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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 | [509](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 886 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [543](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [426](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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| |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | |  | [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) | | [negative regulation of chromosome condensation](http://amigo.geneontology.org/amigo/term/GO:1902340) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902340&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902340&list=upload_1&organism=Homo%20sapiens) | .13 | 23.24 | + | 1.27E-03 | 3.03E-02 | | [regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0033044) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 10.84 | 2.95 | + | 2.81E-07 | 2.07E-05 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 51.17 | 1.50 | + | 5.95E-04 | 1.66E-02 | | [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) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 101.73 | 1.69 | + | 2.92E-11 | 3.85E-09 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [647](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 481.41 | 1.34 | + | 4.42E-29 | 1.48E-26 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [675](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 508.04 | 1.33 | + | 1.87E-30 | 6.37E-28 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [709](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 539.80 | 1.31 | + | 6.98E-33 | 2.61E-30 | | [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) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 29.69 | 2.02 | + | 1.29E-06 | 8.22E-05 | | [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) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 203.63 | 1.89 | + | 5.36E-39 | 4.20E-36 | | [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) | [406](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 228.68 | 1.78 | + | 6.12E-36 | 3.20E-33 | | [negative regulation of calcium ion export across plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1905913) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905913&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905913&list=upload_1&organism=Homo%20sapiens) | .17 | 23.24 | + | 1.76E-04 | 6.02E-03 | | [regulation of calcium ion export across plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1905912) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905912&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905912&list=upload_1&organism=Homo%20sapiens) | .17 | 23.24 | + | 1.76E-04 | 6.01E-03 | | [response to fungicide](http://amigo.geneontology.org/amigo/term/GO:0060992) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060992&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060992&list=upload_1&organism=Homo%20sapiens) | .17 | 23.24 | + | 1.76E-04 | 6.00E-03 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 174.71 | 1.56 | + | 1.82E-14 | 3.49E-12 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [479](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 353.26 | 1.36 | + | 7.94E-17 | 1.89E-14 | | [response to antibiotic](http://amigo.geneontology.org/amigo/term/GO:0046677) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046677&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046677&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.27 | + | 5.76E-04 | 1.62E-02 | | [positive regulation of histone H4 acetylation](http://amigo.geneontology.org/amigo/term/GO:0090240) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090240&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090240&list=upload_1&organism=Homo%20sapiens) | .30 | 19.92 | + | 6.49E-06 | 3.41E-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) | .60 | 9.96 | + | 1.14E-04 | 4.24E-03 | | [regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035065) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&list=upload_1&organism=Homo%20sapiens) | 2.93 | 7.18 | + | 6.08E-11 | 7.62E-09 | | [regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031056) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&list=upload_1&organism=Homo%20sapiens) | 7.79 | 5.78 | + | 9.03E-19 | 2.62E-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) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 67.26 | 2.14 | + | 7.13E-17 | 1.72E-14 | | [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) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&list=upload_1&organism=Homo%20sapiens) | 111.33 | 1.84 | + | 3.61E-17 | 8.99E-15 | | [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) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 252.69 | 1.78 | + | 9.24E-42 | 1.04E-38 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 290.64 | 1.70 | + | 2.62E-42 | 5.13E-39 | | [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) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 267.41 | 1.76 | + | 1.88E-43 | 7.38E-40 | | [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) | [443](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 245.67 | 1.80 | + | 1.64E-42 | 3.68E-39 | | [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) | 3.31 | 7.24 | + | 2.22E-12 | 3.35E-10 | | [regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901983) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&list=upload_1&organism=Homo%20sapiens) | 3.83 | 6.53 | + | 5.28E-12 | 7.52E-10 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&list=upload_1&organism=Homo%20sapiens) | 1.59 | 8.79 | + | 1.16E-08 | 1.07E-06 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&list=upload_1&organism=Homo%20sapiens) | 1.85 | 8.65 | + | 1.28E-09 | 1.33E-07 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&list=upload_1&organism=Homo%20sapiens) | 2.28 | 7.45 | + | 2.51E-09 | 2.53E-07 | | [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) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 43.85 | 2.10 | + | 1.70E-10 | 1.97E-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) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 65.19 | 1.95 | + | 3.93E-12 | 5.75E-10 | | [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) | [287](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 136.59 | 2.10 | + | 1.98E-34 | 8.39E-32 | | [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) | [327](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 166.02 | 1.97 | + | 5.45E-35 | 2.67E-32 | | [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) | [429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 271.28 | 1.58 | + | 3.15E-27 | 9.88E-25 | | [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) | [310](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 152.42 | 2.03 | + | 2.84E-35 | 1.44E-32 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 4.60 | 6.73 | + | 7.33E-15 | 1.53E-12 | | [C-5 methylation of cytosine](http://amigo.geneontology.org/amigo/term/GO:0090116) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090116&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090116&list=upload_1&organism=Homo%20sapiens) | .22 | 18.59 | + | 3.07E-04 | 9.63E-03 | | [DNA methylation on cytosine](http://amigo.geneontology.org/amigo/term/GO:0032776) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032776&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032776&list=upload_1&organism=Homo%20sapiens) | .30 | 16.60 | + | 7.35E-05 | 2.89E-03 | | [DNA methylation](http://amigo.geneontology.org/amigo/term/GO:0006306) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006306&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006306&list=upload_1&organism=Homo%20sapiens) | 2.45 | 4.89 | + | 2.28E-05 | 1.05E-03 | | [DNA methylation or demethylation](http://amigo.geneontology.org/amigo/term/GO:0044728) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044728&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044728&list=upload_1&organism=Homo%20sapiens) | 3.27 | 3.67 | + | 2.59E-04 | 8.41E-03 | | [DNA modification](http://amigo.geneontology.org/amigo/term/GO:0006304) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006304&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006304&list=upload_1&organism=Homo%20sapiens) | 4.30 | 3.49 | + | 7.75E-05 | 3.03E-03 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [196](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 124.06 | 1.58 | + | 2.05E-10 | 2.35E-08 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [380](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 255.66 | 1.49 | + | 3.85E-18 | 1.08E-15 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [446](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 331.22 | 1.35 | + | 2.13E-14 | 3.98E-12 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 349.90 | 1.31 | + | 2.59E-13 | 4.57E-11 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 34.17 | 2.14 | + | 7.79E-09 | 7.50E-07 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 108.36 | 1.52 | + | 1.03E-07 | 8.35E-06 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [389](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 284.27 | 1.37 | + | 7.33E-13 | 1.22E-10 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [770](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 647.38 | 1.19 | + | 1.72E-22 | 5.08E-20 | | [nucleic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090304) | [2276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&reflist=1) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 97.94 | 1.83 | + | 1.41E-14 | 2.73E-12 | | [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) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 121.57 | 1.65 | + | 3.47E-12 | 5.18E-10 | | [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) | [227](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 141.66 | 1.60 | + | 8.98E-13 | 1.47E-10 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 129.06 | 1.60 | + | 1.17E-11 | 1.61E-09 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [418](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 311.04 | 1.34 | + | 6.03E-13 | 1.03E-10 | | [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) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 131.25 | 1.62 | + | 2.02E-12 | 3.11E-10 | | [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) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 153.76 | 1.50 | + | 2.51E-10 | 2.83E-08 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 288.75 | 1.39 | + | 3.27E-14 | 6.03E-12 | | [DNA alkylation](http://amigo.geneontology.org/amigo/term/GO:0006305) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006305&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006305&list=upload_1&organism=Homo%20sapiens) | 2.45 | 4.89 | + | 2.28E-05 | 1.05E-03 | | [macromolecule methylation](http://amigo.geneontology.org/amigo/term/GO:0043414) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&list=upload_1&organism=Homo%20sapiens) | 12.05 | 2.82 | + | 3.09E-07 | 2.27E-05 | | [methylation](http://amigo.geneontology.org/amigo/term/GO:0032259) | [329](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032259&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032259&list=upload_1&organism=Homo%20sapiens) | 14.16 | 2.54 | + | 1.52E-06 | 9.59E-05 | | [cellular heat acclimation](http://amigo.geneontology.org/amigo/term/GO:0070370) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070370&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070370&list=upload_1&organism=Homo%20sapiens) | .22 | 18.59 | + | 3.07E-04 | 9.61E-03 | | [heat acclimation](http://amigo.geneontology.org/amigo/term/GO:0010286) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010286&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010286&list=upload_1&organism=Homo%20sapiens) | .22 | 18.59 | + | 3.07E-04 | 9.65E-03 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [244](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 149.15 | 1.64 | + | 7.38E-15 | 1.52E-12 | | [response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009628) | [1121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&list=upload_1&organism=Homo%20sapiens) | 48.24 | 2.28 | + | 1.28E-14 | 2.51E-12 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 68.81 | 2.14 | + | 4.80E-17 | 1.18E-14 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [390](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 282.68 | 1.38 | + | 1.75E-13 | 3.15E-11 | | [maintenance of mitotic sister chromatid cohesion](http://amigo.geneontology.org/amigo/term/GO:0034088) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034088&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034088&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.72E-02 | | [maintenance of sister chromatid cohesion](http://amigo.geneontology.org/amigo/term/GO:0034086) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034086&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034086&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.72E-02 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 36.19 | 2.13 | + | 4.22E-09 | 4.16E-07 | | [cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007049) | [1249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&list=upload_1&organism=Homo%20sapiens) | 53.75 | 2.25 | + | 1.52E-15 | 3.35E-13 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 19.11 | 2.09 | + | 3.75E-05 | 1.61E-03 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [354](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 237.67 | 1.49 | + | 1.51E-16 | 3.48E-14 | | [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) | [357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 246.45 | 1.45 | + | 5.60E-15 | 1.20E-12 | | [mitotic cell cycle process](http://amigo.geneontology.org/amigo/term/GO:1903047) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&list=upload_1&organism=Homo%20sapiens) | 22.94 | 2.66 | + | 6.56E-11 | 8.10E-09 | | [mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000278) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&list=upload_1&organism=Homo%20sapiens) | 26.98 | 2.52 | + | 4.10E-11 | 5.32E-09 | | [mitotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0140014) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&list=upload_1&organism=Homo%20sapiens) | 7.44 | 2.42 | + | 1.28E-03 | 3.05E-02 | | [histone H4 deacetylation](http://amigo.geneontology.org/amigo/term/GO:0070933) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&list=upload_1&organism=Homo%20sapiens) | .34 | 17.43 | + | 1.10E-05 | 5.51E-04 | | [histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0016575) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&list=upload_1&organism=Homo%20sapiens) | 2.58 | 6.20 | + | 6.54E-08 | 5.31E-06 | | [histone modification](http://amigo.geneontology.org/amigo/term/GO:0016570) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&list=upload_1&organism=Homo%20sapiens) | 15.71 | 4.01 | + | 1.20E-18 | 3.42E-16 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 114.38 | 1.59 | + | 6.85E-10 | 7.51E-08 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 168.69 | 1.36 | + | 1.31E-06 | 8.28E-05 | | [organonitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901564) | [5013](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&reflist=1) | [278](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 215.72 | 1.29 | + | 3.68E-06 | 2.06E-04 | | [protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0006476) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&list=upload_1&organism=Homo%20sapiens) | 2.75 | 5.81 | + | 1.39E-07 | 1.09E-05 | | [protein deacylation](http://amigo.geneontology.org/amigo/term/GO:0035601) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&list=upload_1&organism=Homo%20sapiens) | 3.23 | 4.96 | + | 8.81E-07 | 5.98E-05 | | [macromolecule deacylation](http://amigo.geneontology.org/amigo/term/GO:0098732) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&list=upload_1&organism=Homo%20sapiens) | 3.40 | 4.71 | + | 1.60E-06 | 1.00E-04 | | [protein localization to CENP-A containing chromatin](http://amigo.geneontology.org/amigo/term/GO:0061644) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061644&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061644&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.71E-02 | | [protein localization to chromatin](http://amigo.geneontology.org/amigo/term/GO:0071168) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071168&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071168&list=upload_1&organism=Homo%20sapiens) | 1.29 | 5.42 | + | 6.92E-04 | 1.88E-02 | | [protein localization to chromosome](http://amigo.geneontology.org/amigo/term/GO:0034502) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&list=upload_1&organism=Homo%20sapiens) | 3.23 | 4.03 | + | 6.29E-05 | 2.53E-03 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 29.86 | 1.81 | + | 7.17E-05 | 2.83E-03 | | [protein localization to chromosome, centromeric region](http://amigo.geneontology.org/amigo/term/GO:0071459) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071459&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071459&list=upload_1&organism=Homo%20sapiens) | 1.08 | 7.44 | + | 4.50E-05 | 1.87E-03 | | [cellular response to bisphenol A](http://amigo.geneontology.org/amigo/term/GO:1903926) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903926&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903926&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.70E-02 | | [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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 22.12 | 2.67 | + | 1.29E-10 | 1.53E-08 | | [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) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 87.18 | 1.86 | + | 8.50E-14 | 1.55E-11 | | [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) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 112.57 | 1.70 | + | 9.53E-13 | 1.54E-10 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 116.36 | 1.82 | + | 2.44E-17 | 6.16E-15 | | [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) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 37.83 | 2.38 | + | 5.22E-13 | 9.09E-11 | | [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) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&list=upload_1&organism=Homo%20sapiens) | 45.57 | 2.06 | + | 2.26E-10 | 2.57E-08 | | [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) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 66.74 | 1.93 | + | 4.23E-12 | 6.15E-10 | | [response to bisphenol A](http://amigo.geneontology.org/amigo/term/GO:1903925) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903925&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903925&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.70E-02 | | [actin filament fragmentation](http://amigo.geneontology.org/amigo/term/GO:0030043) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030043&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030043&list=upload_1&organism=Homo%20sapiens) | .17 | 17.43 | + | 2.16E-03 | 4.69E-02 | | [protein-containing complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032984) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&list=upload_1&organism=Homo%20sapiens) | 5.77 | 2.95 | + | 1.70E-04 | 5.84E-03 | | [cellular component disassembly](http://amigo.geneontology.org/amigo/term/GO:0022411) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&list=upload_1&organism=Homo%20sapiens) | 13.68 | 2.27 | + | 6.12E-05 | 2.47E-03 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 61.24 | 1.80 | + | 1.06E-08 | 9.81E-07 | | [maintenance of DNA methylation](http://amigo.geneontology.org/amigo/term/GO:0010216) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010216&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010216&list=upload_1&organism=Homo%20sapiens) | .30 | 13.28 | + | 7.53E-04 | 2.02E-02 | | [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) | .30 | 13.28 | + | 7.53E-04 | 2.02E-02 | | [facultative heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0140718) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&list=upload_1&organism=Homo%20sapiens) | .56 | 12.51 | + | 9.61E-06 | 4.89E-04 | | [heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0031507) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031507&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031507&list=upload_1&organism=Homo%20sapiens) | 2.24 | 7.15 | + | 1.21E-08 | 1.10E-06 | | [heterochromatin organization](http://amigo.geneontology.org/amigo/term/GO:0070828) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070828&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070828&list=upload_1&organism=Homo%20sapiens) | 2.67 | 7.50 | + | 9.11E-11 | 1.10E-08 | | [chromatin remodeling](http://amigo.geneontology.org/amigo/term/GO:0006338) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&list=upload_1&organism=Homo%20sapiens) | 13.90 | 5.76 | + | 1.85E-32 | 6.61E-30 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006325) | [585](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&list=upload_1&organism=Homo%20sapiens) | 25.17 | 4.61 | + | 8.63E-39 | 6.45E-36 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045814&list=upload_1&organism=Homo%20sapiens) | 2.84 | 5.63 | + | 2.00E-07 | 1.51E-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) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 38.82 | 1.93 | + | 2.32E-07 | 1.72E-05 | | [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) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 118.94 | 2.30 | + | 1.16E-38 | 8.26E-36 | | [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) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 128.58 | 2.19 | + | 1.89E-36 | 1.06E-33 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [392](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 208.92 | 1.88 | + | 1.47E-39 | 1.22E-36 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040029&list=upload_1&organism=Homo%20sapiens) | 5.08 | 5.32 | + | 4.30E-11 | 5.52E-09 | | [negative regulation of histone H3-K9 trimethylation](http://amigo.geneontology.org/amigo/term/GO:1900113) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900113&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900113&list=upload_1&organism=Homo%20sapiens) | .30 | 13.28 | + | 7.53E-04 | 2.01E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051573&list=upload_1&organism=Homo%20sapiens) | .56 | 14.30 | + | 1.03E-06 | 6.78E-05 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051570&list=upload_1&organism=Homo%20sapiens) | 1.16 | 12.91 | + | 5.28E-11 | 6.68E-09 | | [regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031060) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&list=upload_1&organism=Homo%20sapiens) | 3.61 | 7.75 | + | 8.10E-15 | 1.65E-12 | | [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) | [439](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 243.01 | 1.81 | + | 4.39E-42 | 6.25E-39 | | [negative regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031061) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031061&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031061&list=upload_1&organism=Homo%20sapiens) | 1.08 | 8.37 | + | 6.88E-06 | 3.58E-04 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031057&list=upload_1&organism=Homo%20sapiens) | 2.11 | 5.22 | + | 2.98E-05 | 1.33E-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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 21.65 | 2.13 | + | 5.74E-06 | 3.06E-04 | | [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) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 44.84 | 1.67 | + | 3.68E-05 | 1.59E-03 | | [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) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 103.67 | 2.45 | + | 5.38E-40 | 5.63E-37 | | [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) | [241](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 97.43 | 2.47 | + | 1.92E-38 | 1.21E-35 | | [regulation of histone H3-K9 trimethylation](http://amigo.geneontology.org/amigo/term/GO:1900112) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900112&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900112&list=upload_1&organism=Homo%20sapiens) | .56 | 12.51 | + | 9.61E-06 | 4.86E-04 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006336) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006336&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006336&list=upload_1&organism=Homo%20sapiens) | .56 | 12.51 | + | 9.61E-06 | 4.88E-04 | | [regulation of DNA-templated DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:0030174) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&list=upload_1&organism=Homo%20sapiens) | .65 | 12.39 | + | 2.30E-06 | 1.36E-04 | | [regulation of DNA-templated DNA replication](http://amigo.geneontology.org/amigo/term/GO:0090329) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090329&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090329&list=upload_1&organism=Homo%20sapiens) | 2.45 | 5.30 | + | 4.93E-06 | 2.67E-04 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 5.85 | 3.42 | + | 6.90E-06 | 3.58E-04 | | [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) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 23.28 | 2.62 | + | 1.04E-10 | 1.24E-08 | | [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) | [356](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 175.01 | 2.03 | + | 6.20E-42 | 8.11E-39 | | [positive regulation of histone H3-K9 acetylation](http://amigo.geneontology.org/amigo/term/GO:2000617) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000617&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000617&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.73E-02 | | [regulation of histone H3-K9 acetylation](http://amigo.geneontology.org/amigo/term/GO:2000615) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000615&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000615&list=upload_1&organism=Homo%20sapiens) | .56 | 10.73 | + | 8.29E-05 | 3.19E-03 | | [positive regulation of attachment of mitotic spindle microtubules to kinetochore](http://amigo.geneontology.org/amigo/term/GO:1902425) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902425&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902425&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.73E-02 | | [regulation of attachment of mitotic spindle microtubules to kinetochore](http://amigo.geneontology.org/amigo/term/GO:1902423) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902423&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902423&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.72E-02 | | [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) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 30.77 | 2.50 | + | 3.53E-12 | 5.22E-10 | | [regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051726) | [1122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 48.28 | 2.30 | + | 6.87E-15 | 1.46E-12 | | [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) | [402](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 244.00 | 1.65 | + | 2.53E-28 | 8.10E-26 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 15.19 | 2.24 | + | 4.22E-05 | 1.79E-03 | | [transcription initiation at RNA polymerase III promoter](http://amigo.geneontology.org/amigo/term/GO:0006384) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006384&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006384&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.72E-02 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 26.38 | 3.11 | + | 7.32E-18 | 2.01E-15 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 26.42 | 3.10 | + | 7.98E-18 | 2.16E-15 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 26.85 | 3.05 | + | 1.88E-17 | 4.91E-15 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 63.99 | 1.78 | + | 9.45E-09 | 8.93E-07 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 109.04 | 1.37 | + | 1.46E-04 | 5.13E-03 | | [biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009058) | [2603](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&reflist=1) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&list=upload_1&organism=Homo%20sapiens) | 112.01 | 1.37 | + | 1.14E-04 | 4.27E-03 | | [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) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 43.33 | 2.17 | + | 1.68E-11 | 2.25E-09 | | [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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 68.34 | 1.67 | + | 2.22E-07 | 1.66E-05 | | [cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044249) | [2464](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&reflist=1) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&list=upload_1&organism=Homo%20sapiens) | 106.03 | 1.38 | + | 1.21E-04 | 4.44E-03 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 46.43 | 2.09 | + | 6.80E-11 | 8.34E-09 | | [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) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 52.33 | 2.01 | + | 7.26E-11 | 8.83E-09 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 46.86 | 2.09 | + | 4.93E-11 | 6.29E-09 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 70.36 | 1.73 | + | 9.34E-09 | 8.88E-07 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 99.58 | 1.67 | + | 1.73E-10 | 2.00E-08 | | [DNA replication-dependent chromatin assembly](http://amigo.geneontology.org/amigo/term/GO:0006335) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006335&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006335&list=upload_1&organism=Homo%20sapiens) | .43 | 11.62 | + | 2.51E-04 | 8.19E-03 | | [histone H3-K27 methylation](http://amigo.geneontology.org/amigo/term/GO:0070734) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070734&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070734&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.71E-02 | | [histone lysine methylation](http://amigo.geneontology.org/amigo/term/GO:0034968) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034968&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034968&list=upload_1&organism=Homo%20sapiens) | 3.31 | 4.53 | + | 5.11E-06 | 2.76E-04 | | [histone methylation](http://amigo.geneontology.org/amigo/term/GO:0016571) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016571&list=upload_1&organism=Homo%20sapiens) | 4.65 | 4.73 | + | 1.70E-08 | 1.52E-06 | | [protein methylation](http://amigo.geneontology.org/amigo/term/GO:0006479) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006479&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006479&list=upload_1&organism=Homo%20sapiens) | 6.41 | 3.59 | + | 6.85E-07 | 4.77E-05 | | [protein alkylation](http://amigo.geneontology.org/amigo/term/GO:0008213) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008213&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008213&list=upload_1&organism=Homo%20sapiens) | 6.41 | 3.59 | + | 6.85E-07 | 4.75E-05 | | [peptidyl-lysine methylation](http://amigo.geneontology.org/amigo/term/GO:0018022) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018022&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018022&list=upload_1&organism=Homo%20sapiens) | 3.92 | 3.83 | + | 2.96E-05 | 1.32E-03 | | [peptidyl-lysine modification](http://amigo.geneontology.org/amigo/term/GO:0018205) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&list=upload_1&organism=Homo%20sapiens) | 13.38 | 2.54 | + | 3.10E-06 | 1.78E-04 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 37.95 | 2.00 | + | 4.39E-08 | 3.68E-06 | | [histone H3-K36 demethylation](http://amigo.geneontology.org/amigo/term/GO:0070544) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070544&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070544&list=upload_1&organism=Homo%20sapiens) | .43 | 11.62 | + | 2.51E-04 | 8.17E-03 | | [histone lysine demethylation](http://amigo.geneontology.org/amigo/term/GO:0070076) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&list=upload_1&organism=Homo%20sapiens) | 1.20 | 8.30 | + | 2.24E-06 | 1.35E-04 | | [histone demethylation](http://amigo.geneontology.org/amigo/term/GO:0016577) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&list=upload_1&organism=Homo%20sapiens) | 1.25 | 8.01 | + | 2.90E-06 | 1.68E-04 | | [protein demethylation](http://amigo.geneontology.org/amigo/term/GO:0006482) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006482&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006482&list=upload_1&organism=Homo%20sapiens) | 1.38 | 7.26 | + | 6.01E-06 | 3.19E-04 | | [protein dealkylation](http://amigo.geneontology.org/amigo/term/GO:0008214) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008214&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008214&list=upload_1&organism=Homo%20sapiens) | 1.38 | 7.26 | + | 6.01E-06 | 3.18E-04 | | [demethylation](http://amigo.geneontology.org/amigo/term/GO:0070988) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070988&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070988&list=upload_1&organism=Homo%20sapiens) | 2.75 | 3.99 | + | 2.43E-04 | 7.94E-03 | | [tRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0009304) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009304&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009304&list=upload_1&organism=Homo%20sapiens) | .34 | 11.62 | + | 1.09E-03 | 2.71E-02 | | [ncRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0098781) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098781&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098781&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.43 | + | 9.37E-04 | 2.40E-02 | | [histone H3-K9 methylation](http://amigo.geneontology.org/amigo/term/GO:0051567) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051567&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051567&list=upload_1&organism=Homo%20sapiens) | .56 | 10.73 | + | 8.29E-05 | 3.18E-03 | | [histone H3-K9 modification](http://amigo.geneontology.org/amigo/term/GO:0061647) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061647&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061647&list=upload_1&organism=Homo%20sapiens) | .69 | 10.17 | + | 2.73E-05 | 1.23E-03 | | [positive regulation of histone H3-K9 methylation](http://amigo.geneontology.org/amigo/term/GO:0051574) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051574&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051574&list=upload_1&organism=Homo%20sapiens) | .47 | 10.56 | + | 3.53E-04 | 1.08E-02 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031062&list=upload_1&organism=Homo%20sapiens) | 2.24 | 7.60 | + | 1.98E-09 | 2.03E-07 | | [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) | [283](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 134.35 | 2.11 | + | 4.43E-34 | 1.78E-31 | | [DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator](http://amigo.geneontology.org/amigo/term/GO:0006978) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006978&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006978&list=upload_1&organism=Homo%20sapiens) | .60 | 9.96 | + | 1.14E-04 | 4.26E-03 | | [DNA damage response, signal transduction resulting in transcription](http://amigo.geneontology.org/amigo/term/GO:0042772) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042772&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042772&list=upload_1&organism=Homo%20sapiens) | .65 | 9.30 | + | 1.54E-04 | 5.39E-03 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042770&list=upload_1&organism=Homo%20sapiens) | 5.81 | 3.27 | + | 2.02E-05 | 9.48E-04 | | [cellular response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:0006974) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 32.53 | 2.37 | + | 3.13E-11 | 4.09E-09 | | [intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:0035556) | [1511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&reflist=1) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&list=upload_1&organism=Homo%20sapiens) | 65.02 | 1.97 | + | 1.49E-12 | 2.33E-10 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 210.30 | 1.27 | + | 2.00E-05 | 9.41E-04 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 225.10 | 1.26 | + | 1.51E-05 | 7.33E-04 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [295](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 229.88 | 1.28 | + | 2.25E-06 | 1.34E-04 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072331&list=upload_1&organism=Homo%20sapiens) | 3.96 | 3.03 | + | 1.20E-03 | 2.91E-02 | | [histone H3-K9 demethylation](http://amigo.geneontology.org/amigo/term/GO:0033169) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033169&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033169&list=upload_1&organism=Homo%20sapiens) | .60 | 9.96 | + | 1.14E-04 | 4.25E-03 | | [double-strand break repair via break-induced replication](http://amigo.geneontology.org/amigo/term/GO:0000727) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000727&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000727&list=upload_1&organism=Homo%20sapiens) | .52 | 9.68 | + | 4.83E-04 | 1.40E-02 | | [double-strand break repair via homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0000724) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000724&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000724&list=upload_1&organism=Homo%20sapiens) | 4.86 | 3.29 | + | 8.37E-05 | 3.20E-03 | | [recombinational repair](http://amigo.geneontology.org/amigo/term/GO:0000725) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&list=upload_1&organism=Homo%20sapiens) | 5.03 | 3.38 | + | 3.79E-05 | 1.62E-03 | | [DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006281) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&list=upload_1&organism=Homo%20sapiens) | 21.86 | 2.38 | + | 5.90E-08 | 4.82E-06 | | [double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:0006302) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&list=upload_1&organism=Homo%20sapiens) | 8.74 | 2.98 | + | 3.13E-06 | 1.79E-04 | | [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) | .52 | 9.68 | + | 4.83E-04 | 1.40E-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) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 102.12 | 1.50 | + | 8.56E-07 | 5.84E-05 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 133.14 | 1.52 | + | 2.27E-09 | 2.31E-07 | | [mitotic DNA replication](http://amigo.geneontology.org/amigo/term/GO:1902969) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902969&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902969&list=upload_1&organism=Homo%20sapiens) | .52 | 9.68 | + | 4.83E-04 | 1.39E-02 | | [nuclear DNA replication](http://amigo.geneontology.org/amigo/term/GO:0033260) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&list=upload_1&organism=Homo%20sapiens) | 1.03 | 7.75 | + | 3.54E-05 | 1.54E-03 | | [cell cycle DNA replication](http://amigo.geneontology.org/amigo/term/GO:0044786) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&list=upload_1&organism=Homo%20sapiens) | 1.08 | 7.44 | + | 4.50E-05 | 1.88E-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) | 5.98 | 3.18 | + | 2.90E-05 | 1.30E-03 | | [DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006260) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&list=upload_1&organism=Homo%20sapiens) | 8.82 | 3.40 | + | 4.18E-08 | 3.53E-06 | | [DNA ligation](http://amigo.geneontology.org/amigo/term/GO:0006266) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006266&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006266&list=upload_1&organism=Homo%20sapiens) | .43 | 9.30 | + | 2.07E-03 | 4.56E-02 | | [endothelial cell activation](http://amigo.geneontology.org/amigo/term/GO:0042118) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042118&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042118&list=upload_1&organism=Homo%20sapiens) | .43 | 9.30 | + | 2.07E-03 | 4.55E-02 | | [cell activation](http://amigo.geneontology.org/amigo/term/GO:0001775) | [700](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&list=upload_1&organism=Homo%20sapiens) | 30.12 | 1.76 | + | 1.66E-04 | 5.70E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000083&list=upload_1&organism=Homo%20sapiens) | .90 | 8.85 | + | 1.61E-05 | 7.75E-04 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&list=upload_1&organism=Homo%20sapiens) | 3.66 | 4.10 | + | 1.45E-05 | 7.10E-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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&list=upload_1&organism=Homo%20sapiens) | 7.44 | 3.22 | + | 2.16E-06 | 1.31E-04 | | [cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044770) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&list=upload_1&organism=Homo%20sapiens) | 7.87 | 3.43 | + | 1.70E-07 | 1.31E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&list=upload_1&organism=Homo%20sapiens) | 3.74 | 4.27 | + | 4.78E-06 | 2.61E-04 | | [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) | [322](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&list=upload_1&organism=Homo%20sapiens) | 148.63 | 2.17 | + | 2.73E-42 | 4.76E-39 | | [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) | [322](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&list=upload_1&organism=Homo%20sapiens) | 148.72 | 2.17 | + | 2.96E-42 | 4.63E-39 | | [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) | [322](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 149.11 | 2.16 | + | 6.38E-42 | 7.69E-39 | | [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) | [343](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 169.46 | 2.02 | + | 1.10E-39 | 1.01E-36 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [353](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 179.15 | 1.97 | + | 1.23E-38 | 8.39E-36 | | [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) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 161.46 | 2.06 | + | 7.85E-40 | 7.69E-37 | | [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) | [352](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 176.52 | 1.99 | + | 1.42E-39 | 1.24E-36 | | [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) | 1.16 | 8.61 | + | 1.71E-06 | 1.06E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051569&list=upload_1&organism=Homo%20sapiens) | 1.68 | 8.34 | + | 2.00E-08 | 1.77E-06 | | [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) | .95 | 8.45 | + | 2.12E-05 | 9.92E-04 | | [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) | 1.81 | 4.98 | + | 2.13E-04 | 7.10E-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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051568&list=upload_1&organism=Homo%20sapiens) | 1.98 | 5.56 | + | 1.80E-05 | 8.48E-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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060765&list=upload_1&organism=Homo%20sapiens) | 1.20 | 8.30 | + | 2.24E-06 | 1.34E-04 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&list=upload_1&organism=Homo%20sapiens) | 3.14 | 6.05 | + | 5.43E-09 | 5.32E-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) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 128.62 | 1.55 | + | 7.13E-10 | 7.71E-08 | | [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) | [259](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 173.59 | 1.49 | + | 2.26E-11 | 3.01E-09 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 144.98 | 1.49 | + | 2.45E-09 | 2.48E-07 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 145.49 | 1.50 | + | 1.13E-09 | 1.18E-07 | | [cardiac muscle hypertrophy in response to stress](http://amigo.geneontology.org/amigo/term/GO:0014898) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014898&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014898&list=upload_1&organism=Homo%20sapiens) | .60 | 8.30 | + | 8.48E-04 | 2.22E-02 | | [cardiac muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0003300) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003300&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003300&list=upload_1&organism=Homo%20sapiens) | 1.29 | 6.20 | + | 1.32E-04 | 4.76E-03 | | [striated muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014897) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014897&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014897&list=upload_1&organism=Homo%20sapiens) | 1.33 | 6.00 | + | 1.60E-04 | 5.55E-03 | | [muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0014896) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014896&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014896&list=upload_1&organism=Homo%20sapiens) | 1.42 | 5.63 | + | 2.31E-04 | 7.64E-03 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [395](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 283.20 | 1.39 | + | 1.85E-14 | 3.49E-12 | | [muscle hypertrophy in response to stress](http://amigo.geneontology.org/amigo/term/GO:0003299) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003299&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003299&list=upload_1&organism=Homo%20sapiens) | .60 | 8.30 | + | 8.48E-04 | 2.21E-02 | | [muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043500) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043500&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043500&list=upload_1&organism=Homo%20sapiens) | 1.51 | 5.98 | + | 6.42E-05 | 2.57E-03 | | [cardiac muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0014887) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014887&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014887&list=upload_1&organism=Homo%20sapiens) | .60 | 8.30 | + | 8.48E-04 | 2.22E-02 | | [striated muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0014888) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014888&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014888&list=upload_1&organism=Homo%20sapiens) | 1.25 | 5.61 | + | 5.81E-04 | 1.63E-02 | | [cellular response to nitric oxide](http://amigo.geneontology.org/amigo/term/GO:0071732) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071732&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071732&list=upload_1&organism=Homo%20sapiens) | .73 | 8.20 | + | 2.68E-04 | 8.64E-03 | | [cellular response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0071241) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&list=upload_1&organism=Homo%20sapiens) | 9.90 | 2.83 | + | 3.22E-06 | 1.84E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 22.94 | 2.27 | + | 2.28E-07 | 1.70E-05 | | [response to nitric oxide](http://amigo.geneontology.org/amigo/term/GO:0071731) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071731&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071731&list=upload_1&organism=Homo%20sapiens) | .90 | 6.64 | + | 6.82E-04 | 1.86E-02 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 45.70 | 1.79 | + | 1.16E-06 | 7.61E-05 | | [cellular response to reactive nitrogen species](http://amigo.geneontology.org/amigo/term/GO:1902170) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902170&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902170&list=upload_1&organism=Homo%20sapiens) | .82 | 7.34 | + | 4.38E-04 | 1.29E-02 | | [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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 27.58 | 1.99 | + | 4.02E-06 | 2.22E-04 | | [regulation of gene expression by genomic imprinting](http://amigo.geneontology.org/amigo/term/GO:0006349) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006349&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006349&list=upload_1&organism=Homo%20sapiens) | .73 | 8.20 | + | 2.68E-04 | 8.62E-03 | | [negative regulation by host of viral transcription](http://amigo.geneontology.org/amigo/term/GO:0043922) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043922&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043922&list=upload_1&organism=Homo%20sapiens) | .65 | 7.75 | + | 1.09E-03 | 2.74E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&list=upload_1&organism=Homo%20sapiens) | 3.57 | 4.48 | + | 2.81E-06 | 1.64E-04 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 4.86 | 3.91 | + | 2.07E-06 | 1.26E-04 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 11.23 | 2.31 | + | 2.26E-04 | 7.49E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&list=upload_1&organism=Homo%20sapiens) | 1.08 | 7.44 | + | 4.50E-05 | 1.87E-03 | | [DNA unwinding involved in DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006268) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&list=upload_1&organism=Homo%20sapiens) | .95 | 7.39 | + | 1.40E-04 | 4.98E-03 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 3.96 | 3.03 | + | 1.20E-03 | 2.91E-02 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 4.22 | 2.85 | + | 1.95E-03 | 4.33E-02 | | [androgen receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030521) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030521&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030521&list=upload_1&organism=Homo%20sapiens) | .95 | 7.39 | + | 1.40E-04 | 4.97E-03 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.56 | + | 8.59E-05 | 3.27E-03 | | [intracellular receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030522) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&list=upload_1&organism=Homo%20sapiens) | 6.37 | 2.83 | + | 1.79E-04 | 6.07E-03 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.92 | + | 7.98E-05 | 3.10E-03 | | [hormone-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0009755) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&list=upload_1&organism=Homo%20sapiens) | 5.64 | 3.02 | + | 1.33E-04 | 4.79E-03 | | [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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 21.04 | 2.42 | + | 3.80E-08 | 3.25E-06 | | [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) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 47.64 | 2.14 | + | 5.01E-12 | 7.20E-10 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 59.00 | 2.05 | + | 5.79E-13 | 9.97E-11 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 33.01 | 2.24 | + | 8.09E-10 | 8.68E-08 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 6.54 | 3.97 | + | 2.11E-08 | 1.85E-06 | | [cellular response to lipid](http://amigo.geneontology.org/amigo/term/GO:0071396) | [519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&list=upload_1&organism=Homo%20sapiens) | 22.33 | 2.55 | + | 1.54E-09 | 1.59E-07 | | [response to lipid](http://amigo.geneontology.org/amigo/term/GO:0033993) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&list=upload_1&organism=Homo%20sapiens) | 36.28 | 2.54 | + | 1.00E-14 | 1.99E-12 | | [response to steroid hormone](http://amigo.geneontology.org/amigo/term/GO:0048545) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 12.22 | 2.95 | + | 5.32E-08 | 4.41E-06 | | [nucleosome disassembly](http://amigo.geneontology.org/amigo/term/GO:0006337) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006337&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006337&list=upload_1&organism=Homo%20sapiens) | .82 | 7.34 | + | 4.38E-04 | 1.29E-02 | | [protein-DNA complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032986) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&list=upload_1&organism=Homo%20sapiens) | .90 | 6.64 | + | 6.82E-04 | 1.86E-02 | | [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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&list=upload_1&organism=Homo%20sapiens) | 10.03 | 3.89 | + | 1.16E-11 | 1.61E-09 | | [nucleosome organization](http://amigo.geneontology.org/amigo/term/GO:0034728) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&list=upload_1&organism=Homo%20sapiens) | 5.38 | 5.76 | + | 2.54E-13 | 4.52E-11 | | [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) | .82 | 7.34 | + | 4.38E-04 | 1.28E-02 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 73.80 | 2.67 | + | 9.63E-35 | 4.31E-32 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 73.80 | 2.67 | + | 9.63E-35 | 4.44E-32 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 74.06 | 2.66 | + | 1.34E-34 | 5.84E-32 | | [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) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 79.52 | 2.58 | + | 2.54E-34 | 1.05E-31 | | [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) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 88.56 | 2.48 | + | 7.63E-35 | 3.62E-32 | | [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) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 88.13 | 2.45 | + | 2.30E-33 | 8.81E-31 | | [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) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 89.81 | 2.41 | + | 2.25E-32 | 7.85E-30 | | [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) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 83.61 | 2.51 | + | 1.04E-33 | 4.08E-31 | | [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) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060253&list=upload_1&organism=Homo%20sapiens) | .69 | 7.26 | + | 1.38E-03 | 3.24E-02 | | [regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060251) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 1.51 | 5.98 | + | 6.42E-05 | 2.57E-03 | | [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) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 72.04 | 1.93 | + | 6.19E-13 | 1.04E-10 | | [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) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 30.68 | 2.31 | + | 6.04E-10 | 6.67E-08 | | [negative regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014014) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&list=upload_1&organism=Homo%20sapiens) | 1.76 | 4.53 | + | 8.16E-04 | 2.16E-02 | | [regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014013) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&list=upload_1&organism=Homo%20sapiens) | 4.35 | 3.91 | + | 6.96E-06 | 3.60E-04 | | [regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050767) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&list=upload_1&organism=Homo%20sapiens) | 16.05 | 2.43 | + | 1.84E-06 | 1.13E-04 | | [regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051960) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&list=upload_1&organism=Homo%20sapiens) | 19.45 | 2.01 | + | 1.18E-04 | 4.35E-03 | | [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) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 59.51 | 1.87 | + | 1.26E-09 | 1.32E-07 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 118.34 | 1.66 | + | 1.96E-12 | 3.04E-10 | | [regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0050793) | [2489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&reflist=1) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 107.11 | 1.80 | + | 3.36E-15 | 7.31E-13 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 22.08 | 2.26 | + | 4.28E-07 | 3.08E-05 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 68.03 | 2.13 | + | 9.97E-17 | 2.33E-14 | | [negative regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050768) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050768&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050768&list=upload_1&organism=Homo%20sapiens) | 6.20 | 3.07 | + | 4.49E-05 | 1.88E-03 | | [negative regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051961) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051961&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051961&list=upload_1&organism=Homo%20sapiens) | 6.41 | 3.12 | + | 2.29E-05 | 1.05E-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) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&list=upload_1&organism=Homo%20sapiens) | 44.71 | 1.88 | + | 1.17E-07 | 9.37E-06 | | [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) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&list=upload_1&organism=Homo%20sapiens) | 39.72 | 2.14 | + | 3.44E-10 | 3.85E-08 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010721&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.41 | + | 9.24E-04 | 2.37E-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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 29.09 | 2.23 | + | 9.52E-09 | 8.94E-07 | | [uterus development](http://amigo.geneontology.org/amigo/term/GO:0060065) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060065&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060065&list=upload_1&organism=Homo%20sapiens) | .99 | 7.07 | + | 1.76E-04 | 6.02E-03 | | [reproductive structure development](http://amigo.geneontology.org/amigo/term/GO:0048608) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&list=upload_1&organism=Homo%20sapiens) | 12.91 | 2.79 | + | 1.82E-07 | 1.38E-05 | | [anatomical structure development](http://amigo.geneontology.org/amigo/term/GO:0048856) | [5144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&reflist=1) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&list=upload_1&organism=Homo%20sapiens) | 221.36 | 1.50 | + | 1.17E-15 | 2.66E-13 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 244.30 | 1.49 | + | 1.48E-17 | 3.94E-15 | | [reproductive system development](http://amigo.geneontology.org/amigo/term/GO:0061458) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&list=upload_1&organism=Homo%20sapiens) | 13.08 | 2.75 | + | 2.43E-07 | 1.80E-05 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [263](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 165.16 | 1.59 | + | 9.66E-15 | 1.94E-12 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [286](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 181.94 | 1.57 | + | 1.48E-15 | 3.31E-13 | | [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) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&list=upload_1&organism=Homo%20sapiens) | 40.75 | 1.82 | + | 2.36E-06 | 1.40E-04 | | [reproductive process](http://amigo.geneontology.org/amigo/term/GO:0022414) | [1437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&list=upload_1&organism=Homo%20sapiens) | 61.84 | 1.55 | + | 4.36E-05 | 1.84E-03 | | [reproduction](http://amigo.geneontology.org/amigo/term/GO:0000003) | [1447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&list=upload_1&organism=Homo%20sapiens) | 62.27 | 1.54 | + | 4.75E-05 | 1.96E-03 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 140.03 | 1.73 | + | 1.97E-17 | 5.07E-15 | | [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) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&list=upload_1&organism=Homo%20sapiens) | .73 | 6.83 | + | 1.73E-03 | 3.92E-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) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905269&list=upload_1&organism=Homo%20sapiens) | .73 | 6.83 | + | 1.73E-03 | 3.92E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 4.56 | 3.07 | + | 4.32E-04 | 1.28E-02 | | [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) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 45.36 | 1.63 | + | 7.93E-05 | 3.09E-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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902275&list=upload_1&organism=Homo%20sapiens) | 1.89 | 5.81 | + | 1.26E-05 | 6.17E-04 | | [regulation of megakaryocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045652) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045652&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045652&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.78 | + | 2.19E-04 | 7.30E-03 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 8.61 | 2.44 | + | 4.30E-04 | 1.27E-02 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 17.13 | 2.39 | + | 1.20E-06 | 7.84E-05 | | [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) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 65.41 | 1.51 | + | 7.00E-05 | 2.77E-03 | | [aortic valve morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003180) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003180&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003180&list=upload_1&organism=Homo%20sapiens) | 1.38 | 6.54 | + | 3.54E-05 | 1.54E-03 | | [aortic valve development](http://amigo.geneontology.org/amigo/term/GO:0003176) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&list=upload_1&organism=Homo%20sapiens) | 1.59 | 6.28 | + | 1.75E-05 | 8.33E-04 | | [semi-lunar valve development](http://amigo.geneontology.org/amigo/term/GO:1905314) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&list=upload_1&organism=Homo%20sapiens) | 1.76 | 5.67 | + | 3.73E-05 | 1.61E-03 | | [heart valve development](http://amigo.geneontology.org/amigo/term/GO:0003170) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&list=upload_1&organism=Homo%20sapiens) | 2.80 | 5.01 | + | 3.83E-06 | 2.13E-04 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 23.88 | 2.22 | + | 3.88E-07 | 2.83E-05 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 39.12 | 1.79 | + | 7.40E-06 | 3.81E-04 | | [heart valve morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003179) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003179&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003179&list=upload_1&organism=Homo%20sapiens) | 2.37 | 5.07 | + | 1.67E-05 | 7.99E-04 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 96.26 | 1.58 | + | 4.07E-08 | 3.45E-06 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902455&list=upload_1&organism=Homo%20sapiens) | 1.08 | 6.51 | + | 2.71E-04 | 8.70E-03 | | [regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:2000036) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&list=upload_1&organism=Homo%20sapiens) | 3.01 | 3.65 | + | 4.80E-04 | 1.39E-02 | | [nucleosome assembly](http://amigo.geneontology.org/amigo/term/GO:0006334) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006334&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006334&list=upload_1&organism=Homo%20sapiens) | 4.00 | 6.50 | + | 2.17E-12 | 3.31E-10 | | [protein-DNA complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065004) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&list=upload_1&organism=Homo%20sapiens) | 8.61 | 4.18 | + | 1.17E-11 | 1.60E-09 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 54.65 | 1.72 | + | 9.79E-07 | 6.53E-05 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 103.02 | 1.47 | + | 3.53E-06 | 2.00E-04 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 113.31 | 1.39 | + | 4.23E-05 | 1.79E-03 | | [stress fiber assembly](http://amigo.geneontology.org/amigo/term/GO:0043149) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043149&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043149&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.14E-03 | 4.68E-02 | | [actomyosin structure organization](http://amigo.geneontology.org/amigo/term/GO:0031032) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&list=upload_1&organism=Homo%20sapiens) | 4.91 | 2.85 | + | 8.29E-04 | 2.18E-02 | | [contractile actin filament bundle assembly](http://amigo.geneontology.org/amigo/term/GO:0030038) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030038&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030038&list=upload_1&organism=Homo%20sapiens) | .77 | 6.46 | + | 2.14E-03 | 4.68E-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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071392&list=upload_1&organism=Homo%20sapiens) | 1.72 | 5.81 | + | 3.11E-05 | 1.38E-03 | | [response to estradiol](http://amigo.geneontology.org/amigo/term/GO:0032355) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&list=upload_1&organism=Homo%20sapiens) | 5.29 | 3.59 | + | 6.21E-06 | 3.28E-04 | | [rRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0009303) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009303&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009303&list=upload_1&organism=Homo%20sapiens) | 1.03 | 5.81 | + | 1.23E-03 | 2.95E-02 | | [intestinal epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060575) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060575&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060575&list=upload_1&organism=Homo%20sapiens) | 1.03 | 5.81 | + | 1.23E-03 | 2.95E-02 | | [digestive tract development](http://amigo.geneontology.org/amigo/term/GO:0048565) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048565&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048565&list=upload_1&organism=Homo%20sapiens) | 5.68 | 2.82 | + | 4.15E-04 | 1.23E-02 | | [tube development](http://amigo.geneontology.org/amigo/term/GO:0035295) | [885](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&list=upload_1&organism=Homo%20sapiens) | 38.08 | 1.63 | + | 3.09E-04 | 9.65E-03 | | [digestive system development](http://amigo.geneontology.org/amigo/term/GO:0055123) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055123&list=upload_1&organism=Homo%20sapiens) | 6.15 | 2.60 | + | 9.12E-04 | 2.36E-02 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 46.13 | 1.54 | + | 5.56E-04 | 1.58E-02 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 74.27 | 1.68 | + | 3.03E-08 | 2.63E-06 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [234](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 151.43 | 1.55 | + | 1.24E-11 | 1.68E-09 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 152.42 | 1.55 | + | 7.51E-12 | 1.05E-09 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071480&list=upload_1&organism=Homo%20sapiens) | 1.25 | 5.61 | + | 5.81E-04 | 1.63E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&list=upload_1&organism=Homo%20sapiens) | 2.41 | 3.73 | + | 1.34E-03 | 3.14E-02 | | [response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0010212) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&list=upload_1&organism=Homo%20sapiens) | 6.20 | 3.07 | + | 4.49E-05 | 1.88E-03 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 19.32 | 2.79 | + | 1.44E-10 | 1.68E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&list=upload_1&organism=Homo%20sapiens) | 3.23 | 4.65 | + | 3.86E-06 | 2.14E-04 | | [cellular response to radiation](http://amigo.geneontology.org/amigo/term/GO:0071478) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 7.83 | 3.06 | + | 4.74E-06 | 2.60E-04 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 14.03 | 2.28 | + | 4.15E-05 | 1.77E-03 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&list=upload_1&organism=Homo%20sapiens) | 14.03 | 2.28 | + | 4.15E-05 | 1.76E-03 | | [protein refolding](http://amigo.geneontology.org/amigo/term/GO:0042026) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042026&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042026&list=upload_1&organism=Homo%20sapiens) | 1.08 | 5.58 | + | 1.47E-03 | 3.41E-02 | | [protein folding](http://amigo.geneontology.org/amigo/term/GO:0006457) | [221](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&list=upload_1&organism=Homo%20sapiens) | 9.51 | 2.63 | + | 3.27E-05 | 1.45E-03 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&list=upload_1&organism=Homo%20sapiens) | 1.46 | 5.47 | + | 2.76E-04 | 8.80E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.96E-02 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&list=upload_1&organism=Homo%20sapiens) | 2.02 | 5.44 | + | 2.13E-05 | 9.96E-04 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&list=upload_1&organism=Homo%20sapiens) | 2.28 | 5.26 | + | 1.21E-05 | 6.01E-04 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 3.18 | 5.34 | + | 1.62E-07 | 1.25E-05 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 2.71 | 5.53 | + | 5.83E-07 | 4.16E-05 | | [response to X-ray](http://amigo.geneontology.org/amigo/term/GO:0010165) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010165&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010165&list=upload_1&organism=Homo%20sapiens) | 1.33 | 5.25 | + | 8.18E-04 | 2.16E-02 | | [negative regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033144) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&list=upload_1&organism=Homo%20sapiens) | 1.59 | 5.02 | + | 4.51E-04 | 1.32E-02 | | [negative regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009968) | [1257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 54.09 | 1.87 | + | 7.59E-09 | 7.35E-07 | | [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) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 58.40 | 1.82 | + | 1.15E-08 | 1.06E-06 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 58.65 | 1.81 | + | 1.78E-08 | 1.58E-06 | | [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) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 69.71 | 1.76 | + | 3.63E-09 | 3.62E-07 | | [response to testosterone](http://amigo.geneontology.org/amigo/term/GO:0033574) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033574&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033574&list=upload_1&organism=Homo%20sapiens) | 1.81 | 4.98 | + | 2.13E-04 | 7.11E-03 | | [response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901654) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&list=upload_1&organism=Homo%20sapiens) | 8.86 | 2.48 | + | 2.66E-04 | 8.60E-03 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902459&list=upload_1&organism=Homo%20sapiens) | 2.02 | 4.94 | + | 1.01E-04 | 3.80E-03 | | [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) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051094&list=upload_1&organism=Homo%20sapiens) | 57.62 | 2.05 | + | 1.47E-12 | 2.32E-10 | | [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) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 65.19 | 1.79 | + | 3.91E-09 | 3.88E-07 | | [response to fluid shear stress](http://amigo.geneontology.org/amigo/term/GO:0034405) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034405&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034405&list=upload_1&organism=Homo%20sapiens) | 1.46 | 4.78 | + | 1.31E-03 | 3.09E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045663&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.65 | + | 3.33E-04 | 1.03E-02 | | [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) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 38.04 | 2.34 | + | 1.40E-12 | 2.24E-10 | | [regulation of natural killer cell activation](http://amigo.geneontology.org/amigo/term/GO:0032814) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032814&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032814&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.65 | + | 3.33E-04 | 1.03E-02 | | [regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051249) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&list=upload_1&organism=Homo%20sapiens) | 25.43 | 1.69 | + | 1.53E-03 | 3.52E-02 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 29.43 | 1.70 | + | 6.05E-04 | 1.68E-02 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 31.89 | 1.69 | + | 3.54E-04 | 1.08E-02 | | [regulation of intracellular estrogen receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033146) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033146&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033146&list=upload_1&organism=Homo%20sapiens) | 1.55 | 4.52 | + | 1.75E-03 | 3.95E-02 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070316&list=upload_1&organism=Homo%20sapiens) | 1.59 | 4.40 | + | 2.01E-03 | 4.44E-02 | | [response to cocaine](http://amigo.geneontology.org/amigo/term/GO:0042220) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042220&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042220&list=upload_1&organism=Homo%20sapiens) | 2.07 | 4.36 | + | 5.04E-04 | 1.45E-02 | | [response to alkaloid](http://amigo.geneontology.org/amigo/term/GO:0043279) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043279&list=upload_1&organism=Homo%20sapiens) | 4.30 | 2.79 | + | 2.27E-03 | 4.87E-02 | | [response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0010243) | [968](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&reflist=1) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 41.66 | 1.87 | + | 3.89E-07 | 2.83E-05 | | [myeloid leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002444) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002444&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002444&list=upload_1&organism=Homo%20sapiens) | 2.54 | 4.33 | + | 1.29E-04 | 4.68E-03 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 104.53 | 1.35 | + | 3.85E-04 | 1.16E-02 | | [chromosome condensation](http://amigo.geneontology.org/amigo/term/GO:0030261) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030261&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030261&list=upload_1&organism=Homo%20sapiens) | 1.85 | 4.32 | + | 1.07E-03 | 2.69E-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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046329&list=upload_1&organism=Homo%20sapiens) | 1.64 | 4.28 | + | 2.29E-03 | 4.91E-02 | | [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) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 30.51 | 1.90 | + | 1.07E-05 | 5.42E-04 | | [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) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 59.08 | 1.71 | + | 4.21E-07 | 3.04E-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) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 74.06 | 1.65 | + | 1.57E-07 | 1.22E-05 | | [regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043408) | [672](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&list=upload_1&organism=Homo%20sapiens) | 28.92 | 1.90 | + | 1.56E-05 | 7.55E-04 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032873&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.27 | + | 5.76E-04 | 1.63E-02 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&list=upload_1&organism=Homo%20sapiens) | 7.32 | 2.73 | + | 1.21E-04 | 4.45E-03 | | [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) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&list=upload_1&organism=Homo%20sapiens) | 22.29 | 1.97 | + | 5.44E-05 | 2.22E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070303&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.27 | + | 5.76E-04 | 1.62E-02 | | [cardiac conduction system development](http://amigo.geneontology.org/amigo/term/GO:0003161) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003161&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003161&list=upload_1&organism=Homo%20sapiens) | 1.64 | 4.28 | + | 2.29E-03 | 4.90E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048738&list=upload_1&organism=Homo%20sapiens) | 7.83 | 2.68 | + | 1.06E-04 | 3.97E-03 | | [striated muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0014706) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&list=upload_1&organism=Homo%20sapiens) | 8.09 | 2.60 | + | 1.60E-04 | 5.54E-03 | | [muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0060537) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&list=upload_1&organism=Homo%20sapiens) | 14.03 | 2.64 | + | 6.29E-07 | 4.42E-05 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000378&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.96E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051602&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.95E-02 | | [regulation of protein autophosphorylation](http://amigo.geneontology.org/amigo/term/GO:0031952) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031952&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031952&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.95E-02 | | [regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001932) | [1105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 47.55 | 1.62 | + | 8.20E-05 | 3.17E-03 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 53.70 | 1.79 | + | 1.23E-07 | 9.80E-06 | | [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) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 60.42 | 1.74 | + | 1.27E-07 | 1.00E-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) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 60.46 | 1.74 | + | 1.28E-07 | 1.01E-05 | | [regulation of oligodendrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0048713) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048713&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048713&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.94E-02 | | [regulation of glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045685) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&list=upload_1&organism=Homo%20sapiens) | 3.18 | 3.45 | + | 7.28E-04 | 1.97E-02 | | [endodermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0035987) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&list=upload_1&organism=Homo%20sapiens) | 1.89 | 4.23 | + | 1.22E-03 | 2.94E-02 | | [endoderm formation](http://amigo.geneontology.org/amigo/term/GO:0001706) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&list=upload_1&organism=Homo%20sapiens) | 2.32 | 4.30 | + | 2.72E-04 | 8.73E-03 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 3.49 | 4.02 | + | 3.41E-05 | 1.51E-03 | | [formation of primary germ layer](http://amigo.geneontology.org/amigo/term/GO:0001704) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&list=upload_1&organism=Homo%20sapiens) | 5.16 | 3.10 | + | 1.57E-04 | 5.47E-03 | | [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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&list=upload_1&organism=Homo%20sapiens) | 40.49 | 1.78 | + | 7.02E-06 | 3.62E-04 | | [gastrulation](http://amigo.geneontology.org/amigo/term/GO:0007369) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&list=upload_1&organism=Homo%20sapiens) | 7.27 | 2.61 | + | 2.99E-04 | 9.45E-03 | | [embryonic morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048598) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&list=upload_1&organism=Homo%20sapiens) | 25.43 | 2.20 | + | 1.79E-07 | 1.37E-05 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 45.57 | 1.91 | + | 4.02E-08 | 3.43E-06 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043525&list=upload_1&organism=Homo%20sapiens) | 2.37 | 4.23 | + | 3.10E-04 | 9.65E-03 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 63.17 | 1.84 | + | 1.06E-09 | 1.12E-07 | | [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) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 64.46 | 1.85 | + | 4.44E-10 | 4.94E-08 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 71.18 | 1.83 | + | 1.43E-10 | 1.68E-08 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&list=upload_1&organism=Homo%20sapiens) | 4.00 | 3.25 | + | 4.22E-04 | 1.25E-02 | | [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) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 25.09 | 1.99 | + | 1.52E-05 | 7.36E-04 | | [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) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&list=upload_1&organism=Homo%20sapiens) | 21.65 | 2.03 | + | 2.64E-05 | 1.20E-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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&list=upload_1&organism=Homo%20sapiens) | 22.20 | 2.03 | + | 2.14E-05 | 9.95E-04 | | [regulation of smooth muscle cell migration](http://amigo.geneontology.org/amigo/term/GO:0014910) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014910&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014910&list=upload_1&organism=Homo%20sapiens) | 2.84 | 4.23 | + | 7.99E-05 | 3.09E-03 | | [regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030334) | [929](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 39.98 | 1.88 | + | 8.01E-07 | 5.51E-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) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&list=upload_1&organism=Homo%20sapiens) | 42.56 | 1.79 | + | 3.66E-06 | 2.06E-04 | | [regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040012) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&list=upload_1&organism=Homo%20sapiens) | 44.50 | 1.80 | + | 1.29E-06 | 8.20E-05 | | [nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006289) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.15 | + | 3.52E-04 | 1.08E-02 | | [negative regulation of DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0045910) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045910&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045910&list=upload_1&organism=Homo%20sapiens) | 1.94 | 4.13 | + | 1.39E-03 | 3.24E-02 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051053&list=upload_1&organism=Homo%20sapiens) | 6.37 | 2.98 | + | 6.26E-05 | 2.52E-03 | | [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) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 67.22 | 3.06 | + | 1.06E-44 | 1.66E-40 | | [Fc receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038093) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&list=upload_1&organism=Homo%20sapiens) | 2.24 | 4.02 | + | 8.40E-04 | 2.20E-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) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 93.55 | 1.34 | + | 1.26E-03 | 3.00E-02 | | [substantia nigra development](http://amigo.geneontology.org/amigo/term/GO:0021762) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&list=upload_1&organism=Homo%20sapiens) | 2.02 | 3.96 | + | 1.77E-03 | 4.00E-02 | | [midbrain development](http://amigo.geneontology.org/amigo/term/GO:0030901) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&list=upload_1&organism=Homo%20sapiens) | 3.83 | 3.39 | + | 2.88E-04 | 9.14E-03 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 33.35 | 1.95 | + | 1.26E-06 | 8.08E-05 | | [central nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007417) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 44.50 | 1.93 | + | 2.81E-08 | 2.45E-06 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 94.28 | 1.78 | + | 8.44E-13 | 1.39E-10 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 35.42 | 1.89 | + | 2.52E-06 | 1.48E-04 | | [replication fork processing](http://amigo.geneontology.org/amigo/term/GO:0031297) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031297&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031297&list=upload_1&organism=Homo%20sapiens) | 2.02 | 3.96 | + | 1.77E-03 | 4.00E-02 | | [DNA-templated DNA replication maintenance of fidelity](http://amigo.geneontology.org/amigo/term/GO:0045005) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045005&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045005&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.15 | + | 3.52E-04 | 1.08E-02 | | [negative regulation of fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045599) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&list=upload_1&organism=Homo%20sapiens) | 2.28 | 3.95 | + | 9.47E-04 | 2.41E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&list=upload_1&organism=Homo%20sapiens) | 5.81 | 2.58 | + | 1.39E-03 | 3.24E-02 | | [negative regulation of muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051148) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051148&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051148&list=upload_1&organism=Homo%20sapiens) | 2.54 | 3.94 | + | 5.08E-04 | 1.45E-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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032922&list=upload_1&organism=Homo%20sapiens) | 3.06 | 3.93 | + | 1.47E-04 | 5.19E-03 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 5.94 | 3.54 | + | 2.53E-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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 11.70 | 3.67 | + | 5.40E-12 | 7.63E-10 | | [cellular senescence](http://amigo.geneontology.org/amigo/term/GO:0090398) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&list=upload_1&organism=Homo%20sapiens) | 2.58 | 3.87 | + | 5.71E-04 | 1.62E-02 | | [cellular response to glucose starvation](http://amigo.geneontology.org/amigo/term/GO:0042149) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042149&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042149&list=upload_1&organism=Homo%20sapiens) | 2.37 | 3.80 | + | 1.19E-03 | 2.91E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&list=upload_1&organism=Homo%20sapiens) | 7.66 | 2.74 | + | 7.96E-05 | 3.10E-03 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&list=upload_1&organism=Homo%20sapiens) | 9.73 | 2.67 | + | 1.76E-05 | 8.35E-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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&list=upload_1&organism=Homo%20sapiens) | 20.23 | 2.13 | + | 1.34E-05 | 6.56E-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) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&list=upload_1&organism=Homo%20sapiens) | 21.52 | 2.04 | + | 2.45E-05 | 1.12E-03 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 106.25 | 1.47 | + | 2.19E-06 | 1.32E-04 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&list=upload_1&organism=Homo%20sapiens) | 11.02 | 2.45 | + | 5.52E-05 | 2.25E-03 | | [cellular response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0071496) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&list=upload_1&organism=Homo%20sapiens) | 13.99 | 2.22 | + | 1.17E-04 | 4.33E-03 | | [response to starvation](http://amigo.geneontology.org/amigo/term/GO:0042594) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&list=upload_1&organism=Homo%20sapiens) | 9.25 | 2.70 | + | 2.16E-05 | 1.00E-03 | | [protein sumoylation](http://amigo.geneontology.org/amigo/term/GO:0016925) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016925&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016925&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.79 | + | 2.24E-03 | 4.82E-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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&list=upload_1&organism=Homo%20sapiens) | 3.18 | 3.77 | + | 2.08E-04 | 6.98E-03 | | [intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097193) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&list=upload_1&organism=Homo%20sapiens) | 7.01 | 2.42 | + | 1.79E-03 | 4.03E-02 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 44.45 | 1.60 | + | 2.38E-04 | 7.80E-03 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 46.22 | 1.60 | + | 1.29E-04 | 4.68E-03 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 47.68 | 1.57 | + | 2.12E-04 | 7.11E-03 | | [regulation of extracellular matrix organization](http://amigo.geneontology.org/amigo/term/GO:1903053) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903053&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903053&list=upload_1&organism=Homo%20sapiens) | 2.41 | 3.73 | + | 1.34E-03 | 3.15E-02 | | [negative regulation of G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:2000134) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000134&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000134&list=upload_1&organism=Homo%20sapiens) | 3.23 | 3.72 | + | 2.32E-04 | 7.65E-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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000045&list=upload_1&organism=Homo%20sapiens) | 7.06 | 3.40 | + | 9.28E-07 | 6.27E-05 | | [regulation of cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:1902806) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 8.26 | 3.39 | + | 1.25E-07 | 9.93E-06 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&list=upload_1&organism=Homo%20sapiens) | 18.55 | 2.59 | + | 1.57E-08 | 1.41E-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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&list=upload_1&organism=Homo%20sapiens) | 14.29 | 2.80 | + | 3.44E-08 | 2.97E-06 | | [regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007346) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 21.22 | 2.73 | + | 6.42E-11 | 7.99E-09 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901991&list=upload_1&organism=Homo%20sapiens) | 7.14 | 2.52 | + | 6.30E-04 | 1.74E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045930&list=upload_1&organism=Homo%20sapiens) | 9.17 | 2.40 | + | 3.57E-04 | 1.09E-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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045786&list=upload_1&organism=Homo%20sapiens) | 15.45 | 2.52 | + | 6.22E-07 | 4.39E-05 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901988&list=upload_1&organism=Homo%20sapiens) | 9.64 | 2.80 | + | 5.66E-06 | 3.03E-04 | | [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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010948&list=upload_1&organism=Homo%20sapiens) | 11.70 | 2.82 | + | 4.69E-07 | 3.36E-05 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902807&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.87 | + | 4.86E-05 | 1.99E-03 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&list=upload_1&organism=Homo%20sapiens) | 3.53 | 3.68 | + | 1.40E-04 | 4.98E-03 | | [regulation of circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0042752) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&list=upload_1&organism=Homo%20sapiens) | 5.16 | 3.68 | + | 4.52E-06 | 2.49E-04 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&list=upload_1&organism=Homo%20sapiens) | 5.03 | 3.58 | + | 1.14E-05 | 5.68E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 5.64 | 3.73 | + | 1.21E-06 | 7.83E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 9.04 | 2.77 | + | 1.51E-05 | 7.32E-04 | | [regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902105) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 13.60 | 2.35 | + | 2.76E-05 | 1.24E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&list=upload_1&organism=Homo%20sapiens) | 7.87 | 3.17 | + | 1.71E-06 | 1.07E-04 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 7.87 | 3.17 | + | 1.71E-06 | 1.06E-04 | | [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) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 41.61 | 1.51 | + | 1.69E-03 | 3.86E-02 | | [positive regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051251) | [421](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051251&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051251&list=upload_1&organism=Homo%20sapiens) | 18.12 | 1.82 | + | 1.72E-03 | 3.92E-02 | | [positive regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002696) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&list=upload_1&organism=Homo%20sapiens) | 20.18 | 1.83 | + | 8.98E-04 | 2.32E-02 | | [positive regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050867) | [486](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&list=upload_1&organism=Homo%20sapiens) | 20.91 | 1.82 | + | 7.64E-04 | 2.04E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 10.89 | 2.11 | + | 1.86E-03 | 4.15E-02 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 11.88 | 2.02 | + | 1.89E-03 | 4.21E-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) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 33.95 | 1.68 | + | 2.74E-04 | 8.78E-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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 13.94 | 2.15 | + | 2.07E-04 | 6.98E-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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 21.00 | 1.86 | + | 4.99E-04 | 1.44E-02 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&list=upload_1&organism=Homo%20sapiens) | 7.70 | 2.73 | + | 8.56E-05 | 3.26E-03 | | [positive regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014015) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&list=upload_1&organism=Homo%20sapiens) | 2.84 | 3.52 | + | 1.10E-03 | 2.72E-02 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 9.94 | 2.21 | + | 1.11E-03 | 2.72E-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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 13.25 | 2.26 | + | 8.27E-05 | 3.18E-03 | | [regulation of muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043502) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&list=upload_1&organism=Homo%20sapiens) | 3.44 | 3.49 | + | 3.94E-04 | 1.19E-02 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090257&list=upload_1&organism=Homo%20sapiens) | 10.16 | 2.46 | + | 1.02E-04 | 3.84E-03 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030512&list=upload_1&organism=Homo%20sapiens) | 4.05 | 3.46 | + | 1.42E-04 | 5.02E-03 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017015&list=upload_1&organism=Homo%20sapiens) | 5.98 | 3.18 | + | 2.90E-05 | 1.30E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903844&list=upload_1&organism=Homo%20sapiens) | 6.11 | 3.27 | + | 1.22E-05 | 6.04E-04 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090287&list=upload_1&organism=Homo%20sapiens) | 13.51 | 2.52 | + | 3.61E-06 | 2.04E-04 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090092&list=upload_1&organism=Homo%20sapiens) | 11.83 | 2.28 | + | 1.85E-04 | 6.25E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090101&list=upload_1&organism=Homo%20sapiens) | 6.28 | 2.55 | + | 1.11E-03 | 2.73E-02 | | [osteoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0001649) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&list=upload_1&organism=Homo%20sapiens) | 6.11 | 3.44 | + | 3.79E-06 | 2.11E-04 | | [ossification](http://amigo.geneontology.org/amigo/term/GO:0001503) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001503&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001503&list=upload_1&organism=Homo%20sapiens) | 12.48 | 2.24 | + | 1.65E-04 | 5.68E-03 | | [negative regulation of neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0045665) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045665&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045665&list=upload_1&organism=Homo%20sapiens) | 3.23 | 3.41 | + | 8.04E-04 | 2.13E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045664&list=upload_1&organism=Homo%20sapiens) | 8.39 | 2.50 | + | 3.59E-04 | 1.09E-02 | | [regulation of lipid kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043550) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043550&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043550&list=upload_1&organism=Homo%20sapiens) | 2.97 | 3.37 | + | 1.49E-03 | 3.44E-02 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 33.69 | 1.72 | + | 1.28E-04 | 4.67E-03 | | [regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051338) | [915](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 39.37 | 1.73 | + | 3.45E-05 | 1.52E-03 | | [ovulation cycle](http://amigo.geneontology.org/amigo/term/GO:0042698) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042698&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042698&list=upload_1&organism=Homo%20sapiens) | 2.97 | 3.37 | + | 1.49E-03 | 3.43E-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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048609&list=upload_1&organism=Homo%20sapiens) | 37.44 | 1.74 | + | 4.65E-05 | 1.92E-03 | | [multicellular organism reproduction](http://amigo.geneontology.org/amigo/term/GO:0032504) | [908](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032504&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032504&list=upload_1&organism=Homo%20sapiens) | 39.07 | 1.69 | + | 6.97E-05 | 2.76E-03 | | [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) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 41.91 | 3.32 | + | 1.12E-32 | 4.09E-30 | | [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) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 56.93 | 3.27 | + | 1.62E-43 | 8.44E-40 | | [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) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 57.02 | 3.26 | + | 1.96E-43 | 6.14E-40 | | [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) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 57.10 | 3.26 | + | 2.37E-43 | 6.20E-40 | | [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) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 61.75 | 3.16 | + | 7.97E-44 | 6.25E-40 | | [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) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 68.59 | 2.80 | + | 2.00E-36 | 1.08E-33 | | [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) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 69.89 | 2.79 | + | 7.22E-37 | 4.20E-34 | | [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) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 65.97 | 2.91 | + | 1.50E-38 | 9.77E-36 | | [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) | [259](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 112.14 | 2.31 | + | 6.59E-37 | 3.98E-34 | | [metanephros development](http://amigo.geneontology.org/amigo/term/GO:0001656) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001656&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001656&list=upload_1&organism=Homo%20sapiens) | 3.66 | 3.28 | + | 6.41E-04 | 1.76E-02 | | [urogenital system development](http://amigo.geneontology.org/amigo/term/GO:0001655) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&list=upload_1&organism=Homo%20sapiens) | 15.06 | 2.06 | + | 3.55E-04 | 1.09E-02 | | [positive regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048661) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&list=upload_1&organism=Homo%20sapiens) | 3.66 | 3.28 | + | 6.41E-04 | 1.76E-02 | | [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) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 40.84 | 1.74 | + | 1.63E-05 | 7.81E-04 | | [regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048660) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&list=upload_1&organism=Homo%20sapiens) | 6.11 | 3.11 | + | 3.78E-05 | 1.62E-03 | | [ventricular septum development](http://amigo.geneontology.org/amigo/term/GO:0003281) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003281&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003281&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.18 | + | 2.17E-03 | 4.69E-02 | | [cardiac ventricle development](http://amigo.geneontology.org/amigo/term/GO:0003231) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003231&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003231&list=upload_1&organism=Homo%20sapiens) | 5.42 | 2.58 | + | 1.97E-03 | 4.38E-02 | | [mitotic DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0044773) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044773&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044773&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.16 | + | 1.41E-03 | 3.29E-02 | | [DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000077) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&list=upload_1&organism=Homo%20sapiens) | 4.52 | 3.10 | + | 3.96E-04 | 1.19E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031570&list=upload_1&organism=Homo%20sapiens) | 4.86 | 3.08 | + | 2.60E-04 | 8.43E-03 | | [cell cycle checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000075) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&list=upload_1&organism=Homo%20sapiens) | 6.76 | 2.52 | + | 8.93E-04 | 2.32E-02 | | [mitotic DNA integrity checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0044774) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044774&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044774&list=upload_1&organism=Homo%20sapiens) | 3.66 | 3.01 | + | 2.00E-03 | 4.42E-02 | | [negative regulation of neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0010977) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010977&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010977&list=upload_1&organism=Homo%20sapiens) | 6.07 | 3.13 | + | 3.46E-05 | 1.51E-03 | | [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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010975&list=upload_1&organism=Homo%20sapiens) | 19.15 | 2.19 | + | 7.72E-06 | 3.96E-04 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&list=upload_1&organism=Homo%20sapiens) | 27.54 | 1.74 | + | 4.05E-04 | 1.21E-02 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&list=upload_1&organism=Homo%20sapiens) | 28.23 | 1.70 | + | 6.80E-04 | 1.86E-02 | | [negative regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031345) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031345&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031345&list=upload_1&organism=Homo%20sapiens) | 8.22 | 2.31 | + | 1.30E-03 | 3.08E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 4.48 | 3.13 | + | 3.63E-04 | 1.10E-02 | | [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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&list=upload_1&organism=Homo%20sapiens) | 3.57 | 3.08 | + | 1.68E-03 | 3.85E-02 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 31.97 | 1.69 | + | 3.63E-04 | 1.10E-02 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&list=upload_1&organism=Homo%20sapiens) | 8.31 | 2.29 | + | 1.43E-03 | 3.31E-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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&list=upload_1&organism=Homo%20sapiens) | 16.05 | 1.87 | + | 2.10E-03 | 4.61E-02 | | [positive regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051345) | [589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&list=upload_1&organism=Homo%20sapiens) | 25.35 | 1.74 | + | 7.45E-04 | 2.00E-02 | | [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) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 51.38 | 1.60 | + | 6.08E-05 | 2.47E-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) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 68.42 | 1.75 | + | 8.49E-09 | 8.12E-07 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&list=upload_1&organism=Homo%20sapiens) | 3.92 | 3.06 | + | 1.10E-03 | 2.72E-02 | | [regulation of endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010594) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&list=upload_1&organism=Homo%20sapiens) | 7.27 | 2.48 | + | 1.13E-03 | 2.76E-02 | | [regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010632) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&list=upload_1&organism=Homo%20sapiens) | 9.85 | 2.54 | + | 7.67E-05 | 3.01E-03 | | [stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0019827) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&list=upload_1&organism=Homo%20sapiens) | 4.91 | 3.06 | + | 2.84E-04 | 9.00E-03 | | [maintenance of cell number](http://amigo.geneontology.org/amigo/term/GO:0098727) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&list=upload_1&organism=Homo%20sapiens) | 5.08 | 2.95 | + | 3.95E-04 | 1.19E-02 | | [regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0051101) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 5.34 | 3.00 | + | 2.20E-04 | 7.31E-03 | | [regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051098) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&list=upload_1&organism=Homo%20sapiens) | 16.09 | 2.49 | + | 6.19E-07 | 4.39E-05 | | [cellular response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990830) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&list=upload_1&organism=Homo%20sapiens) | 4.00 | 3.00 | + | 1.30E-03 | 3.07E-02 | | [response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990823) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&list=upload_1&organism=Homo%20sapiens) | 4.05 | 2.97 | + | 1.41E-03 | 3.28E-02 | | [response to cytokine](http://amigo.geneontology.org/amigo/term/GO:0034097) | [808](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&list=upload_1&organism=Homo%20sapiens) | 34.77 | 1.87 | + | 4.83E-06 | 2.63E-04 | | [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) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 30.73 | 1.95 | + | 3.07E-06 | 1.77E-04 | | [cellular glucose homeostasis](http://amigo.geneontology.org/amigo/term/GO:0001678) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001678&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001678&list=upload_1&organism=Homo%20sapiens) | 4.35 | 2.99 | + | 8.50E-04 | 2.21E-02 | | [glucose homeostasis](http://amigo.geneontology.org/amigo/term/GO:0042593) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042593&list=upload_1&organism=Homo%20sapiens) | 8.65 | 2.31 | + | 9.59E-04 | 2.43E-02 | | [carbohydrate homeostasis](http://amigo.geneontology.org/amigo/term/GO:0033500) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033500&list=upload_1&organism=Homo%20sapiens) | 8.69 | 2.30 | + | 1.01E-03 | 2.53E-02 | | [homeostatic process](http://amigo.geneontology.org/amigo/term/GO:0042592) | [1424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&reflist=1) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&list=upload_1&organism=Homo%20sapiens) | 61.28 | 1.60 | + | 1.22E-05 | 6.04E-04 | | [regulation of biological quality](http://amigo.geneontology.org/amigo/term/GO:0065008) | [3677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&reflist=1) | [225](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 158.23 | 1.42 | + | 5.03E-08 | 4.19E-06 | | [cellular homeostasis](http://amigo.geneontology.org/amigo/term/GO:0019725) | [641](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019725&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019725&list=upload_1&organism=Homo%20sapiens) | 27.58 | 1.70 | + | 8.31E-04 | 2.18E-02 | | [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) | 9.38 | 2.98 | + | 1.26E-06 | 8.08E-05 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 14.33 | 2.51 | + | 1.88E-06 | 1.15E-04 | | [male gonad development](http://amigo.geneontology.org/amigo/term/GO:0008584) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008584&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008584&list=upload_1&organism=Homo%20sapiens) | 6.20 | 2.90 | + | 1.31E-04 | 4.74E-03 | | [development of primary male sexual characteristics](http://amigo.geneontology.org/amigo/term/GO:0046546) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046546&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046546&list=upload_1&organism=Homo%20sapiens) | 6.24 | 2.88 | + | 1.42E-04 | 5.02E-03 | | [male sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0046661) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046661&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046661&list=upload_1&organism=Homo%20sapiens) | 7.19 | 2.92 | + | 3.46E-05 | 1.52E-03 | | [sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0007548) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&list=upload_1&organism=Homo%20sapiens) | 12.14 | 2.72 | + | 9.73E-07 | 6.52E-05 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045137&list=upload_1&organism=Homo%20sapiens) | 9.94 | 2.92 | + | 1.24E-06 | 7.99E-05 | | [gonad development](http://amigo.geneontology.org/amigo/term/GO:0008406) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&list=upload_1&organism=Homo%20sapiens) | 9.73 | 2.98 | + | 8.30E-07 | 5.68E-05 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&list=upload_1&organism=Homo%20sapiens) | 4.13 | 2.90 | + | 1.66E-03 | 3.81E-02 | | [cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:0071560) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&list=upload_1&organism=Homo%20sapiens) | 6.63 | 2.72 | + | 2.79E-04 | 8.88E-03 | | [response to transforming growth factor beta](http://amigo.geneontology.org/amigo/term/GO:0071559) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&list=upload_1&organism=Homo%20sapiens) | 6.93 | 2.60 | + | 4.53E-04 | 1.32E-02 | | [response to growth factor](http://amigo.geneontology.org/amigo/term/GO:0070848) | [507](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 21.82 | 2.25 | + | 6.69E-07 | 4.68E-05 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 20.53 | 2.19 | + | 3.28E-06 | 1.86E-04 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&list=upload_1&organism=Homo%20sapiens) | 27.54 | 1.71 | + | 8.23E-04 | 2.17E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&list=upload_1&organism=Homo%20sapiens) | 5.51 | 2.90 | + | 3.04E-04 | 9.58E-03 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 11.92 | 2.18 | + | 4.04E-04 | 1.21E-02 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 12.48 | 2.08 | + | 8.55E-04 | 2.22E-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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 13.73 | 2.11 | + | 3.33E-04 | 1.03E-02 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&list=upload_1&organism=Homo%20sapiens) | 5.85 | 2.73 | + | 5.58E-04 | 1.58E-02 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&list=upload_1&organism=Homo%20sapiens) | 6.58 | 2.58 | + | 6.87E-04 | 1.87E-02 | | [mitotic spindle organization](http://amigo.geneontology.org/amigo/term/GO:0007052) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&list=upload_1&organism=Homo%20sapiens) | 4.17 | 2.87 | + | 1.80E-03 | 4.04E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&list=upload_1&organism=Homo%20sapiens) | 5.55 | 2.70 | + | 9.15E-04 | 2.35E-02 | | [regulation of G2/M transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0010389) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010389&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010389&list=upload_1&organism=Homo%20sapiens) | 4.22 | 2.85 | + | 1.95E-03 | 4.33E-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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902749&list=upload_1&organism=Homo%20sapiens) | 4.73 | 2.75 | + | 1.72E-03 | 3.91E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&list=upload_1&organism=Homo%20sapiens) | 4.95 | 2.83 | + | 8.96E-04 | 2.32E-02 | | [regulation of cyclin-dependent protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:1904029) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&list=upload_1&organism=Homo%20sapiens) | 5.08 | 2.76 | + | 1.12E-03 | 2.75E-02 | | [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) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&list=upload_1&organism=Homo%20sapiens) | 54.18 | 2.82 | + | 4.93E-29 | 1.61E-26 | | [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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&list=upload_1&organism=Homo%20sapiens) | 15.32 | 2.81 | + | 9.87E-09 | 9.21E-07 | | [retina development in camera-type eye](http://amigo.geneontology.org/amigo/term/GO:0060041) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060041&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060041&list=upload_1&organism=Homo%20sapiens) | 6.80 | 2.79 | + | 1.37E-04 | 4.91E-03 | | [camera-type eye development](http://amigo.geneontology.org/amigo/term/GO:0043010) | [334](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043010&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043010&list=upload_1&organism=Homo%20sapiens) | 14.37 | 2.02 | + | 7.25E-04 | 1.96E-02 | | [eye development](http://amigo.geneontology.org/amigo/term/GO:0001654) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001654&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001654&list=upload_1&organism=Homo%20sapiens) | 16.52 | 2.00 | + | 4.02E-04 | 1.20E-02 | | [sensory organ development](http://amigo.geneontology.org/amigo/term/GO:0007423) | [582](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007423&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007423&list=upload_1&organism=Homo%20sapiens) | 25.05 | 1.96 | + | 2.41E-05 | 1.10E-03 | | [visual system development](http://amigo.geneontology.org/amigo/term/GO:0150063) | [388](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0150063&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0150063&list=upload_1&organism=Homo%20sapiens) | 16.70 | 1.98 | + | 4.42E-04 | 1.29E-02 | | [sensory system development](http://amigo.geneontology.org/amigo/term/GO:0048880) | [394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048880&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048880&list=upload_1&organism=Homo%20sapiens) | 16.95 | 1.95 | + | 5.21E-04 | 1.49E-02 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 4.30 | 2.79 | + | 2.27E-03 | 4.87E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006354&list=upload_1&organism=Homo%20sapiens) | 7.96 | 2.76 | + | 4.88E-05 | 2.00E-03 | | [response to glucocorticoid](http://amigo.geneontology.org/amigo/term/GO:0051384) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&list=upload_1&organism=Homo%20sapiens) | 6.15 | 2.76 | + | 3.41E-04 | 1.05E-02 | | [response to corticosteroid](http://amigo.geneontology.org/amigo/term/GO:0031960) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&list=upload_1&organism=Homo%20sapiens) | 7.14 | 2.52 | + | 6.30E-04 | 1.74E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&list=upload_1&organism=Homo%20sapiens) | 8.35 | 2.76 | + | 3.46E-05 | 1.52E-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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007264&list=upload_1&organism=Homo%20sapiens) | 11.62 | 2.32 | + | 1.58E-04 | 5.50E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&list=upload_1&organism=Homo%20sapiens) | 7.79 | 2.70 | + | 9.87E-05 | 3.73E-03 | | [ear morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0042471) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042471&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042471&list=upload_1&organism=Homo%20sapiens) | 5.59 | 2.68 | + | 9.82E-04 | 2.48E-02 | | [ear development](http://amigo.geneontology.org/amigo/term/GO:0043583) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&list=upload_1&organism=Homo%20sapiens) | 9.98 | 2.40 | + | 1.84E-04 | 6.23E-03 | | [sensory organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0090596) | [279](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090596&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090596&list=upload_1&organism=Homo%20sapiens) | 12.01 | 2.33 | + | 1.11E-04 | 4.14E-03 | | [animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009887) | [1003](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&list=upload_1&organism=Homo%20sapiens) | 43.16 | 1.90 | + | 1.10E-07 | 8.83E-06 | | [embryonic organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048562) | [301](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048562&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048562&list=upload_1&organism=Homo%20sapiens) | 12.95 | 2.24 | + | 1.27E-04 | 4.65E-03 | | [embryonic organ development](http://amigo.geneontology.org/amigo/term/GO:0048568) | [454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&list=upload_1&organism=Homo%20sapiens) | 19.54 | 2.00 | + | 1.22E-04 | 4.48E-03 | | [aging](http://amigo.geneontology.org/amigo/term/GO:0007568) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&list=upload_1&organism=Homo%20sapiens) | 7.49 | 2.67 | + | 1.60E-04 | 5.54E-03 | | [myeloid cell homeostasis](http://amigo.geneontology.org/amigo/term/GO:0002262) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002262&list=upload_1&organism=Homo%20sapiens) | 5.68 | 2.64 | + | 1.13E-03 | 2.76E-02 | | [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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&list=upload_1&organism=Homo%20sapiens) | 11.06 | 2.17 | + | 7.36E-04 | 1.99E-02 | | [cardiac chamber morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003206) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003206&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003206&list=upload_1&organism=Homo%20sapiens) | 5.34 | 2.62 | + | 1.72E-03 | 3.91E-02 | | [heart morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003007) | [249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&list=upload_1&organism=Homo%20sapiens) | 10.72 | 2.43 | + | 8.67E-05 | 3.29E-03 | | [positive regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010634) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&list=upload_1&organism=Homo%20sapiens) | 6.50 | 2.62 | + | 6.00E-04 | 1.67E-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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&list=upload_1&organism=Homo%20sapiens) | 22.89 | 1.97 | + | 4.45E-05 | 1.87E-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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&list=upload_1&organism=Homo%20sapiens) | 24.01 | 1.87 | + | 1.53E-04 | 5.35E-03 | | [positive regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040017) | [574](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&list=upload_1&organism=Homo%20sapiens) | 24.70 | 1.86 | + | 1.27E-04 | 4.64E-03 | | [hepaticobiliary system development](http://amigo.geneontology.org/amigo/term/GO:0061008) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&list=upload_1&organism=Homo%20sapiens) | 5.77 | 2.60 | + | 1.30E-03 | 3.07E-02 | | [negative regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051100) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 7.01 | 2.57 | + | 5.18E-04 | 1.48E-02 | | [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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 49.49 | 1.58 | + | 1.51E-04 | 5.30E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 13.64 | 2.57 | + | 1.88E-06 | 1.15E-04 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 11.36 | 2.55 | + | 1.71E-05 | 8.16E-04 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 28.40 | 1.97 | + | 5.19E-06 | 2.79E-04 | | [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) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 30.55 | 2.03 | + | 6.92E-07 | 4.78E-05 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 32.58 | 1.96 | + | 1.01E-06 | 6.73E-05 | | [positive regulation of neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0010976) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010976&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010976&list=upload_1&organism=Homo%20sapiens) | 6.67 | 2.55 | + | 7.84E-04 | 2.08E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043433&list=upload_1&organism=Homo%20sapiens) | 7.49 | 2.54 | + | 4.17E-04 | 1.24E-02 | | [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) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&list=upload_1&organism=Homo%20sapiens) | 18.85 | 2.18 | + | 1.16E-05 | 5.75E-04 | | [peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018108) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&list=upload_1&organism=Homo%20sapiens) | 7.23 | 2.49 | + | 1.10E-03 | 2.72E-02 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 30.94 | 1.68 | + | 5.81E-04 | 1.63E-02 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 39.50 | 1.57 | + | 9.38E-04 | 2.39E-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) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 79.83 | 1.39 | + | 6.72E-04 | 1.84E-02 | | [phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006793) | [1881](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&list=upload_1&organism=Homo%20sapiens) | 80.94 | 1.37 | + | 1.11E-03 | 2.73E-02 | | [peptidyl-tyrosine modification](http://amigo.geneontology.org/amigo/term/GO:0018212) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&list=upload_1&organism=Homo%20sapiens) | 7.32 | 2.46 | + | 1.16E-03 | 2.83E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030308&list=upload_1&organism=Homo%20sapiens) | 8.09 | 2.47 | + | 5.54E-04 | 1.58E-02 | | [regulation of cell growth](http://amigo.geneontology.org/amigo/term/GO:0001558) | [429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&list=upload_1&organism=Homo%20sapiens) | 18.46 | 1.84 | + | 1.25E-03 | 2.99E-02 | | [regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0040008) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&list=upload_1&organism=Homo%20sapiens) | 26.98 | 1.78 | + | 2.46E-04 | 8.02E-03 | | [negative regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0045926) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045926&list=upload_1&organism=Homo%20sapiens) | 10.63 | 2.16 | + | 9.98E-04 | 2.51E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008361&list=upload_1&organism=Homo%20sapiens) | 8.18 | 2.45 | + | 5.95E-04 | 1.66E-02 | | [muscle organ development](http://amigo.geneontology.org/amigo/term/GO:0007517) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007517&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007517&list=upload_1&organism=Homo%20sapiens) | 13.08 | 2.45 | + | 1.12E-05 | 5.61E-04 | | [muscle structure development](http://amigo.geneontology.org/amigo/term/GO:0061061) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&list=upload_1&organism=Homo%20sapiens) | 21.47 | 2.47 | + | 1.24E-08 | 1.13E-06 | | [muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0042692) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&list=upload_1&organism=Homo%20sapiens) | 11.53 | 2.43 | + | 4.52E-05 | 1.87E-03 | | [cellular response to xenobiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071466) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071466&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071466&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.41 | + | 9.24E-04 | 2.38E-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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 18.20 | 2.53 | + | 5.70E-08 | 4.71E-06 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 7.87 | 2.41 | + | 9.24E-04 | 2.37E-02 | | [morphogenesis of a branching structure](http://amigo.geneontology.org/amigo/term/GO:0001763) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001763&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001763&list=upload_1&organism=Homo%20sapiens) | 7.53 | 2.39 | + | 1.38E-03 | 3.24E-02 | | [response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0000302) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&list=upload_1&organism=Homo%20sapiens) | 7.19 | 2.37 | + | 2.07E-03 | 4.56E-02 | | [response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0006979) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 15.79 | 1.96 | + | 7.83E-04 | 2.09E-02 | | [production of molecular mediator of immune response](http://amigo.geneontology.org/amigo/term/GO:0002440) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002440&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002440&list=upload_1&organism=Homo%20sapiens) | 7.27 | 2.34 | + | 2.23E-03 | 4.81E-02 | | [cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0045165) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&list=upload_1&organism=Homo%20sapiens) | 10.76 | 2.32 | + | 3.09E-04 | 9.64E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071248&list=upload_1&organism=Homo%20sapiens) | 8.61 | 2.32 | + | 9.14E-04 | 2.36E-02 | | [response to metal ion](http://amigo.geneontology.org/amigo/term/GO:0010038) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&list=upload_1&organism=Homo%20sapiens) | 15.62 | 2.18 | + | 5.92E-05 | 2.41E-03 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 9.47 | 2.32 | + | 4.99E-04 | 1.43E-02 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 8.65 | 2.31 | + | 9.59E-04 | 2.44E-02 | | [regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006282) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&list=upload_1&organism=Homo%20sapiens) | 9.12 | 2.30 | + | 7.44E-04 | 2.00E-02 | | [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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 13.51 | 2.44 | + | 8.35E-06 | 4.27E-04 | | [lung development](http://amigo.geneontology.org/amigo/term/GO:0030324) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&list=upload_1&organism=Homo%20sapiens) | 7.83 | 2.30 | + | 1.85E-03 | 4.15E-02 | | [respiratory tube development](http://amigo.geneontology.org/amigo/term/GO:0030323) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&list=upload_1&organism=Homo%20sapiens) | 8.00 | 2.25 | + | 2.22E-03 | 4.80E-02 | | [inner ear development](http://amigo.geneontology.org/amigo/term/GO:0048839) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048839&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048839&list=upload_1&organism=Homo%20sapiens) | 8.78 | 2.28 | + | 1.11E-03 | 2.73E-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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&list=upload_1&organism=Homo%20sapiens) | 11.53 | 2.25 | + | 2.82E-04 | 8.98E-03 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 17.77 | 2.25 | + | 6.51E-06 | 3.40E-04 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 17.77 | 2.25 | + | 6.51E-06 | 3.41E-04 | | [positive regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070374) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&list=upload_1&organism=Homo%20sapiens) | 9.34 | 2.25 | + | 1.38E-03 | 3.24E-02 | | [regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070372) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&list=upload_1&organism=Homo%20sapiens) | 13.04 | 2.30 | + | 6.72E-05 | 2.67E-03 | | [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) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 42.99 | 1.56 | + | 6.37E-04 | 1.75E-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) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 65.75 | 1.61 | + | 2.81E-06 | 1.63E-04 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 73.20 | 1.52 | + | 2.47E-05 | 1.12E-03 | | [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) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 72.98 | 1.52 | + | 2.40E-05 | 1.10E-03 | | [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) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 95.66 | 1.52 | + | 9.65E-07 | 6.50E-05 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 13.12 | 2.21 | + | 2.25E-04 | 7.47E-03 | | [gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0042063) | [246](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042063&list=upload_1&organism=Homo%20sapiens) | 10.59 | 2.17 | + | 9.61E-04 | 2.43E-02 | | [neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0022008) | [1290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&list=upload_1&organism=Homo%20sapiens) | 55.51 | 1.80 | + | 5.79E-08 | 4.76E-06 | | [anatomical structure homeostasis](http://amigo.geneontology.org/amigo/term/GO:0060249) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&list=upload_1&organism=Homo%20sapiens) | 13.04 | 2.15 | + | 3.75E-04 | 1.13E-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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&list=upload_1&organism=Homo%20sapiens) | 13.60 | 2.13 | + | 3.01E-04 | 9.49E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.11 | + | 1.64E-03 | 3.75E-02 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&list=upload_1&organism=Homo%20sapiens) | 14.03 | 2.00 | + | 1.03E-03 | 2.59E-02 | | [regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009894) | [987](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&list=upload_1&organism=Homo%20sapiens) | 42.47 | 1.58 | + | 4.44E-04 | 1.30E-02 | | [gland development](http://amigo.geneontology.org/amigo/term/GO:0048732) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&list=upload_1&organism=Homo%20sapiens) | 18.16 | 2.09 | + | 6.79E-05 | 2.70E-03 | | [cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008283) | [718](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&list=upload_1&organism=Homo%20sapiens) | 30.90 | 2.07 | + | 1.87E-07 | 1.42E-05 | | [negative regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040013) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&list=upload_1&organism=Homo%20sapiens) | 14.59 | 2.06 | + | 4.71E-04 | 1.37E-02 | | [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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 24.87 | 2.05 | + | 5.28E-06 | 2.83E-04 | | [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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 38.64 | 2.04 | + | 1.26E-08 | 1.14E-06 | | [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) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 39.50 | 2.05 | + | 6.73E-09 | 6.55E-07 | | [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) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&list=upload_1&organism=Homo%20sapiens) | 43.98 | 2.05 | + | 8.49E-10 | 9.06E-08 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 13.47 | 2.00 | + | 1.30E-03 | 3.07E-02 | | [multicellular organismal homeostasis](http://amigo.geneontology.org/amigo/term/GO:0048871) | [380](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048871&list=upload_1&organism=Homo%20sapiens) | 16.35 | 1.96 | + | 6.24E-04 | 1.73E-02 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 17.21 | 1.92 | + | 8.26E-04 | 2.18E-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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&list=upload_1&organism=Homo%20sapiens) | 15.66 | 1.92 | + | 1.24E-03 | 2.96E-02 | | [cell morphogenesis involved in neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0048667) | [440](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048667&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048667&list=upload_1&organism=Homo%20sapiens) | 18.93 | 1.90 | + | 6.11E-04 | 1.70E-02 | | [cell morphogenesis involved in differentiation](http://amigo.geneontology.org/amigo/term/GO:0000904) | [556](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000904&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000904&list=upload_1&organism=Homo%20sapiens) | 23.93 | 1.84 | + | 2.33E-04 | 7.65E-03 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 74.23 | 1.58 | + | 2.16E-06 | 1.31E-04 | | [cell morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0000902) | [713](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&list=upload_1&organism=Homo%20sapiens) | 30.68 | 1.60 | + | 2.11E-03 | 4.62E-02 | | [neuron development](http://amigo.geneontology.org/amigo/term/GO:0048666) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048666&list=upload_1&organism=Homo%20sapiens) | 36.28 | 1.76 | + | 3.57E-05 | 1.54E-03 | | [neuron differentiation](http://amigo.geneontology.org/amigo/term/GO:0030182) | [1065](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&list=upload_1&organism=Homo%20sapiens) | 45.83 | 1.79 | + | 1.21E-06 | 7.85E-05 | | [generation of neurons](http://amigo.geneontology.org/amigo/term/GO:0048699) | [1134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&list=upload_1&organism=Homo%20sapiens) | 48.80 | 1.76 | + | 1.16E-06 | 7.64E-05 | | [forebrain development](http://amigo.geneontology.org/amigo/term/GO:0030900) | [388](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&list=upload_1&organism=Homo%20sapiens) | 16.70 | 1.86 | + | 1.72E-03 | 3.91E-02 | | [chordate embryonic development](http://amigo.geneontology.org/amigo/term/GO:0043009) | [655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&list=upload_1&organism=Homo%20sapiens) | 28.19 | 1.84 | + | 6.64E-05 | 2.65E-03 | | [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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&list=upload_1&organism=Homo%20sapiens) | 29.13 | 1.82 | + | 8.69E-05 | 3.29E-03 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&list=upload_1&organism=Homo%20sapiens) | 16.83 | 1.84 | + | 1.84E-03 | 4.13E-02 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&list=upload_1&organism=Homo%20sapiens) | 41.87 | 1.55 | + | 7.54E-04 | 2.01E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002009&list=upload_1&organism=Homo%20sapiens) | 19.75 | 1.77 | + | 1.85E-03 | 4.14E-02 | | [tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048729) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&list=upload_1&organism=Homo%20sapiens) | 24.44 | 2.09 | + | 2.79E-06 | 1.63E-04 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 20.70 | 1.74 | + | 2.30E-03 | 4.91E-02 | | [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) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 49.53 | 1.98 | + | 7.03E-10 | 7.66E-08 | | [tube morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0035239) | [673](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035239&list=upload_1&organism=Homo%20sapiens) | 28.96 | 1.73 | + | 3.86E-04 | 1.16E-02 | | [cell division](http://amigo.geneontology.org/amigo/term/GO:0051301) | [514](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&list=upload_1&organism=Homo%20sapiens) | 22.12 | 1.72 | + | 2.20E-03 | 4.75E-02 | | [positive regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051347) | [590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&list=upload_1&organism=Homo%20sapiens) | 25.39 | 1.69 | + | 1.52E-03 | 3.49E-02 | | [cellular component morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032989) | [604](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&list=upload_1&organism=Homo%20sapiens) | 25.99 | 1.69 | + | 1.23E-03 | 2.95E-02 | | [spermatogenesis](http://amigo.geneontology.org/amigo/term/GO:0007283) | [592](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007283&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007283&list=upload_1&organism=Homo%20sapiens) | 25.48 | 1.69 | + | 1.55E-03 | 3.56E-02 | | [gamete generation](http://amigo.geneontology.org/amigo/term/GO:0007276) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007276&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007276&list=upload_1&organism=Homo%20sapiens) | 32.53 | 1.60 | + | 1.52E-03 | 3.49E-02 | | [leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0045321) | [581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&list=upload_1&organism=Homo%20sapiens) | 25.00 | 1.68 | + | 1.99E-03 | 4.41E-02 | | [positive regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001934) | [748](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&list=upload_1&organism=Homo%20sapiens) | 32.19 | 1.62 | + | 1.41E-03 | 3.27E-02 | | [positive regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042327) | [826](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&list=upload_1&organism=Homo%20sapiens) | 35.54 | 1.69 | + | 1.84E-04 | 6.24E-03 | | [positive regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045937) | [911](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&list=upload_1&organism=Homo%20sapiens) | 39.20 | 1.66 | + | 1.39E-04 | 4.95E-03 | | [positive regulation of phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010562) | [911](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&list=upload_1&organism=Homo%20sapiens) | 39.20 | 1.66 | + | 1.39E-04 | 4.97E-03 | | [neuron projection development](http://amigo.geneontology.org/amigo/term/GO:0031175) | [677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031175&list=upload_1&organism=Homo%20sapiens) | 29.13 | 1.61 | + | 2.22E-03 | 4.79E-02 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 38.86 | 1.60 | + | 6.31E-04 | 1.74E-02 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 40.92 | 1.59 | + | 4.73E-04 | 1.37E-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) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&list=upload_1&organism=Homo%20sapiens) | 39.76 | 1.56 | + | 9.84E-04 | 2.48E-02 | | [catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009056) | [1974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&list=upload_1&organism=Homo%20sapiens) | 84.95 | 1.37 | + | 9.40E-04 | 2.40E-02 | | Unclassified | [2725](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&list=upload_1&organism=Homo%20sapiens) | 117.26 | .21 | - | 3.10E-26 | 9.53E-24 | | [sphingolipid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006665) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006665&reflist=1) | [0](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006665&list=upload_1&organism=Homo%20sapiens) | 6.89 | < 0.01 | - | 2.13E-03 | 4.66E-02 | |

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