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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 | [546](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 943 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [614](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [487](http://pantherdb.org/tools/multipleMap.jsp?&listName=upload_1) |

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

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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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 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) | .18 | 21.83 | + | 2.22E-04 | 7.52E-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) | .18 | 21.83 | + | 2.22E-04 | 7.51E-03 | | [regulation of calcium ion transport](http://amigo.geneontology.org/amigo/term/GO:0051924) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051924&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051924&list=upload_1&organism=Homo%20sapiens) | 12.09 | 2.23 | + | 2.38E-04 | 7.97E-03 | | [regulation of metal ion transport](http://amigo.geneontology.org/amigo/term/GO:0010959) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010959&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010959&list=upload_1&organism=Homo%20sapiens) | 18.78 | 1.92 | + | 4.03E-04 | 1.21E-02 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [715](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 540.73 | 1.32 | + | 5.72E-31 | 2.72E-28 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [744](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 574.53 | 1.29 | + | 8.55E-31 | 3.94E-28 | | [regulation of cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1904062) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904062&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904062&list=upload_1&organism=Homo%20sapiens) | 17.59 | 1.82 | + | 2.21E-03 | 4.93E-02 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 512.38 | 1.33 | + | 3.03E-29 | 1.28E-26 | | [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) | [396](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 216.73 | 1.83 | + | 1.89E-36 | 1.18E-33 | | [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) | [421](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 243.39 | 1.73 | + | 4.96E-34 | 2.51E-31 | | [negative regulation of calcium ion transport](http://amigo.geneontology.org/amigo/term/GO:0051926) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051926&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051926&list=upload_1&organism=Homo%20sapiens) | 3.07 | 3.58 | + | 5.69E-04 | 1.62E-02 | | [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) | .14 | 21.83 | + | 1.52E-03 | 3.63E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 11.54 | 3.03 | + | 4.63E-08 | 4.06E-06 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 54.46 | 1.60 | + | 3.89E-05 | 1.74E-03 | | [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) | [177](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 108.27 | 1.63 | + | 2.24E-10 | 2.84E-08 | | [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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 31.60 | 1.87 | + | 1.54E-05 | 7.70E-04 | | [histone H4 deacetylation](http://amigo.geneontology.org/amigo/term/GO:0070933) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070933&list=upload_1&organism=Homo%20sapiens) | .37 | 19.10 | + | 1.43E-06 | 9.03E-05 | | [histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0016575) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&list=upload_1&organism=Homo%20sapiens) | 2.75 | 4.73 | + | 1.51E-05 | 7.56E-04 | | [histone modification](http://amigo.geneontology.org/amigo/term/GO:0016570) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&list=upload_1&organism=Homo%20sapiens) | 16.72 | 3.95 | + | 4.69E-19 | 1.31E-16 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 121.74 | 1.63 | + | 1.77E-11 | 2.57E-09 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 132.04 | 1.61 | + | 5.77E-12 | 8.96E-10 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 272.10 | 1.41 | + | 4.98E-14 | 9.75E-12 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [456](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 352.53 | 1.29 | + | 2.31E-11 | 3.24E-09 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 372.41 | 1.26 | + | 5.42E-10 | 6.39E-08 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [244](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 179.54 | 1.36 | + | 4.92E-07 | 3.49E-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) | [298](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 229.60 | 1.30 | + | 8.77E-07 | 5.90E-05 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [416](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 307.33 | 1.35 | + | 6.93E-13 | 1.29E-10 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [432](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 331.05 | 1.30 | + | 4.19E-11 | 5.71E-09 | | [protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0006476) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&list=upload_1&organism=Homo%20sapiens) | 2.93 | 4.78 | + | 6.50E-06 | 3.61E-04 | | [protein deacylation](http://amigo.geneontology.org/amigo/term/GO:0035601) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&list=upload_1&organism=Homo%20sapiens) | 3.44 | 4.08 | + | 3.10E-05 | 1.42E-03 | | [macromolecule deacylation](http://amigo.geneontology.org/amigo/term/GO:0098732) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&list=upload_1&organism=Homo%20sapiens) | 3.62 | 3.87 | + | 5.12E-05 | 2.18E-03 | | [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) | .23 | 17.47 | + | 3.86E-04 | 1.18E-02 | | [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) | .32 | 15.60 | + | 9.76E-05 | 3.77E-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) | 2.61 | 4.60 | + | 4.08E-05 | 1.80E-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) | 3.48 | 3.45 | + | 4.44E-04 | 1.32E-02 | | [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) | 4.58 | 3.28 | + | 1.50E-04 | 5.40E-03 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 36.37 | 1.98 | + | 1.67E-07 | 1.35E-05 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 115.33 | 1.47 | + | 9.18E-07 | 6.10E-05 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [405](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 302.56 | 1.34 | + | 9.56E-12 | 1.46E-09 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [816](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 689.03 | 1.18 | + | 1.53E-22 | 4.60E-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) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 104.24 | 1.74 | + | 9.61E-13 | 1.71E-10 | | [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) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 129.39 | 1.63 | + | 2.70E-12 | 4.51E-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) | [233](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 150.78 | 1.55 | + | 2.06E-11 | 2.93E-09 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 137.36 | 1.57 | + | 3.34E-11 | 4.59E-09 | | [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) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 139.69 | 1.59 | + | 6.54E-12 | 1.01E-09 | | [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) | [244](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 163.65 | 1.49 | + | 1.59E-10 | 2.05E-08 | | [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) | 2.61 | 4.60 | + | 4.08E-05 | 1.80E-03 | | [macromolecule methylation](http://amigo.geneontology.org/amigo/term/GO:0043414) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043414&list=upload_1&organism=Homo%20sapiens) | 12.82 | 2.73 | + | 4.55E-07 | 3.29E-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) | 15.07 | 2.39 | + | 6.42E-06 | 3.58E-04 | | [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) | .23 | 17.47 | + | 3.86E-04 | 1.18E-02 | | [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) | .23 | 17.47 | + | 3.86E-04 | 1.18E-02 | | [response to heat](http://amigo.geneontology.org/amigo/term/GO:0009408) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&list=upload_1&organism=Homo%20sapiens) | 4.72 | 3.18 | + | 2.00E-04 | 6.90E-03 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 158.75 | 1.61 | + | 1.13E-14 | 2.36E-12 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 375.98 | 1.33 | + | 3.34E-15 | 7.81E-13 | | [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) | 51.34 | 2.14 | + | 7.76E-13 | 1.43E-10 | | [cellular response to heat](http://amigo.geneontology.org/amigo/term/GO:0034605) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034605&list=upload_1&organism=Homo%20sapiens) | 2.47 | 4.04 | + | 4.37E-04 | 1.30E-02 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 73.24 | 1.91 | + | 1.11E-12 | 1.96E-10 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [417](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 300.87 | 1.39 | + | 1.50E-14 | 3.09E-12 | | [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) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090240&list=upload_1&organism=Homo%20sapiens) | .32 | 15.60 | + | 9.76E-05 | 3.76E-03 | | [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) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090239&list=upload_1&organism=Homo%20sapiens) | .64 | 7.80 | + | 1.11E-03 | 2.82E-02 | | [regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035065) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&list=upload_1&organism=Homo%20sapiens) | 3.11 | 6.74 | + | 1.82E-10 | 2.32E-08 | | [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) | 8.29 | 5.43 | + | 8.88E-18 | 2.44E-15 | | [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) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 71.59 | 2.08 | + | 2.41E-16 | 6.20E-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) | 118.49 | 1.73 | + | 2.74E-14 | 5.58E-12 | | [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) | [455](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 268.94 | 1.69 | + | 1.15E-35 | 6.68E-33 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 309.34 | 1.61 | + | 2.78E-35 | 1.55E-32 | | [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) | [479](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 284.61 | 1.68 | + | 7.21E-38 | 6.65E-35 | | [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) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 261.48 | 1.73 | + | 1.48E-37 | 1.22E-34 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000756&list=upload_1&organism=Homo%20sapiens) | 3.53 | 6.52 | + | 4.35E-11 | 5.88E-09 | | [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) | 4.08 | 6.13 | + | 1.91E-11 | 2.75E-09 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&list=upload_1&organism=Homo%20sapiens) | 1.69 | 7.67 | + | 1.58E-07 | 1.28E-05 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&list=upload_1&organism=Homo%20sapiens) | 1.97 | 7.11 | + | 1.15E-07 | 9.64E-06 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&list=upload_1&organism=Homo%20sapiens) | 2.43 | 6.59 | + | 3.48E-08 | 3.12E-06 | | [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) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 46.67 | 2.10 | + | 4.90E-11 | 6.57E-09 | | [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) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 69.39 | 1.82 | + | 5.06E-10 | 6.10E-08 | | [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) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 145.37 | 1.90 | + | 1.24E-25 | 4.06E-23 | | [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) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 176.70 | 1.79 | + | 1.26E-25 | 4.02E-23 | | [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) | [437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 288.73 | 1.51 | + | 6.54E-23 | 2.01E-20 | | [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) | [302](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 162.23 | 1.86 | + | 4.43E-27 | 1.54E-24 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 4.90 | 5.71 | + | 5.02E-12 | 8.03E-10 | | [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) | .32 | 12.48 | + | 9.42E-04 | 2.46E-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) | .60 | 13.44 | + | 1.61E-06 | 1.00E-04 | | [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) | 1.24 | 12.13 | + | 1.22E-10 | 1.58E-08 | | [regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031060) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&list=upload_1&organism=Homo%20sapiens) | 3.85 | 7.54 | + | 5.92E-15 | 1.33E-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) | [448](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 258.64 | 1.73 | + | 2.35E-37 | 1.76E-34 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031061&list=upload_1&organism=Homo%20sapiens) | 1.15 | 8.73 | + | 1.67E-06 | 1.04E-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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031057&list=upload_1&organism=Homo%20sapiens) | 2.24 | 5.79 | + | 2.27E-06 | 1.36E-04 | | [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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 23.04 | 2.30 | + | 1.35E-07 | 1.11E-05 | | [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) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 47.72 | 1.70 | + | 8.87E-06 | 4.78E-04 | | [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) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 126.59 | 2.23 | + | 2.35E-37 | 1.84E-34 | | [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) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 136.85 | 2.12 | + | 6.08E-35 | 3.18E-32 | | [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) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 110.33 | 2.42 | + | 7.24E-41 | 1.42E-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) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 103.69 | 2.43 | + | 1.40E-38 | 1.37E-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) | .60 | 11.76 | + | 1.42E-05 | 7.18E-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) | .60 | 11.76 | + | 1.42E-05 | 7.20E-04 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [392](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 252.96 | 1.55 | + | 1.68E-21 | 4.96E-19 | | [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) | [397](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 262.30 | 1.51 | + | 5.47E-20 | 1.56E-17 | | [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) | .37 | 10.92 | + | 1.36E-03 | 3.34E-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) | .60 | 10.08 | + | 1.15E-04 | 4.36E-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) | .37 | 10.92 | + | 1.36E-03 | 3.34E-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) | .37 | 10.92 | + | 1.36E-03 | 3.33E-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) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 32.75 | 2.47 | + | 1.42E-12 | 2.42E-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) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 51.39 | 2.20 | + | 8.68E-14 | 1.68E-11 | | [regulation of chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0051983) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&list=upload_1&organism=Homo%20sapiens) | 6.00 | 2.67 | + | 7.32E-04 | 2.00E-02 | | [positive regulation of attachment of spindle microtubules to kinetochore](http://amigo.geneontology.org/amigo/term/GO:0051987) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051987&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051987&list=upload_1&organism=Homo%20sapiens) | .50 | 9.92 | + | 4.65E-04 | 1.37E-02 | | [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) | [407](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 259.69 | 1.57 | + | 1.34E-23 | 4.21E-21 | | [positive regulation of cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0090068) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&list=upload_1&organism=Homo%20sapiens) | 11.50 | 2.35 | + | 1.48E-04 | 5.37E-03 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 16.17 | 2.47 | + | 1.08E-06 | 6.97E-05 | | [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) | .46 | 10.92 | + | 3.31E-04 | 1.05E-02 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006325) | [585](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&reflist=1) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&list=upload_1&organism=Homo%20sapiens) | 26.79 | 4.78 | + | 5.78E-44 | 9.07E-40 | | [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) | .37 | 10.92 | + | 1.36E-03 | 3.33E-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) | 3.53 | 4.25 | + | 1.04E-05 | 5.57E-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) | 4.95 | 4.45 | + | 4.90E-08 | 4.27E-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) | 6.82 | 3.37 | + | 1.89E-06 | 1.15E-04 | | [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) | 6.82 | 3.37 | + | 1.89E-06 | 1.15E-04 | | [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) | 4.17 | 3.60 | + | 5.84E-05 | 2.43E-03 | | [peptidyl-lysine modification](http://amigo.geneontology.org/amigo/term/GO:0018205) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&list=upload_1&organism=Homo%20sapiens) | 14.24 | 2.88 | + | 1.26E-08 | 1.19E-06 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 40.40 | 2.28 | + | 3.19E-12 | 5.16E-10 | | [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) | .46 | 10.92 | + | 3.31E-04 | 1.04E-02 | | [histone lysine demethylation](http://amigo.geneontology.org/amigo/term/GO:0070076) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070076&list=upload_1&organism=Homo%20sapiens) | 1.28 | 7.02 | + | 2.34E-05 | 1.11E-03 | | [histone demethylation](http://amigo.geneontology.org/amigo/term/GO:0016577) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016577&list=upload_1&organism=Homo%20sapiens) | 1.33 | 6.78 | + | 2.95E-05 | 1.37E-03 | | [protein demethylation](http://amigo.geneontology.org/amigo/term/GO:0006482) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006482&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006482&list=upload_1&organism=Homo%20sapiens) | 1.47 | 6.14 | + | 5.64E-05 | 2.36E-03 | | [protein dealkylation](http://amigo.geneontology.org/amigo/term/GO:0008214) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008214&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008214&list=upload_1&organism=Homo%20sapiens) | 1.47 | 6.14 | + | 5.64E-05 | 2.35E-03 | | [positive regulation of microtubule nucleation](http://amigo.geneontology.org/amigo/term/GO:0090063) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090063&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090063&list=upload_1&organism=Homo%20sapiens) | .37 | 10.92 | + | 1.36E-03 | 3.32E-02 | | [regulation of microtubule polymerization](http://amigo.geneontology.org/amigo/term/GO:0031113) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031113&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031113&list=upload_1&organism=Homo%20sapiens) | 2.52 | 3.97 | + | 4.96E-04 | 1.44E-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) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 43.56 | 1.56 | + | 5.30E-04 | 1.53E-02 | | [positive regulation of microtubule polymerization](http://amigo.geneontology.org/amigo/term/GO:0031116) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031116&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031116&list=upload_1&organism=Homo%20sapiens) | 1.47 | 4.78 | + | 1.36E-03 | 3.34E-02 | | [positive regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0010638) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&list=upload_1&organism=Homo%20sapiens) | 23.27 | 1.72 | + | 1.96E-03 | 4.46E-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) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 48.27 | 1.78 | + | 7.48E-07 | 5.10E-05 | | [histone H3-K4 demethylation](http://amigo.geneontology.org/amigo/term/GO:0034720) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034720&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034720&list=upload_1&organism=Homo%20sapiens) | .37 | 10.92 | + | 1.36E-03 | 3.32E-02 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&list=upload_1&organism=Homo%20sapiens) | .69 | 10.19 | + | 2.89E-05 | 1.34E-03 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090329&list=upload_1&organism=Homo%20sapiens) | 2.61 | 3.45 | + | 2.24E-03 | 4.99E-02 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 6.23 | 2.73 | + | 3.99E-04 | 1.21E-02 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 24.78 | 2.62 | + | 2.64E-11 | 3.66E-09 | | [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) | [372](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 186.27 | 2.00 | + | 1.21E-41 | 3.17E-38 | | [facultative heterochromatin formation](http://amigo.geneontology.org/amigo/term/GO:0140718) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140718&list=upload_1&organism=Homo%20sapiens) | .60 | 10.08 | + | 1.15E-04 | 4.37E-03 | | [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) | 2.38 | 6.72 | + | 2.79E-08 | 2.54E-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) | 2.84 | 7.04 | + | 2.61E-10 | 3.27E-08 | | [chromatin remodeling](http://amigo.geneontology.org/amigo/term/GO:0006338) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&list=upload_1&organism=Homo%20sapiens) | 14.79 | 6.02 | + | 4.76E-37 | 3.24E-34 | | [negative regulation of gene expression, epigenetic](http://amigo.geneontology.org/amigo/term/GO:0045814) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045814&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045814&list=upload_1&organism=Homo%20sapiens) | 3.02 | 5.95 | + | 1.85E-08 | 1.72E-06 | | [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) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 41.31 | 1.96 | + | 4.00E-08 | 3.54E-06 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [405](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 222.36 | 1.82 | + | 3.42E-37 | 2.43E-34 | | [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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040029&list=upload_1&organism=Homo%20sapiens) | 5.40 | 5.55 | + | 1.63E-12 | 2.75E-10 | | [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) | .50 | 9.92 | + | 4.65E-04 | 1.37E-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) | 2.38 | 7.14 | + | 4.84E-09 | 4.86E-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) | [274](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 142.99 | 1.92 | + | 5.59E-26 | 1.86E-23 | | [mitotic nuclear membrane reassembly](http://amigo.geneontology.org/amigo/term/GO:0007084) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007084&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007084&list=upload_1&organism=Homo%20sapiens) | .41 | 9.70 | + | 1.90E-03 | 4.36E-02 | | [nuclear membrane organization](http://amigo.geneontology.org/amigo/term/GO:0071763) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071763&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071763&list=upload_1&organism=Homo%20sapiens) | 2.02 | 3.97 | + | 1.78E-03 | 4.13E-02 | | [nucleus organization](http://amigo.geneontology.org/amigo/term/GO:0006997) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006997&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006997&list=upload_1&organism=Homo%20sapiens) | 6.69 | 2.84 | + | 1.16E-04 | 4.39E-03 | | [organelle organization](http://amigo.geneontology.org/amigo/term/GO:0006996) | [3026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&reflist=1) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&list=upload_1&organism=Homo%20sapiens) | 138.59 | 1.31 | + | 2.56E-04 | 8.43E-03 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 109.65 | 1.50 | + | 2.36E-07 | 1.80E-05 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 120.59 | 1.43 | + | 3.12E-06 | 1.81E-04 | | [mitotic nuclear membrane organization](http://amigo.geneontology.org/amigo/term/GO:0101024) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0101024&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0101024&list=upload_1&organism=Homo%20sapiens) | .41 | 9.70 | + | 1.90E-03 | 4.35E-02 | | [mitotic cell cycle process](http://amigo.geneontology.org/amigo/term/GO:1903047) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&list=upload_1&organism=Homo%20sapiens) | 24.41 | 2.25 | + | 1.77E-07 | 1.41E-05 | | [mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000278) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&list=upload_1&organism=Homo%20sapiens) | 28.72 | 2.12 | + | 1.92E-07 | 1.50E-05 | | [cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007049) | [1249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&list=upload_1&organism=Homo%20sapiens) | 57.21 | 2.13 | + | 3.97E-14 | 7.97E-12 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 38.52 | 1.92 | + | 3.50E-07 | 2.61E-05 | | [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) | 7.92 | 2.27 | + | 2.08E-03 | 4.65E-02 | | [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) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014898&list=upload_1&organism=Homo%20sapiens) | .64 | 9.36 | + | 1.59E-04 | 5.67E-03 | | [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) | 1.37 | 5.82 | + | 1.99E-04 | 6.89E-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) | 1.42 | 5.63 | + | 2.41E-04 | 8.04E-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) | 1.51 | 5.29 | + | 3.46E-04 | 1.08E-02 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [409](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 301.42 | 1.36 | + | 9.05E-13 | 1.63E-10 | | [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) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003299&list=upload_1&organism=Homo%20sapiens) | .64 | 9.36 | + | 1.59E-04 | 5.64E-03 | | [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) | 1.60 | 5.61 | + | 1.01E-04 | 3.89E-03 | | [cardiac muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0014887) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014887&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014887&list=upload_1&organism=Homo%20sapiens) | .64 | 9.36 | + | 1.59E-04 | 5.65E-03 | | [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) | 1.33 | 5.27 | + | 8.28E-04 | 2.20E-02 | | [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) | .55 | 9.10 | + | 6.35E-04 | 1.78E-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) | 5.18 | 3.09 | + | 1.66E-04 | 5.82E-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) | 5.36 | 3.17 | + | 7.93E-05 | 3.20E-03 | | [DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006281) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&list=upload_1&organism=Homo%20sapiens) | 23.27 | 2.11 | + | 4.34E-06 | 2.44E-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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 34.63 | 2.08 | + | 2.94E-08 | 2.65E-06 | | [DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0006310) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006310&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006310&list=upload_1&organism=Homo%20sapiens) | 11.22 | 2.14 | + | 1.30E-03 | 3.21E-02 | | [double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:0006302) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&list=upload_1&organism=Homo%20sapiens) | 9.30 | 2.90 | + | 3.26E-06 | 1.88E-04 | | [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) | .55 | 9.10 | + | 6.35E-04 | 1.78E-02 | | [nuclear DNA replication](http://amigo.geneontology.org/amigo/term/GO:0033260) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&list=upload_1&organism=Homo%20sapiens) | 1.10 | 5.46 | + | 1.67E-03 | 3.92E-02 | | [cell cycle DNA replication](http://amigo.geneontology.org/amigo/term/GO:0044786) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&list=upload_1&organism=Homo%20sapiens) | 1.15 | 5.24 | + | 2.00E-03 | 4.50E-02 | | [DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006260) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&list=upload_1&organism=Homo%20sapiens) | 9.39 | 2.88 | + | 3.85E-06 | 2.19E-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) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060765&list=upload_1&organism=Homo%20sapiens) | 1.28 | 8.58 | + | 5.82E-07 | 4.07E-05 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&list=upload_1&organism=Homo%20sapiens) | 3.34 | 5.98 | + | 2.83E-09 | 2.94E-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) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 136.90 | 1.54 | + | 3.76E-10 | 4.64E-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) | [279](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 184.76 | 1.51 | + | 8.30E-13 | 1.51E-10 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 154.30 | 1.50 | + | 4.55E-10 | 5.53E-08 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 154.85 | 1.49 | + | 1.11E-09 | 1.23E-07 | | [histone H3 deacetylation](http://amigo.geneontology.org/amigo/term/GO:0070932) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070932&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070932&list=upload_1&organism=Homo%20sapiens) | .60 | 8.40 | + | 8.48E-04 | 2.25E-02 | | [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) | .96 | 8.32 | + | 2.48E-05 | 1.17E-03 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&list=upload_1&organism=Homo%20sapiens) | 3.89 | 4.11 | + | 7.83E-06 | 4.26E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&list=upload_1&organism=Homo%20sapiens) | 7.92 | 2.78 | + | 4.76E-05 | 2.06E-03 | | [cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044770) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&list=upload_1&organism=Homo%20sapiens) | 8.38 | 2.86 | + | 1.39E-05 | 7.09E-04 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&list=upload_1&organism=Homo%20sapiens) | 3.98 | 4.27 | + | 2.64E-06 | 1.55E-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) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&list=upload_1&organism=Homo%20sapiens) | 158.20 | 2.14 | + | 3.35E-43 | 1.75E-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) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&list=upload_1&organism=Homo%20sapiens) | 158.29 | 2.14 | + | 3.66E-43 | 1.44E-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) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 158.70 | 2.14 | + | 7.46E-43 | 2.34E-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) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 180.36 | 2.01 | + | 4.33E-41 | 9.70E-38 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 190.67 | 1.96 | + | 6.65E-40 | 7.45E-37 | | [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) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 171.85 | 2.01 | + | 1.05E-38 | 1.09E-35 | | [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) | [371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 187.88 | 1.97 | + | 2.31E-40 | 2.78E-37 | | [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) | 1.24 | 8.09 | + | 2.93E-06 | 1.71E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051569&list=upload_1&organism=Homo%20sapiens) | 1.79 | 8.40 | + | 6.53E-09 | 6.44E-07 | | [protein localization to chromatin](http://amigo.geneontology.org/amigo/term/GO:0071168) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071168&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071168&list=upload_1&organism=Homo%20sapiens) | 1.37 | 8.01 | + | 1.01E-06 | 6.59E-05 | | [protein localization to chromosome](http://amigo.geneontology.org/amigo/term/GO:0034502) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&list=upload_1&organism=Homo%20sapiens) | 3.44 | 5.24 | + | 9.77E-08 | 8.29E-06 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 31.79 | 1.76 | + | 1.17E-04 | 4.41E-03 | | [cellular localization](http://amigo.geneontology.org/amigo/term/GO:0051641) | [2655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&reflist=1) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&list=upload_1&organism=Homo%20sapiens) | 121.60 | 1.33 | + | 2.49E-04 | 8.27E-03 | | [localization](http://amigo.geneontology.org/amigo/term/GO:0051179) | [4566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&reflist=1) | [265](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&list=upload_1&organism=Homo%20sapiens) | 209.13 | 1.27 | + | 3.21E-05 | 1.46E-03 | | [histone H3-K4 trimethylation](http://amigo.geneontology.org/amigo/term/GO:0080182) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080182&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080182&list=upload_1&organism=Homo%20sapiens) | 1.01 | 7.94 | + | 3.25E-05 | 1.48E-03 | | [peptidyl-lysine trimethylation](http://amigo.geneontology.org/amigo/term/GO:0018023) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018023&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018023&list=upload_1&organism=Homo%20sapiens) | 1.92 | 4.68 | + | 3.31E-04 | 1.05E-02 | | [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) | 2.11 | 5.22 | + | 3.11E-05 | 1.42E-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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&list=upload_1&organism=Homo%20sapiens) | 1.15 | 7.86 | + | 1.11E-05 | 5.85E-04 | | [histone H3-K9 demethylation](http://amigo.geneontology.org/amigo/term/GO:0033169) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033169&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033169&list=upload_1&organism=Homo%20sapiens) | .64 | 7.80 | + | 1.11E-03 | 2.82E-02 | | [epigenetic maintenance of chromatin in transcription-competent conformation](http://amigo.geneontology.org/amigo/term/GO:0045815) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045815&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045815&list=upload_1&organism=Homo%20sapiens) | .64 | 7.80 | + | 1.11E-03 | 2.81E-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) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 52.72 | 2.01 | + | 8.50E-11 | 1.12E-08 | | [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) | .78 | 7.71 | + | 3.69E-04 | 1.14E-02 | | [histone H4-K16 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043984) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043984&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043984&list=upload_1&organism=Homo%20sapiens) | .69 | 7.28 | + | 1.43E-03 | 3.45E-02 | | [histone H4 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043967) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&list=upload_1&organism=Homo%20sapiens) | 2.79 | 3.58 | + | 1.01E-03 | 2.61E-02 | | [histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0016573) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&list=upload_1&organism=Homo%20sapiens) | 5.77 | 3.12 | + | 6.02E-05 | 2.49E-03 | | [internal peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:0018393) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018393&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018393&list=upload_1&organism=Homo%20sapiens) | 6.05 | 3.14 | + | 3.46E-05 | 1.57E-03 | | [peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:0018394) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&list=upload_1&organism=Homo%20sapiens) | 6.18 | 3.07 | + | 4.55E-05 | 1.98E-03 | | [protein acetylation](http://amigo.geneontology.org/amigo/term/GO:0006473) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&list=upload_1&organism=Homo%20sapiens) | 7.10 | 3.10 | + | 1.05E-05 | 5.56E-04 | | [protein acylation](http://amigo.geneontology.org/amigo/term/GO:0043543) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&list=upload_1&organism=Homo%20sapiens) | 8.93 | 2.58 | + | 1.47E-04 | 5.32E-03 | | [internal protein amino acid acetylation](http://amigo.geneontology.org/amigo/term/GO:0006475) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006475&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006475&list=upload_1&organism=Homo%20sapiens) | 6.14 | 3.10 | + | 4.16E-05 | 1.83E-03 | | [positive regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060252) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060252&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060252&list=upload_1&organism=Homo%20sapiens) | .82 | 7.28 | + | 4.74E-04 | 1.39E-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) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 43.47 | 1.93 | + | 5.08E-08 | 4.40E-06 | | [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) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 76.67 | 2.02 | + | 6.70E-16 | 1.64E-13 | | [positive regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014015) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&list=upload_1&organism=Homo%20sapiens) | 3.02 | 3.97 | + | 1.40E-04 | 5.15E-03 | | [regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014013) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&list=upload_1&organism=Homo%20sapiens) | 4.63 | 4.54 | + | 7.27E-08 | 6.20E-06 | | [regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050767) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&list=upload_1&organism=Homo%20sapiens) | 17.08 | 2.52 | + | 1.85E-07 | 1.45E-05 | | [regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051960) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&list=upload_1&organism=Homo%20sapiens) | 20.70 | 2.08 | + | 1.91E-05 | 9.28E-04 | | [regulation of multicellular organismal development](http://amigo.geneontology.org/amigo/term/GO:2000026) | [1383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&reflist=1) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 63.34 | 2.02 | + | 3.38E-13 | 6.47E-11 | | [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) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 125.95 | 1.75 | + | 8.07E-16 | 1.95E-13 | | [regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0050793) | [2489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&reflist=1) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 114.00 | 1.82 | + | 1.58E-16 | 4.14E-14 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 23.50 | 2.30 | + | 1.00E-07 | 8.44E-06 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 72.41 | 2.10 | + | 6.45E-17 | 1.71E-14 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.46 | + | 7.64E-05 | 3.09E-03 | | [positive regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051962) | [279](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&list=upload_1&organism=Homo%20sapiens) | 12.78 | 2.03 | + | 1.59E-03 | 3.77E-02 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051094&list=upload_1&organism=Homo%20sapiens) | 61.33 | 2.18 | + | 3.60E-16 | 9.11E-14 | | [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) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 69.39 | 2.05 | + | 5.54E-15 | 1.26E-12 | | [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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 14.11 | 2.62 | + | 6.91E-07 | 4.75E-05 | | [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) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 40.49 | 2.52 | + | 4.28E-16 | 1.06E-13 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 1.60 | 6.24 | + | 1.95E-05 | 9.45E-04 | | [nucleosome assembly](http://amigo.geneontology.org/amigo/term/GO:0006334) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006334&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006334&list=upload_1&organism=Homo%20sapiens) | 4.26 | 7.04 | + | 8.96E-15 | 1.92E-12 | | [protein-DNA complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065004) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&list=upload_1&organism=Homo%20sapiens) | 9.16 | 4.26 | + | 1.16E-12 | 2.02E-10 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 58.17 | 1.75 | + | 1.23E-07 | 1.03E-05 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 65.18 | 1.84 | + | 5.65E-10 | 6.62E-08 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&list=upload_1&organism=Homo%20sapiens) | 10.67 | 4.31 | + | 7.24E-15 | 1.60E-12 | | [nucleosome organization](http://amigo.geneontology.org/amigo/term/GO:0034728) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&list=upload_1&organism=Homo%20sapiens) | 5.73 | 6.64 | + | 1.24E-17 | 3.35E-15 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902455&list=upload_1&organism=Homo%20sapiens) | 1.15 | 6.99 | + | 6.86E-05 | 2.81E-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) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&list=upload_1&organism=Homo%20sapiens) | 47.59 | 1.81 | + | 4.25E-07 | 3.10E-05 | | [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) | 42.27 | 2.01 | + | 8.29E-09 | 8.08E-07 | | [regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:2000036) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&list=upload_1&organism=Homo%20sapiens) | 3.21 | 4.37 | + | 1.58E-05 | 7.81E-04 | | [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) | 1.15 | 6.99 | + | 6.86E-05 | 2.80E-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) | 1.01 | 6.95 | + | 2.02E-04 | 6.94E-03 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 4.21 | 3.32 | + | 2.16E-04 | 7.34E-03 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 4.49 | 3.34 | + | 1.23E-04 | 4.59E-03 | | [DNA conformation change](http://amigo.geneontology.org/amigo/term/GO:0071103) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&list=upload_1&organism=Homo%20sapiens) | 4.90 | 3.06 | + | 2.90E-04 | 9.35E-03 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 20.34 | 2.31 | + | 5.27E-07 | 3.71E-05 | | [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) | 1.01 | 6.95 | + | 2.02E-04 | 6.92E-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) | 2.56 | 4.29 | + | 1.45E-04 | 5.31E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&list=upload_1&organism=Homo%20sapiens) | 6.78 | 2.51 | + | 1.55E-03 | 3.69E-02 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 223.83 | 1.29 | + | 3.35E-06 | 1.93E-04 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [305](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 239.59 | 1.27 | + | 3.21E-06 | 1.86E-04 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 244.67 | 1.27 | + | 2.60E-06 | 1.54E-04 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&list=upload_1&organism=Homo%20sapiens) | 3.53 | 3.97 | + | 4.00E-05 | 1.78E-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) | 6.00 | 2.83 | + | 2.69E-04 | 8.79E-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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 22.40 | 2.05 | + | 1.39E-05 | 7.11E-04 | | [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) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 92.79 | 1.86 | + | 1.02E-14 | 2.16E-12 | | [cellular response to chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0070887) | [2616](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&reflist=1) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 119.82 | 1.74 | + | 5.29E-15 | 1.22E-12 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [289](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 185.95 | 1.55 | + | 7.86E-15 | 1.71E-12 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 123.85 | 1.74 | + | 1.70E-15 | 4.05E-13 | | [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) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 50.70 | 1.95 | + | 1.74E-09 | 1.88E-07 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 62.79 | 1.88 | + | 2.77E-10 | 3.44E-08 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 35.13 | 1.94 | + | 9.81E-07 | 6.44E-05 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 6.96 | 3.59 | + | 2.39E-07 | 1.81E-05 | | [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) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 23.54 | 2.80 | + | 1.24E-12 | 2.14E-10 | | [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) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 40.26 | 2.33 | + | 4.75E-13 | 8.98E-11 | | [cellular response to lipid](http://amigo.geneontology.org/amigo/term/GO:0071396) | [519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&list=upload_1&organism=Homo%20sapiens) | 23.77 | 2.69 | + | 1.65E-11 | 2.42E-09 | | [response to lipid](http://amigo.geneontology.org/amigo/term/GO:0033993) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&list=upload_1&organism=Homo%20sapiens) | 38.61 | 2.43 | + | 4.52E-14 | 8.96E-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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 13.01 | 2.69 | + | 6.14E-07 | 4.26E-05 | | [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) | .87 | 6.89 | + | 6.01E-04 | 1.70E-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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&list=upload_1&organism=Homo%20sapiens) | .96 | 7.28 | + | 1.59E-04 | 5.66E-03 | | [protein-containing complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032984) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&list=upload_1&organism=Homo%20sapiens) | 6.14 | 2.61 | + | 9.12E-04 | 2.40E-02 | | [histone H3-K9 modification](http://amigo.geneontology.org/amigo/term/GO:0061647) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061647&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061647&list=upload_1&organism=Homo%20sapiens) | .73 | 6.82 | + | 1.80E-03 | 4.16E-02 | | [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) | 1.10 | 6.37 | + | 3.16E-04 | 1.00E-02 | | [regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045637) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 9.16 | 2.84 | + | 7.13E-06 | 3.95E-04 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 18.23 | 2.80 | + | 5.11E-10 | 6.11E-08 | | [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) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 69.62 | 1.71 | + | 3.70E-08 | 3.30E-06 | | [Fc-gamma receptor signaling pathway involved in phagocytosis](http://amigo.geneontology.org/amigo/term/GO:0038096) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038096&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038096&list=upload_1&organism=Homo%20sapiens) | .96 | 6.24 | + | 9.32E-04 | 2.44E-02 | | [Fc receptor mediated stimulatory signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002431) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002431&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002431&list=upload_1&organism=Homo%20sapiens) | 1.10 | 6.37 | + | 3.16E-04 | 1.00E-02 | | [immune response-regulating cell surface receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002768) | [315](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002768&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002768&list=upload_1&organism=Homo%20sapiens) | 14.43 | 2.01 | + | 7.61E-04 | 2.05E-02 | | [immune response-regulating signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002764) | [397](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&list=upload_1&organism=Homo%20sapiens) | 18.18 | 1.87 | + | 1.14E-03 | 2.87E-02 | | [regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050776) | [935](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&list=upload_1&organism=Homo%20sapiens) | 42.82 | 1.63 | + | 1.36E-04 | 5.03E-03 | | [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) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 99.57 | 1.42 | + | 5.22E-05 | 2.20E-03 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 111.25 | 1.43 | + | 7.84E-06 | 4.26E-04 | | [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) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 101.82 | 1.57 | + | 2.81E-08 | 2.55E-06 | | [positive regulation of immune system process](http://amigo.geneontology.org/amigo/term/GO:0002684) | [967](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 44.29 | 1.85 | + | 3.68E-07 | 2.72E-05 | | [Fc-gamma receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038094) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038094&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038094&list=upload_1&organism=Homo%20sapiens) | 1.33 | 5.27 | + | 8.28E-04 | 2.21E-02 | | [Fc receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038093) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038093&list=upload_1&organism=Homo%20sapiens) | 2.38 | 4.62 | + | 8.18E-05 | 3.26E-03 | | [immune response-regulating cell surface receptor signaling pathway involved in phagocytosis](http://amigo.geneontology.org/amigo/term/GO:0002433) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002433&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002433&list=upload_1&organism=Homo%20sapiens) | .96 | 6.24 | + | 9.32E-04 | 2.44E-02 | | [immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002252) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&list=upload_1&organism=Homo%20sapiens) | 21.53 | 1.86 | + | 3.95E-04 | 1.20E-02 | | [cellular response to zinc ion](http://amigo.geneontology.org/amigo/term/GO:0071294) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071294&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071294&list=upload_1&organism=Homo%20sapiens) | 1.15 | 6.11 | + | 3.89E-04 | 1.18E-02 | | [response to zinc ion](http://amigo.geneontology.org/amigo/term/GO:0010043) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010043&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010043&list=upload_1&organism=Homo%20sapiens) | 2.43 | 4.53 | + | 9.49E-05 | 3.69E-03 | | [response to metal ion](http://amigo.geneontology.org/amigo/term/GO:0010038) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&list=upload_1&organism=Homo%20sapiens) | 16.63 | 2.65 | + | 4.51E-08 | 3.97E-06 | | [response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0010035) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 24.41 | 2.46 | + | 2.32E-09 | 2.45E-07 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071248&list=upload_1&organism=Homo%20sapiens) | 9.16 | 2.95 | + | 2.54E-06 | 1.51E-04 | | [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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071241&list=upload_1&organism=Homo%20sapiens) | 10.53 | 2.94 | + | 4.84E-07 | 3.46E-05 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902459&list=upload_1&organism=Homo%20sapiens) | 2.15 | 6.04 | + | 1.53E-06 | 9.60E-05 | | [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) | 2.02 | 5.46 | + | 2.19E-05 | 1.05E-03 | | [regulation of nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:2000819) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000819&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000819&list=upload_1&organism=Homo%20sapiens) | 1.28 | 5.46 | + | 6.93E-04 | 1.90E-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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&list=upload_1&organism=Homo%20sapiens) | 9.71 | 2.47 | + | 1.40E-04 | 5.13E-03 | | [regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001020) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 14.38 | 2.57 | + | 9.22E-07 | 6.10E-05 | | [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) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 32.47 | 2.16 | + | 1.12E-08 | 1.08E-06 | | [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) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 62.88 | 1.86 | + | 6.66E-10 | 7.67E-08 | | [Fc-epsilon receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0038095) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038095&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0038095&list=upload_1&organism=Homo%20sapiens) | 1.10 | 5.46 | + | 1.67E-03 | 3.91E-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) | 1.10 | 5.46 | + | 1.67E-03 | 3.91E-02 | | [tube development](http://amigo.geneontology.org/amigo/term/GO:0035295) | [885](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&list=upload_1&organism=Homo%20sapiens) | 40.53 | 1.58 | + | 6.15E-04 | 1.74E-02 | | [anatomical structure development](http://amigo.geneontology.org/amigo/term/GO:0048856) | [5144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&reflist=1) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&list=upload_1&organism=Homo%20sapiens) | 235.60 | 1.38 | + | 3.85E-10 | 4.71E-08 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 260.01 | 1.38 | + | 5.70E-12 | 8.94E-10 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 193.65 | 1.43 | + | 5.42E-10 | 6.44E-08 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 175.78 | 1.44 | + | 1.11E-09 | 1.23E-07 | | [columnar/cuboidal epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002065) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.70 | + | 2.00E-03 | 4.52E-02 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 49.10 | 1.51 | + | 8.05E-04 | 2.15E-02 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 79.05 | 1.53 | + | 7.37E-06 | 4.07E-04 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [238](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 161.17 | 1.48 | + | 8.81E-10 | 9.94E-08 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 162.23 | 1.47 | + | 9.72E-10 | 1.09E-07 | | [positive regulation of protein maturation](http://amigo.geneontology.org/amigo/term/GO:1903319) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903319&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903319&list=upload_1&organism=Homo%20sapiens) | 1.33 | 5.27 | + | 8.28E-04 | 2.20E-02 | | [regulation of protein maturation](http://amigo.geneontology.org/amigo/term/GO:1903317) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903317&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903317&list=upload_1&organism=Homo%20sapiens) | 3.44 | 3.20 | + | 1.30E-03 | 3.22E-02 | | [lung epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060487) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&list=upload_1&organism=Homo%20sapiens) | 1.15 | 5.24 | + | 2.00E-03 | 4.51E-02 | | [lung cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060479) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&list=upload_1&organism=Homo%20sapiens) | 1.15 | 5.24 | + | 2.00E-03 | 4.50E-02 | | [lung development](http://amigo.geneontology.org/amigo/term/GO:0030324) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&list=upload_1&organism=Homo%20sapiens) | 8.34 | 2.76 | + | 3.53E-05 | 1.60E-03 | | [respiratory system development](http://amigo.geneontology.org/amigo/term/GO:0060541) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&list=upload_1&organism=Homo%20sapiens) | 9.44 | 2.44 | + | 2.25E-04 | 7.60E-03 | | [respiratory tube development](http://amigo.geneontology.org/amigo/term/GO:0030323) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&list=upload_1&organism=Homo%20sapiens) | 8.52 | 2.82 | + | 1.77E-05 | 8.69E-04 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 149.04 | 1.55 | + | 2.25E-11 | 3.18E-09 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045910&list=upload_1&organism=Homo%20sapiens) | 2.06 | 4.85 | + | 1.20E-04 | 4.52E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051053&list=upload_1&organism=Homo%20sapiens) | 6.78 | 2.95 | + | 4.85E-05 | 2.09E-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) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 71.54 | 2.96 | + | 1.62E-43 | 1.27E-39 | | [negative regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014014) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014014&list=upload_1&organism=Homo%20sapiens) | 1.88 | 4.79 | + | 2.83E-04 | 9.20E-03 | | [negative regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050768) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050768&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050768&list=upload_1&organism=Homo%20sapiens) | 6.60 | 3.18 | + | 1.14E-05 | 5.97E-04 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051961&list=upload_1&organism=Homo%20sapiens) | 6.82 | 3.08 | + | 1.81E-05 | 8.85E-04 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010721&list=upload_1&organism=Homo%20sapiens) | 8.38 | 2.51 | + | 3.59E-04 | 1.11E-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) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 30.96 | 2.07 | + | 2.07E-07 | 1.60E-05 | | [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) | 1.69 | 4.72 | + | 6.69E-04 | 1.86E-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) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 57.57 | 1.86 | + | 4.13E-09 | 4.18E-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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 62.15 | 1.83 | + | 1.96E-09 | 2.10E-07 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 62.43 | 1.83 | + | 3.07E-09 | 3.15E-07 | | [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) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 74.20 | 1.74 | + | 3.55E-09 | 3.62E-07 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070316&list=upload_1&organism=Homo%20sapiens) | 1.69 | 4.72 | + | 6.69E-04 | 1.86E-02 | | [aortic valve development](http://amigo.geneontology.org/amigo/term/GO:0003176) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&list=upload_1&organism=Homo%20sapiens) | 1.69 | 4.72 | + | 6.69E-04 | 1.85E-02 | | [semi-lunar valve development](http://amigo.geneontology.org/amigo/term/GO:1905314) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&list=upload_1&organism=Homo%20sapiens) | 1.88 | 4.26 | + | 1.20E-03 | 3.00E-02 | | [heart valve development](http://amigo.geneontology.org/amigo/term/GO:0003170) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&list=upload_1&organism=Homo%20sapiens) | 2.98 | 3.69 | + | 4.53E-04 | 1.34E-02 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 25.42 | 1.85 | + | 1.55E-04 | 5.56E-03 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 41.63 | 1.54 | + | 1.27E-03 | 3.15E-02 | | [cellular response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0071276) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071276&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071276&list=upload_1&organism=Homo%20sapiens) | 1.74 | 4.60 | + | 7.80E-04 | 2.10E-02 | | [response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0046686) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&list=upload_1&organism=Homo%20sapiens) | 2.79 | 4.30 | + | 7.25E-05 | 2.95E-03 | | [positive regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0043388) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&list=upload_1&organism=Homo%20sapiens) | 2.66 | 4.52 | + | 4.73E-05 | 2.05E-03 | | [regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0051101) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 5.68 | 3.17 | + | 4.99E-05 | 2.14E-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) | 17.13 | 2.34 | + | 4.15E-06 | 2.34E-04 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 141.71 | 1.51 | + | 1.23E-09 | 1.34E-07 | | [positive regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051099) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&list=upload_1&organism=Homo%20sapiens) | 8.29 | 2.90 | + | 1.18E-05 | 6.15E-04 | | [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) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 72.82 | 1.77 | + | 1.21E-09 | 1.32E-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) | 1.56 | 4.50 | + | 1.84E-03 | 4.24E-02 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&list=upload_1&organism=Homo%20sapiens) | 1.56 | 4.50 | + | 1.84E-03 | 4.23E-02 | | [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) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&list=upload_1&organism=Homo%20sapiens) | 2.02 | 4.47 | + | 4.46E-04 | 1.33E-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) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 78.55 | 2.44 | + | 7.68E-29 | 3.09E-26 | | [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) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 78.55 | 2.44 | + | 7.68E-29 | 3.17E-26 | | [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) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 78.82 | 2.44 | + | 9.96E-29 | 3.90E-26 | | [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) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 84.64 | 2.34 | + | 1.62E-27 | 5.91E-25 | | [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) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 94.26 | 2.26 | + | 5.78E-28 | 2.21E-25 | | [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) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 93.80 | 2.26 | + | 8.22E-28 | 3.07E-25 | | [positive regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009891) | [2087](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&reflist=1) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 95.59 | 2.23 | + | 2.75E-27 | 9.78E-25 | | [positive regulation of macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010557) | [1943](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&reflist=1) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 88.99 | 2.27 | + | 1.36E-26 | 4.64E-24 | | [myeloid leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002444) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002444&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002444&list=upload_1&organism=Homo%20sapiens) | 2.70 | 4.44 | + | 5.47E-05 | 2.29E-03 | | [leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002443) | [310](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&list=upload_1&organism=Homo%20sapiens) | 14.20 | 2.18 | + | 1.36E-04 | 5.03E-03 | | [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) | 2.06 | 4.37 | + | 5.14E-04 | 1.48E-02 | | [somatic stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0035019) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&list=upload_1&organism=Homo%20sapiens) | 2.56 | 4.29 | + | 1.45E-04 | 5.29E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&list=upload_1&organism=Homo%20sapiens) | 5.22 | 3.06 | + | 1.82E-04 | 6.33E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&list=upload_1&organism=Homo%20sapiens) | 5.40 | 3.15 | + | 8.70E-05 | 3.42E-03 | | [negative regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000059) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&list=upload_1&organism=Homo%20sapiens) | 2.34 | 4.28 | + | 2.93E-04 | 9.39E-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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 11.08 | 2.53 | + | 2.80E-05 | 1.30E-03 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&list=upload_1&organism=Homo%20sapiens) | 14.93 | 2.28 | + | 3.70E-05 | 1.66E-03 | | [negative regulation of proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1903051) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903051&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903051&list=upload_1&organism=Homo%20sapiens) | 2.98 | 3.36 | + | 1.55E-03 | 3.70E-02 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 34.03 | 1.76 | + | 6.51E-05 | 2.69E-03 | | [regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000058) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&list=upload_1&organism=Homo%20sapiens) | 7.88 | 2.54 | + | 4.82E-04 | 1.41E-02 | | [substantia nigra development](http://amigo.geneontology.org/amigo/term/GO:0021762) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&list=upload_1&organism=Homo%20sapiens) | 2.15 | 4.18 | + | 6.78E-04 | 1.87E-02 | | [midbrain development](http://amigo.geneontology.org/amigo/term/GO:0030901) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&list=upload_1&organism=Homo%20sapiens) | 4.08 | 2.94 | + | 1.54E-03 | 3.67E-02 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 35.50 | 1.66 | + | 2.72E-04 | 8.88E-03 | | [central nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007417) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 47.36 | 1.77 | + | 1.26E-06 | 8.01E-05 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 100.35 | 1.64 | + | 6.60E-10 | 7.66E-08 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 37.69 | 1.67 | + | 1.49E-04 | 5.37E-03 | | [response to testosterone](http://amigo.geneontology.org/amigo/term/GO:0033574) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033574&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033574&list=upload_1&organism=Homo%20sapiens) | 1.92 | 4.16 | + | 1.37E-03 | 3.34E-02 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 71.04 | 1.89 | + | 1.20E-11 | 1.80E-09 | | [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) | 1.97 | 4.06 | + | 1.57E-03 | 3.72E-02 | | [negative regulation of stress-activated MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0032873) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032873&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032873&list=upload_1&organism=Homo%20sapiens) | 2.24 | 4.01 | + | 8.81E-04 | 2.33E-02 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 78.82 | 1.70 | + | 6.46E-09 | 6.41E-07 | | [regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043408) | [672](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&list=upload_1&organism=Homo%20sapiens) | 30.78 | 1.88 | + | 1.23E-05 | 6.32E-04 | | [negative regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043409) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&list=upload_1&organism=Homo%20sapiens) | 7.79 | 2.57 | + | 2.65E-04 | 8.70E-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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&list=upload_1&organism=Homo%20sapiens) | 23.72 | 1.94 | + | 5.89E-05 | 2.44E-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) | 2.24 | 4.01 | + | 8.81E-04 | 2.33E-02 | | [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) | 2.24 | 4.01 | + | 8.81E-04 | 2.32E-02 | | [cellular senescence](http://amigo.geneontology.org/amigo/term/GO:0090398) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&list=upload_1&organism=Homo%20sapiens) | 2.75 | 4.00 | + | 2.47E-04 | 8.23E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&list=upload_1&organism=Homo%20sapiens) | 3.76 | 3.99 | + | 2.01E-05 | 9.65E-04 | | [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) | 2.02 | 3.97 | + | 1.78E-03 | 4.12E-02 | | [endoderm formation](http://amigo.geneontology.org/amigo/term/GO:0001706) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&list=upload_1&organism=Homo%20sapiens) | 2.47 | 3.64 | + | 1.61E-03 | 3.80E-02 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 3.71 | 3.23 | + | 7.38E-04 | 2.01E-02 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 102.46 | 1.37 | + | 2.39E-04 | 7.98E-03 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 48.50 | 1.65 | + | 2.79E-05 | 1.30E-03 | | [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) | 3.02 | 3.97 | + | 1.40E-04 | 5.14E-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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 42.55 | 1.86 | + | 5.17E-07 | 3.65E-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) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&list=upload_1&organism=Homo%20sapiens) | 45.30 | 1.83 | + | 4.87E-07 | 3.47E-05 | | [regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040012) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&list=upload_1&organism=Homo%20sapiens) | 47.36 | 1.84 | + | 1.81E-07 | 1.44E-05 | | [post-translational protein modification](http://amigo.geneontology.org/amigo/term/GO:0043687) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043687&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043687&list=upload_1&organism=Homo%20sapiens) | 2.29 | 3.93 | + | 1.00E-03 | 2.58E-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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&list=upload_1&organism=Homo%20sapiens) | 2.56 | 3.90 | + | 5.62E-04 | 1.61E-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) | 6.60 | 2.88 | + | 9.88E-05 | 3.80E-03 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 20.56 | 2.48 | + | 2.33E-08 | 2.14E-06 | | [regulation of erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045646) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&list=upload_1&organism=Homo%20sapiens) | 2.06 | 3.88 | + | 2.02E-03 | 4.55E-02 | | [positive regulation of lyase activity](http://amigo.geneontology.org/amigo/term/GO:0051349) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051349&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051349&list=upload_1&organism=Homo%20sapiens) | 2.34 | 3.85 | + | 1.13E-03 | 2.86E-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) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 54.69 | 1.63 | + | 1.58E-05 | 7.81E-04 | | [regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0050790) | [2373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&reflist=1) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 108.69 | 1.46 | + | 2.32E-06 | 1.38E-04 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 2.89 | 3.81 | + | 3.58E-04 | 1.11E-02 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 3.39 | 3.54 | + | 3.58E-04 | 1.11E-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) | 3.25 | 3.69 | + | 2.56E-04 | 8.43E-03 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.85 | + | 1.70E-04 | 5.93E-03 | | [rhythmic process](http://amigo.geneontology.org/amigo/term/GO:0048511) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 12.46 | 3.05 | + | 1.07E-08 | 1.04E-06 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&list=upload_1&organism=Homo%20sapiens) | 3.80 | 3.68 | + | 8.21E-05 | 3.26E-03 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 5.18 | 3.28 | + | 5.39E-05 | 2.27E-03 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 11.95 | 2.26 | + | 2.09E-04 | 7.14E-03 | | [biological process involved in interspecies interaction between organisms](http://amigo.geneontology.org/amigo/term/GO:0044419) | [1602](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&list=upload_1&organism=Homo%20sapiens) | 73.37 | 1.51 | + | 2.67E-05 | 1.25E-03 | | [negative regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031397) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&list=upload_1&organism=Homo%20sapiens) | 3.80 | 3.68 | + | 8.21E-05 | 3.25E-03 | | [negative regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903321) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&list=upload_1&organism=Homo%20sapiens) | 4.35 | 3.22 | + | 2.90E-04 | 9.37E-03 | | [regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903320) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&list=upload_1&organism=Homo%20sapiens) | 11.59 | 2.16 | + | 9.11E-04 | 2.40E-02 | | [regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031396) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&list=upload_1&organism=Homo%20sapiens) | 9.66 | 2.28 | + | 9.42E-04 | 2.46E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&list=upload_1&organism=Homo%20sapiens) | 3.89 | 3.60 | + | 1.03E-04 | 3.93E-03 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&list=upload_1&organism=Homo%20sapiens) | 6.50 | 3.23 | + | 9.44E-06 | 5.07E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&list=upload_1&organism=Homo%20sapiens) | 5.36 | 3.55 | + | 7.66E-06 | 4.20E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 6.00 | 3.67 | + | 9.15E-07 | 6.11E-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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 9.62 | 3.02 | + | 7.21E-07 | 4.94E-05 | | [regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902105) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 14.47 | 2.76 | + | 5.13E-08 | 4.42E-06 | | [regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051249) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&list=upload_1&organism=Homo%20sapiens) | 27.07 | 2.22 | + | 5.26E-08 | 4.51E-06 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 31.33 | 2.20 | + | 6.33E-09 | 6.32E-07 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 33.94 | 2.18 | + | 2.68E-09 | 2.80E-07 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&list=upload_1&organism=Homo%20sapiens) | 8.38 | 3.34 | + | 1.76E-07 | 1.41E-05 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 8.38 | 3.34 | + | 1.76E-07 | 1.40E-05 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051251&list=upload_1&organism=Homo%20sapiens) | 19.28 | 2.39 | + | 4.43E-07 | 3.22E-05 | | [positive regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002696) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&list=upload_1&organism=Homo%20sapiens) | 21.48 | 2.47 | + | 1.35E-08 | 1.27E-06 | | [positive regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050867) | [486](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&list=upload_1&organism=Homo%20sapiens) | 22.26 | 2.52 | + | 3.04E-09 | 3.14E-07 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 11.59 | 2.50 | + | 2.22E-05 | 1.06E-03 | | [positive regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903039) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 12.64 | 2.45 | + | 1.54E-05 | 7.68E-04 | | [regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903037) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&list=upload_1&organism=Homo%20sapiens) | 16.90 | 2.01 | + | 2.93E-04 | 9.42E-03 | | [regulation of cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0022407) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&list=upload_1&organism=Homo%20sapiens) | 22.17 | 2.08 | + | 1.21E-05 | 6.30E-04 | | [regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0030155) | [789](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 36.14 | 1.83 | + | 7.66E-06 | 4.18E-04 | | [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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 14.84 | 2.49 | + | 1.64E-06 | 1.02E-04 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 22.35 | 2.10 | + | 7.92E-06 | 4.28E-04 | | [regulation of T cell activation](http://amigo.geneontology.org/amigo/term/GO:0050863) | [377](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&list=upload_1&organism=Homo%20sapiens) | 17.27 | 2.08 | + | 8.43E-05 | 3.33E-03 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&list=upload_1&organism=Homo%20sapiens) | 8.20 | 3.05 | + | 3.46E-06 | 1.98E-04 | | [regulation of glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045685) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045685&list=upload_1&organism=Homo%20sapiens) | 3.39 | 3.54 | + | 3.58E-04 | 1.11E-02 | | [cellular response to retinoic acid](http://amigo.geneontology.org/amigo/term/GO:0071300) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071300&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071300&list=upload_1&organism=Homo%20sapiens) | 3.11 | 3.53 | + | 6.35E-04 | 1.78E-02 | | [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) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&list=upload_1&organism=Homo%20sapiens) | 48.50 | 2.00 | + | 7.75E-10 | 8.80E-08 | | [response to retinoic acid](http://amigo.geneontology.org/amigo/term/GO:0032526) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032526&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032526&list=upload_1&organism=Homo%20sapiens) | 5.18 | 2.90 | + | 4.88E-04 | 1.42E-02 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&list=upload_1&organism=Homo%20sapiens) | 3.44 | 3.49 | + | 3.99E-04 | 1.21E-02 | | [cellular response to radiation](http://amigo.geneontology.org/amigo/term/GO:0071478) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 8.34 | 2.28 | + | 1.50E-03 | 3.62E-02 | | [cellular response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071214) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 14.93 | 2.14 | + | 1.29E-04 | 4.82E-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) | 14.93 | 2.14 | + | 1.29E-04 | 4.81E-03 | | [positive regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001252) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 4.85 | 3.30 | + | 8.55E-05 | 3.37E-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) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 44.61 | 3.21 | + | 6.11E-32 | 2.99E-29 | | [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) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 60.59 | 3.10 | + | 1.03E-40 | 1.61E-37 | | [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) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 60.69 | 3.10 | + | 1.24E-40 | 1.77E-37 | | [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) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 60.78 | 3.09 | + | 1.50E-40 | 1.96E-37 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 65.72 | 3.00 | + | 7.66E-41 | 1.34E-37 | | [negative regulation of cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0031327) | [1594](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&reflist=1) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 73.01 | 2.70 | + | 5.10E-35 | 2.76E-32 | | [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) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 74.38 | 2.73 | + | 8.94E-37 | 5.84E-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) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 70.21 | 2.82 | + | 1.23E-37 | 1.07E-34 | | [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) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 119.36 | 2.25 | + | 9.11E-36 | 5.49E-33 | | [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) | 3.44 | 3.20 | + | 1.30E-03 | 3.23E-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) | 8.93 | 2.35 | + | 6.13E-04 | 1.73E-02 | | [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) | 7.51 | 3.20 | + | 2.63E-06 | 1.55E-04 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 8.79 | 3.30 | + | 1.36E-07 | 1.11E-05 | | [regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901987) | [431](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&list=upload_1&organism=Homo%20sapiens) | 19.74 | 2.33 | + | 6.11E-07 | 4.26E-05 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&list=upload_1&organism=Homo%20sapiens) | 15.21 | 2.30 | + | 1.56E-05 | 7.74E-04 | | [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) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 22.58 | 2.52 | + | 1.99E-09 | 2.12E-07 | | [telomere organization](http://amigo.geneontology.org/amigo/term/GO:0032200) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&list=upload_1&organism=Homo%20sapiens) | 4.72 | 3.18 | + | 2.00E-04 | 6.92E-03 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 4.76 | 3.15 | + | 2.20E-04 | 7.47E-03 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902807&list=upload_1&organism=Homo%20sapiens) | 3.85 | 3.12 | + | 9.83E-04 | 2.55E-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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045786&list=upload_1&organism=Homo%20sapiens) | 16.44 | 1.95 | + | 6.70E-04 | 1.85E-02 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010976&list=upload_1&organism=Homo%20sapiens) | 7.10 | 3.10 | + | 1.05E-05 | 5.54E-04 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010975&list=upload_1&organism=Homo%20sapiens) | 20.38 | 2.36 | + | 2.70E-07 | 2.03E-05 | | [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) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&list=upload_1&organism=Homo%20sapiens) | 29.31 | 1.81 | + | 9.24E-05 | 3.61E-03 | | [regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031344) | [656](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&list=upload_1&organism=Homo%20sapiens) | 30.05 | 1.76 | + | 1.64E-04 | 5.77E-03 | | [positive regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031346) | [351](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&list=upload_1&organism=Homo%20sapiens) | 16.08 | 1.99 | + | 5.45E-04 | 1.57E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010977&list=upload_1&organism=Homo%20sapiens) | 6.46 | 3.10 | + | 2.62E-05 | 1.23E-03 | | [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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031345&list=upload_1&organism=Homo%20sapiens) | 8.75 | 2.40 | + | 5.03E-04 | 1.46E-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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 4.58 | 3.06 | + | 4.62E-04 | 1.37E-02 | | [response to cAMP](http://amigo.geneontology.org/amigo/term/GO:0051591) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&list=upload_1&organism=Homo%20sapiens) | 4.26 | 3.05 | + | 7.38E-04 | 2.01E-02 | | [response to purine-containing compound](http://amigo.geneontology.org/amigo/term/GO:0014074) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&list=upload_1&organism=Homo%20sapiens) | 6.73 | 2.67 | + | 3.42E-04 | 1.07E-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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 44.34 | 1.78 | + | 2.71E-06 | 1.59E-04 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 48.64 | 1.75 | + | 1.77E-06 | 1.08E-04 | | [response to organophosphorus](http://amigo.geneontology.org/amigo/term/GO:0046683) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&list=upload_1&organism=Homo%20sapiens) | 6.05 | 2.65 | + | 7.89E-04 | 2.11E-02 | | [negative regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010507) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010507&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010507&list=upload_1&organism=Homo%20sapiens) | 3.94 | 3.05 | + | 1.18E-03 | 2.97E-02 | | [negative regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0032091) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&list=upload_1&organism=Homo%20sapiens) | 4.31 | 3.02 | + | 8.07E-04 | 2.15E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 7.47 | 2.55 | + | 4.15E-04 | 1.24E-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) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 52.67 | 1.69 | + | 4.02E-06 | 2.28E-04 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 9.21 | 2.28 | + | 1.31E-03 | 3.22E-02 | | [regulation of muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0043502) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&list=upload_1&organism=Homo%20sapiens) | 3.66 | 3.00 | + | 2.07E-03 | 4.64E-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) | 10.81 | 2.31 | + | 3.20E-04 | 1.01E-02 | | [cellular response to catecholamine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071870) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071870&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071870&list=upload_1&organism=Homo%20sapiens) | 4.44 | 2.93 | + | 1.05E-03 | 2.69E-02 | | [cellular response to monoamine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071868) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071868&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071868&list=upload_1&organism=Homo%20sapiens) | 4.44 | 2.93 | + | 1.05E-03 | 2.69E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 26.47 | 1.96 | + | 1.13E-05 | 5.92E-04 | | [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) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 29.36 | 1.91 | + | 1.22E-05 | 6.30E-04 | | [response to monoamine](http://amigo.geneontology.org/amigo/term/GO:0071867) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071867&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071867&list=upload_1&organism=Homo%20sapiens) | 4.58 | 2.84 | + | 1.34E-03 | 3.31E-02 | | [response to catecholamine](http://amigo.geneontology.org/amigo/term/GO:0071869) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071869&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071869&list=upload_1&organism=Homo%20sapiens) | 4.58 | 2.84 | + | 1.34E-03 | 3.32E-02 | | [regulation of circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0042752) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&list=upload_1&organism=Homo%20sapiens) | 5.50 | 2.91 | + | 3.07E-04 | 9.79E-03 | | [negative regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001237) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&list=upload_1&organism=Homo%20sapiens) | 4.49 | 2.90 | + | 1.14E-03 | 2.87E-02 | | [negative regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001234) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&list=upload_1&organism=Homo%20sapiens) | 10.49 | 2.38 | + | 1.53E-04 | 5.50E-03 | | [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) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 41.13 | 1.99 | + | 2.21E-08 | 2.04E-06 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 67.24 | 1.87 | + | 7.89E-11 | 1.05E-08 | | [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) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 68.61 | 1.89 | + | 1.44E-11 | 2.13E-09 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 75.76 | 1.85 | + | 1.31E-11 | 1.96E-09 | | [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) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 42.05 | 2.00 | + | 1.21E-08 | 1.16E-06 | | [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) | 46.81 | 1.92 | + | 1.71E-08 | 1.60E-06 | | [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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&list=upload_1&organism=Homo%20sapiens) | 16.67 | 2.22 | + | 1.99E-05 | 9.59E-04 | | [regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001236) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&list=upload_1&organism=Homo%20sapiens) | 7.05 | 2.41 | + | 1.86E-03 | 4.27E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&list=upload_1&organism=Homo%20sapiens) | 5.91 | 2.88 | + | 2.28E-04 | 7.69E-03 | | [cellular response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990830) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&list=upload_1&organism=Homo%20sapiens) | 4.26 | 2.82 | + | 2.15E-03 | 4.80E-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) | 37.01 | 1.76 | + | 3.02E-05 | 1.39E-03 | | [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) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 32.70 | 1.90 | + | 6.08E-06 | 3.40E-04 | | [positive regulation of tumor necrosis factor production](http://amigo.geneontology.org/amigo/term/GO:0032760) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032760&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032760&list=upload_1&organism=Homo%20sapiens) | 4.63 | 2.81 | + | 1.46E-03 | 3.52E-02 | | [positive regulation of tumor necrosis factor superfamily cytokine production](http://amigo.geneontology.org/amigo/term/GO:1903557) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903557&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903557&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.70 | + | 2.00E-03 | 4.52E-02 | | [positive regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001819) | [481](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 22.03 | 1.91 | + | 1.93E-04 | 6.70E-03 | | [myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002573) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&list=upload_1&organism=Homo%20sapiens) | 6.14 | 2.77 | + | 3.42E-04 | 1.07E-02 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 12.09 | 2.73 | + | 9.64E-07 | 6.35E-05 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 30.23 | 1.95 | + | 4.13E-06 | 2.34E-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) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 32.52 | 2.03 | + | 2.47E-07 | 1.86E-05 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 34.67 | 2.02 | + | 1.33E-07 | 1.11E-05 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 18.32 | 1.86 | + | 1.19E-03 | 3.00E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043433&list=upload_1&organism=Homo%20sapiens) | 7.97 | 2.76 | + | 5.15E-05 | 2.19E-03 | | [regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051090) | [438](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&list=upload_1&organism=Homo%20sapiens) | 20.06 | 2.34 | + | 4.06E-07 | 2.99E-05 | | [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) | 5.86 | 2.73 | + | 5.84E-04 | 1.66E-02 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 12.69 | 2.13 | + | 5.46E-04 | 1.57E-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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 13.28 | 2.03 | + | 1.20E-03 | 3.00E-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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 14.61 | 2.05 | + | 4.83E-04 | 1.41E-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) | 6.23 | 2.57 | + | 1.05E-03 | 2.69E-02 | | [peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018108) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&list=upload_1&organism=Homo%20sapiens) | 7.69 | 2.73 | + | 8.76E-05 | 3.43E-03 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 32.93 | 1.94 | + | 1.77E-06 | 1.08E-04 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 42.05 | 1.81 | + | 2.27E-06 | 1.36E-04 | | [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) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 84.96 | 1.57 | + | 6.58E-07 | 4.55E-05 | | [phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006793) | [1881](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&reflist=1) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&list=upload_1&organism=Homo%20sapiens) | 86.15 | 1.56 | + | 7.83E-07 | 5.32E-05 | | [peptidyl-tyrosine modification](http://amigo.geneontology.org/amigo/term/GO:0018212) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&list=upload_1&organism=Homo%20sapiens) | 7.79 | 2.70 | + | 1.02E-04 | 3.90E-03 | | [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) | 6.60 | 2.73 | + | 2.73E-04 | 8.87E-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) | 6.64 | 2.71 | + | 2.94E-04 | 9.42E-03 | | [male sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0046661) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046661&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046661&list=upload_1&organism=Homo%20sapiens) | 7.65 | 2.48 | + | 7.77E-04 | 2.09E-02 | | [sex differentiation](http://amigo.geneontology.org/amigo/term/GO:0007548) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007548&list=upload_1&organism=Homo%20sapiens) | 12.92 | 2.17 | + | 3.52E-04 | 1.10E-02 | | [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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&list=upload_1&organism=Homo%20sapiens) | 43.37 | 1.82 | + | 1.00E-06 | 6.55E-05 | | [reproductive process](http://amigo.geneontology.org/amigo/term/GO:0022414) | [1437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&reflist=1) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&list=upload_1&organism=Homo%20sapiens) | 65.82 | 1.64 | + | 1.13E-06 | 7.26E-05 | | [reproduction](http://amigo.geneontology.org/amigo/term/GO:0000003) | [1447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&reflist=1) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&list=upload_1&organism=Homo%20sapiens) | 66.27 | 1.64 | + | 8.86E-07 | 5.94E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045137&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.36 | + | 1.71E-04 | 5.95E-03 | | [gonad development](http://amigo.geneontology.org/amigo/term/GO:0008406) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008406&list=upload_1&organism=Homo%20sapiens) | 10.35 | 2.42 | + | 1.30E-04 | 4.82E-03 | | [reproductive structure development](http://amigo.geneontology.org/amigo/term/GO:0048608) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048608&list=upload_1&organism=Homo%20sapiens) | 13.74 | 2.26 | + | 6.70E-05 | 2.75E-03 | | [reproductive system development](http://amigo.geneontology.org/amigo/term/GO:0061458) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061458&list=upload_1&organism=Homo%20sapiens) | 13.92 | 2.23 | + | 1.14E-04 | 4.34E-03 | | [protein stabilization](http://amigo.geneontology.org/amigo/term/GO:0050821) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&list=upload_1&organism=Homo%20sapiens) | 9.98 | 2.70 | + | 1.06E-05 | 5.62E-04 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 15.25 | 2.49 | + | 1.20E-06 | 7.67E-05 | | [regulation of biological quality](http://amigo.geneontology.org/amigo/term/GO:0065008) | [3677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&reflist=1) | [234](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 168.41 | 1.39 | + | 1.98E-07 | 1.54E-05 | | [positive regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0045739) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&list=upload_1&organism=Homo%20sapiens) | 5.95 | 2.69 | + | 6.80E-04 | 1.87E-02 | | [positive regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001022) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&list=upload_1&organism=Homo%20sapiens) | 7.69 | 2.60 | + | 2.30E-04 | 7.74E-03 | | [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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 13.97 | 2.36 | + | 1.96E-05 | 9.43E-04 | | [hematopoietic progenitor cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002244) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002244&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002244&list=upload_1&organism=Homo%20sapiens) | 4.85 | 2.68 | + | 2.15E-03 | 4.81E-02 | | [response to estradiol](http://amigo.geneontology.org/amigo/term/GO:0032355) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&list=upload_1&organism=Homo%20sapiens) | 5.63 | 2.66 | + | 1.07E-03 | 2.75E-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) | 5.27 | 2.66 | + | 1.58E-03 | 3.74E-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) | 5.40 | 2.59 | + | 1.96E-03 | 4.46E-02 | | [regulation of protein kinase activity](http://amigo.geneontology.org/amigo/term/GO:0045859) | [668](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&list=upload_1&organism=Homo%20sapiens) | 30.60 | 1.73 | + | 2.69E-04 | 8.80E-03 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 35.86 | 1.73 | + | 7.05E-05 | 2.87E-03 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 57.16 | 1.73 | + | 4.10E-07 | 3.00E-05 | | [regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019220) | [1404](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&reflist=1) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 64.30 | 1.70 | + | 2.20E-07 | 1.69E-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) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 64.35 | 1.69 | + | 2.24E-07 | 1.72E-05 | | [regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051338) | [915](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 41.91 | 1.74 | + | 1.45E-05 | 7.27E-04 | | [regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001932) | [1105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 50.61 | 1.62 | + | 4.00E-05 | 1.78E-03 | | [regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071900) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&list=upload_1&organism=Homo%20sapiens) | 17.91 | 1.95 | + | 4.30E-04 | 1.29E-02 | | [positive regulation of protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0051897) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&list=upload_1&organism=Homo%20sapiens) | 5.31 | 2.64 | + | 1.70E-03 | 3.95E-02 | | [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) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 45.76 | 1.66 | + | 4.45E-05 | 1.94E-03 | | [positive regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009967) | [1528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 69.98 | 1.63 | + | 8.38E-07 | 5.66E-05 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 77.91 | 1.58 | + | 1.49E-06 | 9.37E-05 | | [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) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 77.68 | 1.58 | + | 1.08E-06 | 7.00E-05 | | [osteoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0001649) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&list=upload_1&organism=Homo%20sapiens) | 6.50 | 2.61 | + | 6.23E-04 | 1.76E-02 | | [regulation of proteasomal ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0032434) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&list=upload_1&organism=Homo%20sapiens) | 6.50 | 2.61 | + | 6.23E-04 | 1.75E-02 | | [cellular response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0034614) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&list=upload_1&organism=Homo%20sapiens) | 5.36 | 2.61 | + | 1.83E-03 | 4.21E-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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&list=upload_1&organism=Homo%20sapiens) | 7.65 | 2.35 | + | 1.56E-03 | 3.72E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 16.81 | 1.96 | + | 4.81E-04 | 1.41E-02 | | [regulation of double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:2000779) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000779&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000779&list=upload_1&organism=Homo%20sapiens) | 6.18 | 2.59 | + | 9.80E-04 | 2.54E-02 | | [positive regulation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043280) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043280&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043280&list=upload_1&organism=Homo%20sapiens) | 5.91 | 2.54 | + | 1.65E-03 | 3.88E-02 | | [regulation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043281) | [208](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.31 | + | 5.48E-04 | 1.57E-02 | | [regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051336) | [1020](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&list=upload_1&organism=Homo%20sapiens) | 46.72 | 1.50 | + | 1.36E-03 | 3.33E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&list=upload_1&organism=Homo%20sapiens) | 17.08 | 2.17 | + | 4.02E-05 | 1.78E-03 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&list=upload_1&organism=Homo%20sapiens) | 26.98 | 1.67 | + | 1.51E-03 | 3.62E-02 | | [endocrine system development](http://amigo.geneontology.org/amigo/term/GO:0035270) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&list=upload_1&organism=Homo%20sapiens) | 5.95 | 2.52 | + | 1.77E-03 | 4.10E-02 | | [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) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&list=upload_1&organism=Homo%20sapiens) | 16.31 | 2.51 | + | 3.67E-07 | 2.73E-05 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 28.08 | 2.60 | + | 3.01E-12 | 4.96E-10 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 28.12 | 2.60 | + | 3.12E-12 | 5.10E-10 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 28.58 | 2.55 | + | 5.07E-12 | 8.03E-10 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 68.11 | 1.62 | + | 2.21E-06 | 1.33E-04 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 116.06 | 1.32 | + | 5.96E-04 | 1.69E-02 | | [biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009058) | [2603](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&reflist=1) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&list=upload_1&organism=Homo%20sapiens) | 119.22 | 1.31 | + | 6.90E-04 | 1.90E-02 | | [nucleobase-containing compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0034654) | [1007](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 46.12 | 1.99 | + | 2.13E-09 | 2.26E-07 | | [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) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 72.73 | 1.54 | + | 1.39E-05 | 7.12E-04 | | [cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044249) | [2464](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&reflist=1) | [150](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&list=upload_1&organism=Homo%20sapiens) | 112.85 | 1.33 | + | 5.10E-04 | 1.48E-02 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 49.42 | 1.92 | + | 6.82E-09 | 6.69E-07 | | [organic cyclic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901362) | [1216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 55.69 | 1.78 | + | 1.39E-07 | 1.14E-05 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 49.88 | 1.90 | + | 1.23E-08 | 1.17E-06 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 74.88 | 1.64 | + | 1.93E-07 | 1.50E-05 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 105.98 | 1.50 | + | 4.83E-07 | 3.48E-05 | | [regulation of transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0017015) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017015&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017015&list=upload_1&organism=Homo%20sapiens) | 6.37 | 2.51 | + | 1.29E-03 | 3.22E-02 | | [regulation of cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:1903844) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903844&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903844&list=upload_1&organism=Homo%20sapiens) | 6.50 | 2.61 | + | 6.23E-04 | 1.75E-02 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090287&list=upload_1&organism=Homo%20sapiens) | 14.38 | 2.02 | + | 7.39E-04 | 2.00E-02 | | [negative regulation of epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050680) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050680&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050680&list=upload_1&organism=Homo%20sapiens) | 6.41 | 2.50 | + | 1.38E-03 | 3.36E-02 | | [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) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 32.66 | 2.27 | + | 6.67E-10 | 7.64E-08 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 10.08 | 2.48 | + | 9.61E-05 | 3.73E-03 | | [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) | 69.21 | 1.85 | + | 9.64E-11 | 1.26E-08 | | [peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018105) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&list=upload_1&organism=Homo%20sapiens) | 8.52 | 2.47 | + | 4.03E-04 | 1.21E-02 | | [peptidyl-serine modification](http://amigo.geneontology.org/amigo/term/GO:0018209) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&list=upload_1&organism=Homo%20sapiens) | 9.44 | 2.33 | + | 4.93E-04 | 1.43E-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) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&list=upload_1&organism=Homo%20sapiens) | 57.66 | 2.46 | + | 2.65E-21 | 7.69E-19 | | [response to toxic substance](http://amigo.geneontology.org/amigo/term/GO:0009636) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009636&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009636&list=upload_1&organism=Homo%20sapiens) | 10.63 | 2.45 | + | 8.05E-05 | 3.22E-03 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 8.38 | 2.39 | + | 7.34E-04 | 2.00E-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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&list=upload_1&organism=Homo%20sapiens) | 11.77 | 2.38 | + | 9.75E-05 | 3.78E-03 | | [homeostatic process](http://amigo.geneontology.org/amigo/term/GO:0042592) | [1424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&reflist=1) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&list=upload_1&organism=Homo%20sapiens) | 65.22 | 1.58 | + | 1.23E-05 | 6.34E-04 | | [regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001242) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&list=upload_1&organism=Homo%20sapiens) | 7.65 | 2.35 | + | 1.56E-03 | 3.72E-02 | | [epithelial cell development](http://amigo.geneontology.org/amigo/term/GO:0002064) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002064&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002064&list=upload_1&organism=Homo%20sapiens) | 8.75 | 2.29 | + | 1.09E-03 | 2.79E-02 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 79.01 | 1.57 | + | 1.73E-06 | 1.07E-04 | | [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) | 12.27 | 2.28 | + | 1.39E-04 | 5.13E-03 | | [muscle structure development](http://amigo.geneontology.org/amigo/term/GO:0061061) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&list=upload_1&organism=Homo%20sapiens) | 22.85 | 2.19 | + | 1.21E-06 | 7.73E-05 | | [response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0009416) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 14.52 | 2.27 | + | 5.21E-05 | 2.21E-03 | | [aging](http://amigo.geneontology.org/amigo/term/GO:0007568) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&list=upload_1&organism=Homo%20sapiens) | 7.97 | 2.26 | + | 2.18E-03 | 4.86E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&list=upload_1&organism=Homo%20sapiens) | 8.89 | 2.25 | + | 1.92E-03 | 4.39E-02 | | [cellular response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0071222) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&list=upload_1&organism=Homo%20sapiens) | 8.89 | 2.25 | + | 1.92E-03 | 4.38E-02 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 14.34 | 2.23 | + | 8.19E-05 | 3.26E-03 | | [response to molecule of bacterial origin](http://amigo.geneontology.org/amigo/term/GO:0002237) | [331](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&list=upload_1&organism=Homo%20sapiens) | 15.16 | 2.18 | + | 8.01E-05 | 3.22E-03 | | [response to external biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0043207) | [1432](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&reflist=1) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&list=upload_1&organism=Homo%20sapiens) | 65.59 | 1.43 | + | 7.21E-04 | 1.97E-02 | | [response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009607) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&list=upload_1&organism=Homo%20sapiens) | 67.69 | 1.43 | + | 6.69E-04 | 1.86E-02 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 113.08 | 1.41 | + | 1.44E-05 | 7.24E-04 | | [response to bacterium](http://amigo.geneontology.org/amigo/term/GO:0009617) | [754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&list=upload_1&organism=Homo%20sapiens) | 34.53 | 1.59 | + | 1.51E-03 | 3.62E-02 | | [response to other organism](http://amigo.geneontology.org/amigo/term/GO:0051707) | [1429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&list=upload_1&organism=Homo%20sapiens) | 65.45 | 1.41 | + | 1.75E-03 | 4.05E-02 | | [cellular response to molecule of bacterial origin](http://amigo.geneontology.org/amigo/term/GO:0071219) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&list=upload_1&organism=Homo%20sapiens) | 9.34 | 2.25 | + | 1.39E-03 | 3.37E-02 | | [cellular response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071216) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&list=upload_1&organism=Homo%20sapiens) | 10.58 | 2.17 | + | 9.72E-04 | 2.53E-02 | | [protein folding](http://amigo.geneontology.org/amigo/term/GO:0006457) | [221](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006457&list=upload_1&organism=Homo%20sapiens) | 10.12 | 2.17 | + | 1.29E-03 | 3.21E-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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 19.37 | 2.17 | + | 9.50E-06 | 5.08E-04 | | [ear development](http://amigo.geneontology.org/amigo/term/GO:0043583) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043583&list=upload_1&organism=Homo%20sapiens) | 10.63 | 2.16 | + | 1.01E-03 | 2.61E-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) | 13.88 | 2.16 | + | 2.01E-04 | 6.92E-03 | | [muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0060537) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&list=upload_1&organism=Homo%20sapiens) | 14.93 | 2.14 | + | 1.29E-04 | 4.80E-03 | | [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) | 12.27 | 2.12 | + | 7.54E-04 | 2.04E-02 | | [regulation of blood circulation](http://amigo.geneontology.org/amigo/term/GO:1903522) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903522&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903522&list=upload_1&organism=Homo%20sapiens) | 11.50 | 2.09 | + | 1.48E-03 | 3.57E-02 | | [adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains](http://amigo.geneontology.org/amigo/term/GO:0002460) | [265](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002460&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002460&list=upload_1&organism=Homo%20sapiens) | 12.14 | 2.06 | + | 1.25E-03 | 3.13E-02 | | [cellular response to growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0071363) | [477](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 21.85 | 2.06 | + | 1.75E-05 | 8.60E-04 | | [response to growth factor](http://amigo.geneontology.org/amigo/term/GO:0070848) | [507](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 23.22 | 2.07 | + | 7.47E-06 | 4.11E-04 | | [forebrain development](http://amigo.geneontology.org/amigo/term/GO:0030900) | [388](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030900&list=upload_1&organism=Homo%20sapiens) | 17.77 | 2.03 | + | 1.61E-04 | 5.68E-03 | | [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) | 13.88 | 2.02 | + | 9.55E-04 | 2.49E-02 | | [positive regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0045927) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045927&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045927&list=upload_1&organism=Homo%20sapiens) | 11.91 | 2.02 | + | 1.96E-03 | 4.46E-02 | | [regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0040008) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&list=upload_1&organism=Homo%20sapiens) | 28.72 | 1.85 | + | 5.27E-05 | 2.22E-03 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&list=upload_1&organism=Homo%20sapiens) | 24.37 | 1.97 | + | 2.97E-05 | 1.37E-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) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&list=upload_1&organism=Homo%20sapiens) | 25.56 | 1.92 | + | 4.53E-05 | 1.97E-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) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&list=upload_1&organism=Homo%20sapiens) | 26.29 | 1.94 | + | 2.39E-05 | 1.13E-03 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 18.92 | 1.96 | + | 2.54E-04 | 8.40E-03 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 18.92 | 1.96 | + | 2.54E-04 | 8.41E-03 | | [negative regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000146) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000146&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000146&list=upload_1&organism=Homo%20sapiens) | 13.88 | 1.95 | + | 1.69E-03 | 3.94E-02 | | [negative regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040013) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040013&list=upload_1&organism=Homo%20sapiens) | 15.53 | 2.00 | + | 7.04E-04 | 1.93E-02 | | [negative regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042326) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&list=upload_1&organism=Homo%20sapiens) | 16.72 | 1.91 | + | 1.09E-03 | 2.78E-02 | | [negative regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045936) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&list=upload_1&organism=Homo%20sapiens) | 19.33 | 1.81 | + | 1.60E-03 | 3.77E-02 | | [negative regulation of phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010563) | [423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&list=upload_1&organism=Homo%20sapiens) | 19.37 | 1.81 | + | 1.62E-03 | 3.80E-02 | | [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) | 23.04 | 1.91 | + | 1.14E-04 | 4.34E-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) | 23.63 | 1.90 | + | 9.32E-05 | 3.63E-03 | | [positive regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010942) | [583](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 26.70 | 1.87 | + | 6.56E-05 | 2.70E-03 | | [transmembrane receptor protein tyrosine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007169) | [424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007169&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007169&list=upload_1&organism=Homo%20sapiens) | 19.42 | 1.91 | + | 4.66E-04 | 1.37E-02 | | [enzyme-linked receptor protein signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007167) | [640](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007167&list=upload_1&organism=Homo%20sapiens) | 29.31 | 1.74 | + | 2.93E-04 | 9.41E-03 | | [regulation of cell growth](http://amigo.geneontology.org/amigo/term/GO:0001558) | [429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001558&list=upload_1&organism=Homo%20sapiens) | 19.65 | 1.88 | + | 5.13E-04 | 1.48E-02 | | [in utero embryonic development](http://amigo.geneontology.org/amigo/term/GO:0001701) | [395](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&list=upload_1&organism=Homo%20sapiens) | 18.09 | 1.88 | + | 1.11E-03 | 2.81E-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) | 30.00 | 1.73 | + | 2.48E-04 | 8.24E-03 | | [embryo development ending in birth or egg hatching](http://amigo.geneontology.org/amigo/term/GO:0009792) | 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[499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&list=upload_1&organism=Homo%20sapiens) | 22.85 | 1.84 | + | 3.81E-04 | 1.17E-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) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&list=upload_1&organism=Homo%20sapiens) | 27.02 | 1.81 | + | 1.63E-04 | 5.74E-03 | | [positive regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042327) | [826](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&list=upload_1&organism=Homo%20sapiens) | 37.83 | 1.67 | + | 2.06E-04 | 7.05E-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) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&list=upload_1&organism=Homo%20sapiens) | 41.72 | 1.63 | + | 1.61E-04 | 5.68E-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) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&list=upload_1&organism=Homo%20sapiens) | 41.72 | 1.63 | + | 1.61E-04 | 5.69E-03 | | [positive regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032103) | [455](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&list=upload_1&organism=Homo%20sapiens) | 20.84 | 1.82 | + | 7.48E-04 | 2.03E-02 | | [cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008283) | 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phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001934) | [748](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&list=upload_1&organism=Homo%20sapiens) | 34.26 | 1.66 | + | 4.03E-04 | 1.22E-02 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 47.31 | 1.65 | + | 4.23E-05 | 1.85E-03 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 49.19 | 1.61 | + | 8.01E-05 | 3.21E-03 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 50.75 | 1.60 | + | 7.56E-05 | 3.06E-03 | | [regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031347) | [642](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&list=upload_1&organism=Homo%20sapiens) | 29.40 | 1.63 | + | 1.68E-03 | 3.92E-02 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 41.36 | 1.60 | + | 3.80E-04 | 1.17E-02 | | [cell motility](http://amigo.geneontology.org/amigo/term/GO:0048870) | [1061](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&reflist=1) | 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[80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030182&list=upload_1&organism=Homo%20sapiens) | 48.78 | 1.64 | + | 3.95E-05 | 1.76E-03 | | [generation of neurons](http://amigo.geneontology.org/amigo/term/GO:0048699) | [1134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&list=upload_1&organism=Homo%20sapiens) | 51.94 | 1.62 | + | 3.57E-05 | 1.61E-03 | | [neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0022008) | [1290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&list=upload_1&organism=Homo%20sapiens) | 59.08 | 1.68 | + | 1.74E-06 | 1.07E-04 | | Unclassified | [2725](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&list=upload_1&organism=Homo%20sapiens) | 124.81 | .19 | - | 9.07E-30 | 4.06E-27 | |

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