term/GO:0030902) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&list=upload_1&organism=Homo%20sapiens) | 9.23 | 2.17 | + | 2.46E-03 | 3.66E-02 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 45.85 | 1.88 | + | 1.91E-07 | 8.75E-06 | | [hormone transport](http://amigo.geneontology.org/amigo/term/GO:0009914) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009914&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009914&list=upload_1&organism=Homo%20sapiens) | 6.03 | 2.49 | + | 3.38E-03 | 4.64E-02 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031333&list=upload_1&organism=Homo%20sapiens) | 8.46 | 2.48 | + | 4.08E-04 | 8.14E-03 | | [response to hydrogen peroxide](http://amigo.geneontology.org/amigo/term/GO:0042542) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&list=upload_1&organism=Homo%20sapiens) | 6.09 | 2.46 | + | 3.51E-03 | 4.80E-02 | | [regulation of cell cycle G2/M phase transition](http://amigo.geneontology.org/amigo/term/GO:1902749) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902749&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902749&list=upload_1&organism=Homo%20sapiens) | 6.51 | 2.46 | + | 2.47E-03 | 3.66E-02 | | [cytoplasmic translation](http://amigo.geneontology.org/amigo/term/GO:0002181) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&list=upload_1&organism=Homo%20sapiens) | 7.34 | 2.45 | + | 1.24E-03 | 2.08E-02 | | [negative regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903707) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903707&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903707&list=upload_1&organism=Homo%20sapiens) | 6.57 | 2.44 | + | 2.58E-03 | 3.79E-02 | | [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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002683&list=upload_1&organism=Homo%20sapiens) | 25.67 | 1.64 | + | 3.28E-03 | 4.56E-02 | | [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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&list=upload_1&organism=Homo%20sapiens) | 15.85 | 2.40 | + | 3.82E-06 | 1.39E-04 | | [response to retinoic acid](http://amigo.geneontology.org/amigo/term/GO:0032526) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032526&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032526&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.39 | + | 2.84E-03 | 4.06E-02 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&list=upload_1&organism=Homo%20sapiens) | 7.63 | 2.36 | + | 1.64E-03 | 2.62E-02 | | [response to ethanol](http://amigo.geneontology.org/amigo/term/GO:0045471) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045471&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045471&list=upload_1&organism=Homo%20sapiens) | 7.69 | 2.34 | + | 1.75E-03 | 2.77E-02 | | [response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097305) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&list=upload_1&organism=Homo%20sapiens) | 15.03 | 2.13 | + | 2.14E-04 | 4.77E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006261&list=upload_1&organism=Homo%20sapiens) | 8.22 | 2.31 | + | 1.45E-03 | 2.36E-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) | 12.13 | 2.31 | + | 1.34E-04 | 3.17E-03 | | [response to organophosphorus](http://amigo.geneontology.org/amigo/term/GO:0046683) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&list=upload_1&organism=Homo%20sapiens) | 7.81 | 2.31 | + | 1.98E-03 | 3.09E-02 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&list=upload_1&organism=Homo%20sapiens) | 8.70 | 2.30 | + | 1.13E-03 | 1.94E-02 | | [response to insulin](http://amigo.geneontology.org/amigo/term/GO:0032868) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&list=upload_1&organism=Homo%20sapiens) | 12.60 | 2.22 | + | 3.07E-04 | 6.47E-03 | | [response to peptide hormone](http://amigo.geneontology.org/amigo/term/GO:0043434) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&list=upload_1&organism=Homo%20sapiens) | 21.47 | 2.00 | + | 6.65E-05 | 1.71E-03 | | [response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901652) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&list=upload_1&organism=Homo%20sapiens) | 26.33 | 2.01 | + | 6.73E-06 | 2.32E-04 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071375&list=upload_1&organism=Homo%20sapiens) | 14.26 | 2.24 | + | 8.27E-05 | 2.06E-03 | | [cellular response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901653) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&list=upload_1&organism=Homo%20sapiens) | 17.92 | 2.18 | + | 2.35E-05 | 6.88E-04 | | [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) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 34.19 | 2.19 | + | 3.37E-09 | 1.97E-07 | | [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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 37.92 | 2.06 | + | 1.92E-08 | 1.03E-06 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&list=upload_1&organism=Homo%20sapiens) | 8.70 | 2.30 | + | 1.13E-03 | 1.94E-02 | | [epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050673) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050673&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050673&list=upload_1&organism=Homo%20sapiens) | 10.06 | 2.29 | + | 6.83E-04 | 1.28E-02 | | [regulation of tumor necrosis factor production](http://amigo.geneontology.org/amigo/term/GO:0032680) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032680&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032680&list=upload_1&organism=Homo%20sapiens) | 9.64 | 2.28 | + | 9.54E-04 | 1.71E-02 | | [regulation of tumor necrosis factor superfamily cytokine production](http://amigo.geneontology.org/amigo/term/GO:1903555) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903555&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903555&list=upload_1&organism=Homo%20sapiens) | 9.94 | 2.21 | + | 1.18E-03 | 2.01E-02 | | [regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001817) | [742](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&list=upload_1&organism=Homo%20sapiens) | 43.90 | 1.69 | + | 4.68E-05 | 1.28E-03 | | [synaptic vesicle cycle](http://amigo.geneontology.org/amigo/term/GO:0099504) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099504&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099504&list=upload_1&organism=Homo%20sapiens) | 7.45 | 2.28 | + | 2.90E-03 | 4.13E-02 | | [response to glucose](http://amigo.geneontology.org/amigo/term/GO:0009749) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&list=upload_1&organism=Homo%20sapiens) | 8.34 | 2.28 | + | 1.65E-03 | 2.62E-02 | | [response to hexose](http://amigo.geneontology.org/amigo/term/GO:0009746) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.20 | + | 3.01E-03 | 4.26E-02 | | [response to monosaccharide](http://amigo.geneontology.org/amigo/term/GO:0034284) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&list=upload_1&organism=Homo%20sapiens) | 9.11 | 2.31 | + | 1.26E-03 | 2.10E-02 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048639&list=upload_1&organism=Homo%20sapiens) | 9.70 | 2.27 | + | 9.91E-04 | 1.76E-02 | | [osteoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0001649) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&list=upload_1&organism=Homo%20sapiens) | 8.40 | 2.26 | + | 2.65E-03 | 3.85E-02 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030308&list=upload_1&organism=Homo%20sapiens) | 11.12 | 2.25 | + | 4.32E-04 | 8.54E-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) | 25.38 | 2.05 | + | 4.85E-06 | 1.72E-04 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051494&list=upload_1&organism=Homo%20sapiens) | 9.35 | 2.25 | + | 1.44E-03 | 2.36E-02 | | [regulation of cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0051493) | [540](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051493&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051493&list=upload_1&organism=Homo%20sapiens) | 31.95 | 1.75 | + | 1.32E-04 | 3.13E-03 | | [negative regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901991) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901991&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901991&list=upload_1&organism=Homo%20sapiens) | 9.82 | 2.24 | + | 1.08E-03 | 1.87E-02 | | [negative regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045930) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045930&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045930&list=upload_1&organism=Homo%20sapiens) | 12.60 | 2.14 | + | 5.46E-04 | 1.05E-02 | | [regulation of cell size](http://amigo.geneontology.org/amigo/term/GO:0008361) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008361&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008361&list=upload_1&organism=Homo%20sapiens) | 11.24 | 2.22 | + | 4.81E-04 | 9.37E-03 | | [regulation of cellular component size](http://amigo.geneontology.org/amigo/term/GO:0032535) | [372](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032535&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032535&list=upload_1&organism=Homo%20sapiens) | 22.01 | 1.82 | + | 6.95E-04 | 1.29E-02 | | [protein dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006470) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006470&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006470&list=upload_1&organism=Homo%20sapiens) | 10.83 | 2.22 | + | 6.58E-04 | 1.23E-02 | | [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) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 109.74 | 1.42 | + | 2.20E-05 | 6.48E-04 | | [phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006793) | [1881](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&reflist=1) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&list=upload_1&organism=Homo%20sapiens) | 111.28 | 1.41 | + | 3.08E-05 | 8.89E-04 | | [wound healing](http://amigo.geneontology.org/amigo/term/GO:0042060) | [338](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042060&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042060&list=upload_1&organism=Homo%20sapiens) | 20.00 | 2.20 | + | 5.03E-06 | 1.78E-04 | | [response to wounding](http://amigo.geneontology.org/amigo/term/GO:0009611) | [447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&list=upload_1&organism=Homo%20sapiens) | 26.44 | 2.31 | + | 2.08E-08 | 1.10E-06 | | [nucleus organization](http://amigo.geneontology.org/amigo/term/GO:0006997) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006997&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006997&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.20 | + | 3.01E-03 | 4.27E-02 | | [cellular response to starvation](http://amigo.geneontology.org/amigo/term/GO:0009267) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&list=upload_1&organism=Homo%20sapiens) | 10.53 | 2.18 | + | 1.00E-03 | 1.77E-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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&list=upload_1&organism=Homo%20sapiens) | 13.37 | 2.39 | + | 2.57E-05 | 7.46E-04 | | [response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031667) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&list=upload_1&organism=Homo%20sapiens) | 27.80 | 2.01 | + | 4.51E-06 | 1.62E-04 | | [response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0009991) | [500](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&list=upload_1&organism=Homo%20sapiens) | 29.58 | 2.03 | + | 1.40E-06 | 5.51E-05 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&list=upload_1&organism=Homo%20sapiens) | 15.14 | 2.31 | + | 2.48E-05 | 7.25E-04 | | [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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&list=upload_1&organism=Homo%20sapiens) | 19.23 | 2.03 | + | 1.13E-04 | 2.73E-03 | | [response to starvation](http://amigo.geneontology.org/amigo/term/GO:0042594) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&list=upload_1&organism=Homo%20sapiens) | 12.72 | 2.04 | + | 1.57E-03 | 2.52E-02 | | [peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018105) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&list=upload_1&organism=Homo%20sapiens) | 11.00 | 2.18 | + | 7.77E-04 | 1.43E-02 | | [peptidyl-serine modification](http://amigo.geneontology.org/amigo/term/GO:0018209) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&list=upload_1&organism=Homo%20sapiens) | 12.19 | 2.05 | + | 1.39E-03 | 2.29E-02 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 42.53 | 1.97 | + | 2.80E-08 | 1.46E-06 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 54.31 | 1.75 | + | 7.51E-07 | 3.12E-05 | | [protein stabilization](http://amigo.geneontology.org/amigo/term/GO:0050821) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.17 | + | 3.66E-04 | 7.46E-03 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 19.70 | 2.13 | + | 1.92E-05 | 5.73E-04 | | [response to nutrient](http://amigo.geneontology.org/amigo/term/GO:0007584) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&list=upload_1&organism=Homo%20sapiens) | 8.81 | 2.16 | + | 3.40E-03 | 4.66E-02 | | [positive regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045766) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&list=upload_1&organism=Homo%20sapiens) | 9.88 | 2.13 | + | 2.19E-03 | 3.34E-02 | | [regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045765) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&list=upload_1&organism=Homo%20sapiens) | 17.04 | 1.94 | + | 7.98E-04 | 1.46E-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) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&list=upload_1&organism=Homo%20sapiens) | 54.66 | 1.50 | + | 5.50E-04 | 1.06E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901342&list=upload_1&organism=Homo%20sapiens) | 17.27 | 1.91 | + | 8.94E-04 | 1.61E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904018&list=upload_1&organism=Homo%20sapiens) | 9.88 | 2.13 | + | 2.19E-03 | 3.34E-02 | | [gonad development](http://amigo.geneontology.org/amigo/term/GO:0008406) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&list=upload_1&organism=Homo%20sapiens) | 13.37 | 2.09 | + | 7.74E-04 | 1.42E-02 | | [development of primary sexual characteristics](http://amigo.geneontology.org/amigo/term/GO:0045137) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045137&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045137&list=upload_1&organism=Homo%20sapiens) | 13.67 | 2.05 | + | 8.85E-04 | 1.60E-02 | | [sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0007548) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&list=upload_1&organism=Homo%20sapiens) | 16.68 | 2.04 | + | 2.75E-04 | 5.88E-03 | | [response to mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0009612) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&list=upload_1&organism=Homo%20sapiens) | 12.90 | 2.09 | + | 6.86E-04 | 1.28E-02 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&list=upload_1&organism=Homo%20sapiens) | 10.53 | 2.09 | + | 2.69E-03 | 3.91E-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) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 42.24 | 2.01 | + | 1.01E-08 | 5.64E-07 | | [response to cytokine](http://amigo.geneontology.org/amigo/term/GO:0034097) | [808](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&list=upload_1&organism=Homo%20sapiens) | 47.80 | 1.92 | + | 1.83E-08 | 9.91E-07 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&list=upload_1&organism=Homo%20sapiens) | 11.95 | 2.01 | + | 3.03E-03 | 4.28E-02 | | [double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:0006302) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&list=upload_1&organism=Homo%20sapiens) | 12.01 | 2.08 | + | 1.21E-03 | 2.05E-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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&list=upload_1&organism=Homo%20sapiens) | 13.01 | 2.07 | + | 1.09E-03 | 1.89E-02 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060828&list=upload_1&organism=Homo%20sapiens) | 15.09 | 2.05 | + | 3.94E-04 | 7.94E-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) | 19.64 | 2.09 | + | 3.36E-05 | 9.60E-04 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043123&list=upload_1&organism=Homo%20sapiens) | 11.24 | 2.05 | + | 2.35E-03 | 3.53E-02 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043122&list=upload_1&organism=Homo%20sapiens) | 14.91 | 2.08 | + | 3.48E-04 | 7.18E-03 | | [ear development](http://amigo.geneontology.org/amigo/term/GO:0043583) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&list=upload_1&organism=Homo%20sapiens) | 13.72 | 2.04 | + | 9.15E-04 | 1.64E-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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 25.02 | 2.04 | + | 6.83E-06 | 2.35E-04 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 10.83 | 2.03 | + | 3.20E-03 | 4.47E-02 | | [epidermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0009913) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009913&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009913&list=upload_1&organism=Homo%20sapiens) | 11.89 | 2.02 | + | 2.97E-03 | 4.22E-02 | | [tissue homeostasis](http://amigo.geneontology.org/amigo/term/GO:0001894) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&list=upload_1&organism=Homo%20sapiens) | 14.49 | 2.00 | + | 1.24E-03 | 2.08E-02 | | [multicellular organismal homeostasis](http://amigo.geneontology.org/amigo/term/GO:0048871) | [380](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&list=upload_1&organism=Homo%20sapiens) | 22.48 | 1.69 | + | 3.41E-03 | 4.67E-02 | | [anatomical structure homeostasis](http://amigo.geneontology.org/amigo/term/GO:0060249) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&list=upload_1&organism=Homo%20sapiens) | 17.92 | 2.06 | + | 1.09E-04 | 2.65E-03 | | [lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0030098) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&list=upload_1&organism=Homo%20sapiens) | 16.56 | 1.99 | + | 4.42E-04 | 8.70E-03 | | [mononuclear cell differentiation](http://amigo.geneontology.org/amigo/term/GO:1903131) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&list=upload_1&organism=Homo%20sapiens) | 19.29 | 2.18 | + | 1.03E-05 | 3.36E-04 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 23.66 | 1.94 | + | 6.17E-05 | 1.61E-03 | | [lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0046649) | [465](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&list=upload_1&organism=Homo%20sapiens) | 27.51 | 1.64 | + | 2.37E-03 | 3.56E-02 | | [leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0045321) | [581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&list=upload_1&organism=Homo%20sapiens) | 34.37 | 1.60 | + | 1.50E-03 | 2.42E-02 | | [cell activation](http://amigo.geneontology.org/amigo/term/GO:0001775) | [700](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&list=upload_1&organism=Homo%20sapiens) | 41.41 | 1.67 | + | 1.11E-04 | 2.69E-03 | | [response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901654) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&list=upload_1&organism=Homo%20sapiens) | 12.19 | 1.97 | + | 3.36E-03 | 4.62E-02 | | [forebrain development](http://amigo.geneontology.org/amigo/term/GO:0030900) | [388](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&list=upload_1&organism=Homo%20sapiens) | 22.95 | 1.92 | + | 1.18E-04 | 2.83E-03 | | [cell division](http://amigo.geneontology.org/amigo/term/GO:0051301) | [514](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&list=upload_1&organism=Homo%20sapiens) | 30.41 | 1.91 | + | 1.15E-05 | 3.70E-04 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033157&list=upload_1&organism=Homo%20sapiens) | 13.67 | 1.90 | + | 3.61E-03 | 4.94E-02 | | [response to virus](http://amigo.geneontology.org/amigo/term/GO:0009615) | [357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&list=upload_1&organism=Homo%20sapiens) | 21.12 | 1.89 | + | 3.50E-04 | 7.19E-03 | | [cytokine-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0019221) | [366](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&list=upload_1&organism=Homo%20sapiens) | 21.65 | 1.89 | + | 2.74E-04 | 5.88E-03 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001818&list=upload_1&organism=Homo%20sapiens) | 16.92 | 1.89 | + | 1.24E-03 | 2.08E-02 | | [kidney development](http://amigo.geneontology.org/amigo/term/GO:0001822) | [299](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&list=upload_1&organism=Homo%20sapiens) | 17.69 | 1.87 | + | 1.51E-03 | 2.45E-02 | | [renal system development](http://amigo.geneontology.org/amigo/term/GO:0072001) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&list=upload_1&organism=Homo%20sapiens) | 18.22 | 1.81 | + | 2.65E-03 | 3.85E-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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 28.45 | 1.86 | + | 5.12E-05 | 1.37E-03 | | [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) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031331&list=upload_1&organism=Homo%20sapiens) | 24.31 | 1.81 | + | 4.00E-04 | 8.00E-03 | | [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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009896&list=upload_1&organism=Homo%20sapiens) | 30.35 | 1.68 | + | 7.52E-04 | 1.38E-02 | | [regulation of neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0010975) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010975&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010975&list=upload_1&organism=Homo%20sapiens) | 26.33 | 1.79 | + | 3.18E-04 | 6.63E-03 | | [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) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&list=upload_1&organism=Homo%20sapiens) | 37.86 | 1.64 | + | 4.10E-04 | 8.17E-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) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&list=upload_1&organism=Homo%20sapiens) | 38.81 | 1.62 | + | 4.80E-04 | 9.35E-03 | | [regulation of inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0050727) | [372](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&list=upload_1&organism=Homo%20sapiens) | 22.01 | 1.77 | + | 1.48E-03 | 2.41E-02 | | [regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031347) | [642](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&list=upload_1&organism=Homo%20sapiens) | 37.98 | 1.63 | + | 4.19E-04 | 8.34E-03 | | [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) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&list=upload_1&organism=Homo%20sapiens) | 57.56 | 1.67 | + | 4.07E-06 | 1.47E-04 | | [inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0006954) | [540](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&list=upload_1&organism=Homo%20sapiens) | 31.95 | 1.75 | + | 1.32E-04 | 3.14E-03 | | [defense response](http://amigo.geneontology.org/amigo/term/GO:0006952) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&reflist=1) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&list=upload_1&organism=Homo%20sapiens) | 87.44 | 1.35 | + | 1.80E-03 | 2.83E-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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&list=upload_1&organism=Homo%20sapiens) | 20.76 | 1.73 | + | 3.37E-03 | 4.63E-02 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&list=upload_1&organism=Homo%20sapiens) | 23.13 | 1.73 | + | 1.92E-03 | 3.01E-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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&list=upload_1&organism=Homo%20sapiens) | 31.47 | 1.68 | + | 4.95E-04 | 9.56E-03 | | [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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&list=upload_1&organism=Homo%20sapiens) | 33.01 | 1.67 | + | 6.35E-04 | 1.19E-02 | | [positive regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040017) | [574](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&list=upload_1&organism=Homo%20sapiens) | 33.96 | 1.65 | + | 5.64E-04 | 1.08E-02 | | [cell surface receptor signaling pathway involved in cell-cell signaling](http://amigo.geneontology.org/amigo/term/GO:1905114) | [383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905114&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905114&list=upload_1&organism=Homo%20sapiens) | 22.66 | 1.68 | + | 3.58E-03 | 4.90E-02 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&list=upload_1&organism=Homo%20sapiens) | 26.92 | 1.67 | + | 1.54E-03 | 2.48E-02 | | [blood vessel development](http://amigo.geneontology.org/amigo/term/GO:0001568) | [510](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001568&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001568&list=upload_1&organism=Homo%20sapiens) | 30.17 | 1.66 | + | 1.04E-03 | 1.81E-02 | | [regulation of membrane potential](http://amigo.geneontology.org/amigo/term/GO:0042391) | [430](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042391&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042391&list=upload_1&organism=Homo%20sapiens) | 25.44 | 1.65 | + | 3.07E-03 | 4.33E-02 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&list=upload_1&organism=Homo%20sapiens) | 27.75 | 1.62 | + | 3.31E-03 | 4.60E-02 | | [protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0030163) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&list=upload_1&organism=Homo%20sapiens) | 44.72 | 1.59 | + | 3.53E-04 | 7.25E-03 | | [organonitrogen compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901565) | [1112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&list=upload_1&organism=Homo%20sapiens) | 65.78 | 1.52 | + | 8.12E-05 | 2.03E-03 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 53.42 | 1.44 | + | 2.69E-03 | 3.91E-02 | | [G protein-coupled receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007186) | [1223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007186&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007186&list=upload_1&organism=Homo%20sapiens) | 72.35 | .53 | - | 1.20E-05 | 3.81E-04 | | [detection of chemical stimulus involved in sensory perception of smell](http://amigo.geneontology.org/amigo/term/GO:0050911) | [443](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050911&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050911&list=upload_1&organism=Homo%20sapiens) | 26.21 | .38 | - | 5.95E-04 | 1.13E-02 | | [detection of chemical stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050907) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050907&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050907&list=upload_1&organism=Homo%20sapiens) | 28.93 | .35 | - | 1.05E-04 | 2.55E-03 | | [detection of stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050906) | [560](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050906&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050906&list=upload_1&organism=Homo%20sapiens) | 33.13 | .42 | - | 4.15E-04 | 8.27E-03 | | [detection of chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0009593) | [526](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009593&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009593&list=upload_1&organism=Homo%20sapiens) | 31.12 | .45 | - | 1.16E-03 | 1.98E-02 | | [sensory perception of chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0007606) | [551](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007606&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007606&list=upload_1&organism=Homo%20sapiens) | 32.60 | .37 | - | 8.08E-05 | 2.02E-03 | | [sensory perception of smell](http://amigo.geneontology.org/amigo/term/GO:0007608) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007608&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007608&list=upload_1&organism=Homo%20sapiens) | 27.80 | .40 | - | 5.86E-04 | 1.12E-02 | | Unclassified | [2725](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&list=upload_1&organism=Homo%20sapiens) | 161.21 | .23 | - | 1.45E-33 | 3.66E-31 | | [mitochondrial translation](http://amigo.geneontology.org/amigo/term/GO:0032543) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032543&reflist=1) | [0](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032543&list=upload_1&organism=Homo%20sapiens) | 6.51 | < 0.01 | - | 2.95E-03 | 4.19E-02 | |

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