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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 | [705](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 1239 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [778](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [604](http://pantherdb.org/tools/multipleMap.jsp?&listName=upload_1) |

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

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| |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | |  | [Homo sapiens](http://pantherdb.org/tools/gxIdsList.do?reflist=1) (REF) | [upload\_1](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) ( [Hierarchy](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1)  NEW! [Tips](javascript:;)) | | | | | | | [GO biological process complete](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=categories) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=Homo%20sapiens) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=num) | [expected](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=exp) | [Fold Enrichment](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=foldEnrich) | [+/-](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=rep) | [raw P value](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=pval) | [FDR](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=fdr) | | [error-free translesion synthesis](http://amigo.geneontology.org/amigo/term/GO:0070987) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070987&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070987&list=upload_1&organism=Homo%20sapiens) | .30 | 16.62 | + | 1.16E-04 | 3.14E-03 | | [translesion synthesis](http://amigo.geneontology.org/amigo/term/GO:0019985) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019985&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019985&list=upload_1&organism=Homo%20sapiens) | 1.44 | 9.69 | + | 8.96E-09 | 5.64E-07 | | [DNA synthesis involved in DNA repair](http://amigo.geneontology.org/amigo/term/GO:0000731) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000731&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000731&list=upload_1&organism=Homo%20sapiens) | 2.35 | 7.67 | + | 1.24E-09 | 8.79E-08 | | [DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006281) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&reflist=1) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006281&list=upload_1&organism=Homo%20sapiens) | 30.57 | 5.76 | + | 1.29E-68 | 5.05E-65 | | [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) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 45.49 | 4.77 | + | 9.84E-73 | 1.54E-68 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [293](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 96.22 | 3.04 | + | 5.53E-61 | 1.24E-57 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [609](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 395.31 | 1.54 | + | 3.18E-34 | 1.47E-31 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [1114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 905.31 | 1.23 | + | 1.31E-46 | 1.14E-43 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [718](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 494.00 | 1.45 | + | 1.73E-35 | 8.47E-33 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [433](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 208.58 | 2.08 | + | 7.18E-50 | 6.63E-47 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 47.78 | 4.52 | + | 7.60E-69 | 3.97E-65 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [327](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 151.53 | 2.16 | + | 9.61E-39 | 5.80E-36 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [687](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 397.53 | 1.73 | + | 2.24E-60 | 4.40E-57 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [768](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 489.31 | 1.57 | + | 5.45E-54 | 6.10E-51 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [639](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 357.52 | 1.79 | + | 4.19E-59 | 6.57E-56 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [740](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 463.19 | 1.60 | + | 1.08E-53 | 1.13E-50 | | [nucleic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090304) | [2276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&reflist=1) | [377](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 136.96 | 2.75 | + | 2.65E-70 | 2.07E-66 | | [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) | [407](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 170.00 | 2.39 | + | 3.43E-61 | 8.98E-58 | | [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) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 198.11 | 2.20 | + | 2.16E-56 | 2.82E-53 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 180.47 | 2.34 | + | 3.03E-61 | 9.51E-58 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 434.96 | 1.62 | + | 2.79E-51 | 2.73E-48 | | [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) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 183.54 | 2.30 | + | 2.06E-59 | 3.60E-56 | | [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) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 215.02 | 2.14 | + | 2.03E-57 | 2.90E-54 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [683](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 403.79 | 1.69 | + | 4.28E-56 | 5.16E-53 | | [DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0071897) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071897&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071897&list=upload_1&organism=Homo%20sapiens) | 5.90 | 5.43 | + | 1.08E-12 | 1.12E-10 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 89.48 | 2.05 | + | 1.67E-18 | 2.67E-16 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 152.49 | 1.65 | + | 1.12E-14 | 1.31E-12 | | [biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009058) | [2603](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&reflist=1) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009058&list=upload_1&organism=Homo%20sapiens) | 156.64 | 1.65 | + | 7.64E-15 | 9.01E-13 | | [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) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 60.60 | 2.71 | + | 8.48E-28 | 2.71E-25 | | [cellular nitrogen compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044271) | [1588](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&reflist=1) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 95.56 | 2.12 | + | 2.51E-22 | 4.68E-20 | | [cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044249) | [2464](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&reflist=1) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044249&list=upload_1&organism=Homo%20sapiens) | 148.28 | 1.69 | + | 1.80E-15 | 2.35E-13 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 64.93 | 2.65 | + | 4.85E-28 | 1.65E-25 | | [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) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 73.18 | 2.43 | + | 2.55E-25 | 6.88E-23 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 65.53 | 2.59 | + | 7.75E-27 | 2.25E-24 | | [postreplication repair](http://amigo.geneontology.org/amigo/term/GO:0006301) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006301&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006301&list=upload_1&organism=Homo%20sapiens) | 2.05 | 8.80 | + | 2.24E-10 | 1.75E-08 | | [nucleotide-excision repair, DNA incision, 5'-to lesion](http://amigo.geneontology.org/amigo/term/GO:0006296) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006296&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006296&list=upload_1&organism=Homo%20sapiens) | .24 | 16.62 | + | 6.01E-04 | 1.26E-02 | | [nucleotide-excision repair, DNA incision](http://amigo.geneontology.org/amigo/term/GO:0033683) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033683&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033683&list=upload_1&organism=Homo%20sapiens) | .48 | 14.54 | + | 8.03E-06 | 2.93E-04 | | [nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006289) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&list=upload_1&organism=Homo%20sapiens) | 3.37 | 9.79 | + | 6.20E-19 | 1.00E-16 | | [nucleic acid phosphodiester bond hydrolysis](http://amigo.geneontology.org/amigo/term/GO:0090305) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090305&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090305&list=upload_1&organism=Homo%20sapiens) | 15.53 | 2.19 | + | 9.65E-05 | 2.70E-03 | | [lagging strand elongation](http://amigo.geneontology.org/amigo/term/GO:0006273) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006273&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006273&list=upload_1&organism=Homo%20sapiens) | .24 | 16.62 | + | 6.01E-04 | 1.26E-02 | | [DNA strand elongation involved in DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006271) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006271&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006271&list=upload_1&organism=Homo%20sapiens) | .90 | 12.19 | + | 6.61E-08 | 3.64E-06 | | [DNA strand elongation](http://amigo.geneontology.org/amigo/term/GO:0022616) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022616&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022616&list=upload_1&organism=Homo%20sapiens) | 1.20 | 9.97 | + | 8.29E-08 | 4.47E-06 | | [DNA-templated DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006261) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006261&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006261&list=upload_1&organism=Homo%20sapiens) | 8.36 | 6.93 | + | 3.24E-26 | 9.25E-24 | | [DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006260) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&list=upload_1&organism=Homo%20sapiens) | 12.34 | 6.40 | + | 2.17E-33 | 9.71E-31 | | [cellular response to camptothecin](http://amigo.geneontology.org/amigo/term/GO:0072757) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072757&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072757&list=upload_1&organism=Homo%20sapiens) | .24 | 16.62 | + | 6.01E-04 | 1.26E-02 | | [response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097305) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&list=upload_1&organism=Homo%20sapiens) | 15.29 | 2.16 | + | 1.44E-04 | 3.75E-03 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 162.72 | 1.70 | + | 1.74E-17 | 2.62E-15 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [359](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 244.32 | 1.47 | + | 4.81E-14 | 5.43E-12 | | [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) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 93.34 | 1.79 | + | 3.30E-12 | 3.11E-10 | | [cellular response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0071310) | [2026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&reflist=1) | [216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 121.92 | 1.77 | + | 2.25E-15 | 2.84E-13 | | [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) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 157.43 | 1.66 | + | 2.22E-15 | 2.83E-13 | | [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) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901701&list=upload_1&organism=Homo%20sapiens) | 63.73 | 1.80 | + | 8.34E-09 | 5.30E-07 | | [response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0010243) | [968](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 58.25 | 1.79 | + | 6.99E-08 | 3.82E-06 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 63.91 | 1.89 | + | 2.28E-10 | 1.78E-08 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 34.78 | 1.87 | + | 5.78E-06 | 2.16E-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) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 38.57 | 1.92 | + | 6.00E-07 | 2.78E-05 | | [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) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 66.62 | 1.76 | + | 2.42E-08 | 1.45E-06 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 82.50 | 1.75 | + | 7.52E-10 | 5.51E-08 | | [response to camptothecin](http://amigo.geneontology.org/amigo/term/GO:1901563) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901563&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901563&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.00E-02 | | [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) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 52.90 | 2.02 | + | 8.16E-11 | 6.74E-09 | | [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) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 30.93 | 2.07 | + | 3.52E-07 | 1.70E-05 | | [DNA ligation involved in DNA repair](http://amigo.geneontology.org/amigo/term/GO:0051103) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051103&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051103&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.00E-02 | | [DNA ligation](http://amigo.geneontology.org/amigo/term/GO:0006266) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006266&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006266&list=upload_1&organism=Homo%20sapiens) | .60 | 13.29 | + | 2.76E-06 | 1.15E-04 | | [strand invasion](http://amigo.geneontology.org/amigo/term/GO:0042148) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042148&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042148&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.00E-02 | | [DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0006310) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006310&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006310&list=upload_1&organism=Homo%20sapiens) | 14.74 | 5.22 | + | 8.39E-28 | 2.74E-25 | | [mitotic DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:1902975) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902975&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902975&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.00E-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) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903047&list=upload_1&organism=Homo%20sapiens) | 32.07 | 2.99 | + | 4.87E-19 | 7.96E-17 | | [mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000278) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&reflist=1) | [109](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000278&list=upload_1&organism=Homo%20sapiens) | 37.73 | 2.89 | + | 1.80E-20 | 3.10E-18 | | [cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007049) | [1249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&reflist=1) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007049&list=upload_1&organism=Homo%20sapiens) | 75.16 | 2.49 | + | 1.20E-27 | 3.61E-25 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 50.61 | 2.73 | + | 1.35E-23 | 2.91E-21 | | [mitotic DNA replication](http://amigo.geneontology.org/amigo/term/GO:1902969) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902969&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902969&list=upload_1&organism=Homo%20sapiens) | .72 | 12.46 | + | 9.38E-07 | 4.20E-05 | | [nuclear DNA replication](http://amigo.geneontology.org/amigo/term/GO:0033260) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033260&list=upload_1&organism=Homo%20sapiens) | 1.44 | 9.69 | + | 8.96E-09 | 5.67E-07 | | [cell cycle DNA replication](http://amigo.geneontology.org/amigo/term/GO:0044786) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044786&list=upload_1&organism=Homo%20sapiens) | 1.50 | 9.31 | + | 1.32E-08 | 8.21E-07 | | [nuclear cell cycle DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:1902315) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902315&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902315&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.01E-02 | | [cell cycle DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:1902292) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902292&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902292&list=upload_1&organism=Homo%20sapiens) | .30 | 13.29 | + | 1.03E-03 | 2.01E-02 | | [DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:0006270) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006270&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006270&list=upload_1&organism=Homo%20sapiens) | 1.75 | 9.74 | + | 2.15E-10 | 1.71E-08 | | [base-excision repair, gap-filling](http://amigo.geneontology.org/amigo/term/GO:0006287) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006287&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006287&list=upload_1&organism=Homo%20sapiens) | .84 | 13.06 | + | 4.02E-08 | 2.28E-06 | | [base-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006284) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006284&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006284&list=upload_1&organism=Homo%20sapiens) | 2.53 | 10.29 | + | 1.36E-15 | 1.80E-13 | | [t-circle formation](http://amigo.geneontology.org/amigo/term/GO:0090656) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090656&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090656&list=upload_1&organism=Homo%20sapiens) | .66 | 12.09 | + | 4.54E-06 | 1.72E-04 | | [telomere maintenance via telomere trimming](http://amigo.geneontology.org/amigo/term/GO:0090737) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090737&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090737&list=upload_1&organism=Homo%20sapiens) | .66 | 12.09 | + | 4.54E-06 | 1.73E-04 | | [telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0000723) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&list=upload_1&organism=Homo%20sapiens) | 5.66 | 6.54 | + | 1.50E-16 | 2.12E-14 | | [telomere organization](http://amigo.geneontology.org/amigo/term/GO:0032200) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&list=upload_1&organism=Homo%20sapiens) | 6.20 | 6.13 | + | 3.26E-16 | 4.53E-14 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 26.72 | 4.12 | + | 1.40E-31 | 5.64E-29 | | [organelle organization](http://amigo.geneontology.org/amigo/term/GO:0006996) | [3026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&reflist=1) | [298](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&list=upload_1&organism=Homo%20sapiens) | 182.10 | 1.64 | + | 5.74E-17 | 8.33E-15 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [502](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 332.36 | 1.51 | + | 6.26E-24 | 1.42E-21 | | [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) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 344.64 | 1.49 | + | 2.73E-23 | 5.63E-21 | | [formation of extrachromosomal circular DNA](http://amigo.geneontology.org/amigo/term/GO:0001325) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001325&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001325&list=upload_1&organism=Homo%20sapiens) | .66 | 12.09 | + | 4.54E-06 | 1.72E-04 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 144.07 | 1.47 | + | 4.22E-08 | 2.37E-06 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [227](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 158.45 | 1.43 | + | 8.74E-08 | 4.69E-06 | | [replication-born double-strand break repair via sister chromatid exchange](http://amigo.geneontology.org/amigo/term/GO:1990414) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990414&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990414&list=upload_1&organism=Homo%20sapiens) | .42 | 11.87 | + | 3.31E-04 | 7.58E-03 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000724&list=upload_1&organism=Homo%20sapiens) | 6.80 | 7.06 | + | 3.55E-22 | 6.54E-20 | | [recombinational repair](http://amigo.geneontology.org/amigo/term/GO:0000725) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000725&list=upload_1&organism=Homo%20sapiens) | 7.04 | 6.96 | + | 2.12E-22 | 4.00E-20 | | [double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:0006302) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&reflist=1) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006302&list=upload_1&organism=Homo%20sapiens) | 12.22 | 6.88 | + | 2.83E-37 | 1.53E-34 | | [DNA topological change](http://amigo.geneontology.org/amigo/term/GO:0006265) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006265&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006265&list=upload_1&organism=Homo%20sapiens) | .60 | 11.63 | + | 2.19E-05 | 7.38E-04 | | [DNA conformation change](http://amigo.geneontology.org/amigo/term/GO:0071103) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&list=upload_1&organism=Homo%20sapiens) | 6.44 | 6.37 | + | 7.44E-18 | 1.14E-15 | | [error-prone translesion synthesis](http://amigo.geneontology.org/amigo/term/GO:0042276) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042276&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042276&list=upload_1&organism=Homo%20sapiens) | .60 | 11.63 | + | 2.19E-05 | 7.36E-04 | | [somatic hypermutation of immunoglobulin genes](http://amigo.geneontology.org/amigo/term/GO:0016446) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016446&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016446&list=upload_1&organism=Homo%20sapiens) | .90 | 11.08 | + | 5.00E-07 | 2.37E-05 | | [somatic diversification of immunoglobulins](http://amigo.geneontology.org/amigo/term/GO:0016445) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016445&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016445&list=upload_1&organism=Homo%20sapiens) | 2.65 | 7.18 | + | 1.04E-09 | 7.41E-08 | | [somatic diversification of immune receptors](http://amigo.geneontology.org/amigo/term/GO:0002200) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002200&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002200&list=upload_1&organism=Homo%20sapiens) | 3.31 | 6.34 | + | 8.38E-10 | 6.05E-08 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 45.55 | 2.33 | + | 4.92E-14 | 5.51E-12 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [343](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 230.96 | 1.49 | + | 5.93E-14 | 6.59E-12 | | [anatomical structure development](http://amigo.geneontology.org/amigo/term/GO:0048856) | [5144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&reflist=1) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&list=upload_1&organism=Homo%20sapiens) | 309.55 | 1.41 | + | 1.60E-14 | 1.85E-12 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [473](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 341.63 | 1.38 | + | 4.66E-15 | 5.67E-13 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [378](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 254.43 | 1.49 | + | 1.22E-15 | 1.63E-13 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 396.03 | 1.30 | + | 6.90E-12 | 6.25E-10 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 146.17 | 1.52 | + | 1.25E-09 | 8.83E-08 | | [immunoglobulin production](http://amigo.geneontology.org/amigo/term/GO:0002377) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002377&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002377&list=upload_1&organism=Homo%20sapiens) | 9.87 | 3.34 | + | 2.12E-08 | 1.28E-06 | | [production of molecular mediator of immune response](http://amigo.geneontology.org/amigo/term/GO:0002440) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002440&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002440&list=upload_1&organism=Homo%20sapiens) | 10.17 | 3.24 | + | 3.96E-08 | 2.25E-06 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 139.25 | 1.87 | + | 8.42E-22 | 1.50E-19 | | [somatic diversification of immune receptors via somatic mutation](http://amigo.geneontology.org/amigo/term/GO:0002566) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002566&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002566&list=upload_1&organism=Homo%20sapiens) | .96 | 11.42 | + | 1.06E-07 | 5.59E-06 | | [negative regulation of DNA damage checkpoint](http://amigo.geneontology.org/amigo/term/GO:2000002) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000002&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000002&list=upload_1&organism=Homo%20sapiens) | .36 | 11.08 | + | 1.65E-03 | 2.95E-02 | | [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) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902532&list=upload_1&organism=Homo%20sapiens) | 31.17 | 1.96 | + | 3.96E-06 | 1.54E-04 | | [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) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 103.57 | 1.54 | + | 2.82E-07 | 1.40E-05 | | [regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009966) | [2989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&reflist=1) | [259](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 179.87 | 1.44 | + | 4.66E-09 | 3.07E-07 | | [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) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 242.76 | 1.52 | + | 1.16E-16 | 1.65E-14 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 710.46 | 1.25 | + | 8.84E-24 | 1.93E-21 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [932](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 754.87 | 1.23 | + | 5.17E-25 | 1.37E-22 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 202.74 | 1.39 | + | 2.40E-08 | 1.44E-06 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [853](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 673.21 | 1.27 | + | 4.60E-24 | 1.06E-21 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 203.46 | 1.39 | + | 2.47E-08 | 1.47E-06 | | [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) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 75.64 | 1.65 | + | 1.98E-07 | 1.02E-05 | | [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) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 81.66 | 1.57 | + | 1.70E-06 | 7.30E-05 | | [negative regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0048523) | [4732](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&reflist=1) | [468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 284.76 | 1.64 | + | 1.25E-29 | 4.54E-27 | | [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) | [502](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 319.78 | 1.57 | + | 9.74E-28 | 3.05E-25 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 82.02 | 1.56 | + | 2.34E-06 | 9.93E-05 | | [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) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 97.49 | 1.65 | + | 2.34E-09 | 1.60E-07 | | [positive regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901989) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901989&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901989&list=upload_1&organism=Homo%20sapiens) | 6.92 | 2.46 | + | 1.75E-03 | 3.11E-02 | | [regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901987) | [431](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901987&list=upload_1&organism=Homo%20sapiens) | 25.94 | 2.97 | + | 2.56E-15 | 3.18E-13 | | [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) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 43.03 | 2.91 | + | 1.44E-23 | 3.05E-21 | | [regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051726) | [1122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&reflist=1) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 67.52 | 2.59 | + | 1.19E-27 | 3.66E-25 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090068&list=upload_1&organism=Homo%20sapiens) | 15.10 | 2.32 | + | 2.43E-05 | 8.05E-04 | | [positive regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045787) | [353](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 21.24 | 2.26 | + | 1.02E-06 | 4.55E-05 | | [positive regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0048522) | [5670](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&reflist=1) | [543](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 341.21 | 1.59 | + | 2.01E-32 | 8.30E-30 | | [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) | [580](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 379.36 | 1.53 | + | 6.66E-31 | 2.61E-28 | | [regulation of cell cycle checkpoint](http://amigo.geneontology.org/amigo/term/GO:1901976) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901976&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901976&list=upload_1&organism=Homo%20sapiens) | 2.95 | 5.77 | + | 1.05E-07 | 5.57E-06 | | [negative regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001021) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001021&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001021&list=upload_1&organism=Homo%20sapiens) | 4.99 | 4.81 | + | 5.35E-09 | 3.51E-07 | | [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) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 18.90 | 4.34 | + | 5.18E-25 | 1.35E-22 | | [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) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 42.67 | 2.84 | + | 4.65E-22 | 8.47E-20 | | [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) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 82.62 | 2.26 | + | 2.90E-23 | 5.90E-21 | | [regulation of DNA damage checkpoint](http://amigo.geneontology.org/amigo/term/GO:2000001) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000001&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000001&list=upload_1&organism=Homo%20sapiens) | 1.62 | 8.00 | + | 1.70E-07 | 8.87E-06 | | [mitochondrial DNA repair](http://amigo.geneontology.org/amigo/term/GO:0043504) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043504&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043504&list=upload_1&organism=Homo%20sapiens) | .36 | 11.08 | + | 1.65E-03 | 2.95E-02 | | [mitochondrial DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0032042) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032042&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032042&list=upload_1&organism=Homo%20sapiens) | 1.02 | 6.84 | + | 2.75E-04 | 6.53E-03 | | [mitochondrial genome maintenance](http://amigo.geneontology.org/amigo/term/GO:0000002) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000002&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000002&list=upload_1&organism=Homo%20sapiens) | 1.56 | 4.47 | + | 2.17E-03 | 3.70E-02 | | [regulation of DNA ligation](http://amigo.geneontology.org/amigo/term/GO:0051105) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051105&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051105&list=upload_1&organism=Homo%20sapiens) | .36 | 11.08 | + | 1.65E-03 | 2.95E-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) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 32.56 | 3.93 | + | 5.70E-35 | 2.71E-32 | | [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) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 244.74 | 1.83 | + | 9.52E-39 | 5.97E-36 | | [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) | [573](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 343.55 | 1.67 | + | 4.79E-41 | 3.95E-38 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [638](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 406.44 | 1.57 | + | 2.22E-39 | 1.58E-36 | | [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) | [566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 339.82 | 1.67 | + | 3.83E-40 | 3.01E-37 | | [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) | [580](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 353.36 | 1.64 | + | 1.19E-39 | 8.90E-37 | | [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) | [596](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 373.94 | 1.59 | + | 2.32E-37 | 1.30E-34 | | [telomere maintenance via recombination](http://amigo.geneontology.org/amigo/term/GO:0000722) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000722&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000722&list=upload_1&organism=Homo%20sapiens) | .84 | 10.68 | + | 2.35E-06 | 9.94E-05 | | [mitotic recombination](http://amigo.geneontology.org/amigo/term/GO:0006312) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006312&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006312&list=upload_1&organism=Homo%20sapiens) | 1.20 | 9.14 | + | 5.57E-07 | 2.60E-05 | | [cellular response to hydroxyurea](http://amigo.geneontology.org/amigo/term/GO:0072711) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072711&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072711&list=upload_1&organism=Homo%20sapiens) | .66 | 10.57 | + | 3.41E-05 | 1.07E-03 | | [response to hydroxyurea](http://amigo.geneontology.org/amigo/term/GO:0072710) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072710&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072710&list=upload_1&organism=Homo%20sapiens) | .72 | 11.08 | + | 7.18E-06 | 2.64E-04 | | [response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0010035) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 32.07 | 1.78 | + | 9.10E-05 | 2.55E-03 | | [pyrimidine dimer repair](http://amigo.geneontology.org/amigo/term/GO:0006290) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006290&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006290&list=upload_1&organism=Homo%20sapiens) | .48 | 10.39 | + | 5.13E-04 | 1.09E-02 | | [negative regulation of telomere capping](http://amigo.geneontology.org/amigo/term/GO:1904354) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904354&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904354&list=upload_1&organism=Homo%20sapiens) | .48 | 10.39 | + | 5.13E-04 | 1.09E-02 | | [regulation of telomere capping](http://amigo.geneontology.org/amigo/term/GO:1904353) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904353&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904353&list=upload_1&organism=Homo%20sapiens) | 1.56 | 6.39 | + | 2.19E-05 | 7.39E-04 | | [regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032204) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&list=upload_1&organism=Homo%20sapiens) | 6.08 | 4.11 | + | 3.59E-08 | 2.08E-06 | | [regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0033044) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 15.16 | 3.69 | + | 7.57E-15 | 8.99E-13 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 71.55 | 2.03 | + | 2.39E-14 | 2.74E-12 | | [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) | [234](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 142.26 | 1.64 | + | 2.38E-13 | 2.57E-11 | | [negative regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032205) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032205&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032205&list=upload_1&organism=Homo%20sapiens) | 2.17 | 4.62 | + | 2.09E-04 | 5.15E-03 | | [negative regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001251) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001251&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001251&list=upload_1&organism=Homo%20sapiens) | 4.93 | 4.26 | + | 2.70E-07 | 1.35E-05 | | [negative regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0010639) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&list=upload_1&organism=Homo%20sapiens) | 20.76 | 2.46 | + | 6.23E-08 | 3.44E-06 | | [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) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 41.52 | 1.85 | + | 1.02E-06 | 4.55E-05 | | [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) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051053&list=upload_1&organism=Homo%20sapiens) | 8.91 | 4.38 | + | 1.13E-12 | 1.16E-10 | | [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) | [305](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 166.33 | 1.83 | + | 2.30E-24 | 5.74E-22 | | [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) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 179.81 | 1.76 | + | 6.55E-23 | 1.27E-20 | | [negative regulation of nucleobase-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045934) | [1562](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&reflist=1) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 94.00 | 2.19 | + | 4.05E-24 | 9.47E-22 | | [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) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 144.97 | 1.95 | + | 6.49E-26 | 1.82E-23 | | [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) | [266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 136.24 | 1.95 | + | 1.26E-24 | 3.24E-22 | | [UV protection](http://amigo.geneontology.org/amigo/term/GO:0009650) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009650&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009650&list=upload_1&organism=Homo%20sapiens) | .78 | 10.23 | + | 1.10E-05 | 3.86E-04 | | [response to UV](http://amigo.geneontology.org/amigo/term/GO:0009411) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&list=upload_1&organism=Homo%20sapiens) | 9.09 | 4.51 | + | 1.29E-13 | 1.42E-11 | | [response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0009416) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 19.08 | 3.04 | + | 3.21E-12 | 3.07E-10 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 27.02 | 3.44 | + | 4.93E-22 | 8.88E-20 | | [response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009628) | [1121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&reflist=1) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&list=upload_1&organism=Homo%20sapiens) | 67.46 | 2.43 | + | 3.74E-23 | 7.52E-21 | | [lymphoid progenitor cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002320) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002320&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002320&list=upload_1&organism=Homo%20sapiens) | .72 | 9.69 | + | 5.14E-05 | 1.55E-03 | | [hematopoietic progenitor cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002244) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002244&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002244&list=upload_1&organism=Homo%20sapiens) | 6.38 | 3.45 | + | 2.98E-06 | 1.23E-04 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 39.72 | 2.14 | + | 7.78E-10 | 5.67E-08 | | [hematopoietic or lymphoid organ development](http://amigo.geneontology.org/amigo/term/GO:0048534) | [710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 42.73 | 2.13 | + | 2.40E-10 | 1.86E-08 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [285](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 195.82 | 1.46 | + | 1.81E-10 | 1.45E-08 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 211.77 | 1.48 | + | 2.11E-12 | 2.11E-10 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 213.15 | 1.48 | + | 1.33E-12 | 1.36E-10 | | [maintenance of DNA methylation](http://amigo.geneontology.org/amigo/term/GO:0010216) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010216&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010216&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.14E-02 | | [DNA strand resection involved in replication fork processing](http://amigo.geneontology.org/amigo/term/GO:0110025) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110025&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110025&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.14E-02 | | [replication fork processing](http://amigo.geneontology.org/amigo/term/GO:0031297) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031297&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031297&list=upload_1&organism=Homo%20sapiens) | 2.83 | 5.30 | + | 1.40E-06 | 6.12E-05 | | [DNA-templated DNA replication maintenance of fidelity](http://amigo.geneontology.org/amigo/term/GO:0045005) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045005&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045005&list=upload_1&organism=Homo%20sapiens) | 3.37 | 5.64 | + | 2.54E-08 | 1.50E-06 | | [G-quadruplex DNA unwinding](http://amigo.geneontology.org/amigo/term/GO:0044806) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044806&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044806&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.13E-02 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 5.90 | 6.10 | + | 2.19E-15 | 2.82E-13 | | [fatty acid alpha-oxidation](http://amigo.geneontology.org/amigo/term/GO:0001561) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001561&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001561&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.13E-02 | | [fatty acid oxidation](http://amigo.geneontology.org/amigo/term/GO:0019395) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019395&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019395&list=upload_1&organism=Homo%20sapiens) | 5.12 | 3.13 | + | 1.75E-04 | 4.48E-03 | | [lipid oxidation](http://amigo.geneontology.org/amigo/term/GO:0034440) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034440&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034440&list=upload_1&organism=Homo%20sapiens) | 5.42 | 2.95 | + | 3.10E-04 | 7.22E-03 | | [cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044248) | [1625](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&reflist=1) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044248&list=upload_1&organism=Homo%20sapiens) | 97.79 | 1.57 | + | 1.03E-07 | 5.45E-06 | | [catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009056) | [1974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&reflist=1) | [180](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009056&list=upload_1&organism=Homo%20sapiens) | 118.79 | 1.52 | + | 7.94E-08 | 4.31E-06 | | [organic substance catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901575) | [1679](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&reflist=1) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&list=upload_1&organism=Homo%20sapiens) | 101.04 | 1.56 | + | 9.04E-08 | 4.84E-06 | | [carboxylic acid catabolic process](http://amigo.geneontology.org/amigo/term/GO:0046395) | [224](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046395&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046395&list=upload_1&organism=Homo%20sapiens) | 13.48 | 2.15 | + | 3.05E-04 | 7.12E-03 | | [organic acid catabolic process](http://amigo.geneontology.org/amigo/term/GO:0016054) | [228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016054&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016054&list=upload_1&organism=Homo%20sapiens) | 13.72 | 2.11 | + | 5.48E-04 | 1.16E-02 | | [T-helper 2 cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045064) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045064&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045064&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.13E-02 | | [immune response](http://amigo.geneontology.org/amigo/term/GO:0006955) | [1621](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&list=upload_1&organism=Homo%20sapiens) | 97.55 | 1.42 | + | 6.64E-05 | 1.94E-03 | | [T cell activation](http://amigo.geneontology.org/amigo/term/GO:0042110) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&list=upload_1&organism=Homo%20sapiens) | 18.05 | 1.94 | + | 4.86E-04 | 1.04E-02 | | [lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0046649) | [465](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&list=upload_1&organism=Homo%20sapiens) | 27.98 | 1.97 | + | 8.27E-06 | 3.00E-04 | | [leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0045321) | [581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045321&list=upload_1&organism=Homo%20sapiens) | 34.96 | 1.86 | + | 8.51E-06 | 3.07E-04 | | [cell activation](http://amigo.geneontology.org/amigo/term/GO:0001775) | [700](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&list=upload_1&organism=Homo%20sapiens) | 42.12 | 1.88 | + | 5.20E-07 | 2.44E-05 | | [lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0030098) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&list=upload_1&organism=Homo%20sapiens) | 16.85 | 2.02 | + | 3.03E-04 | 7.09E-03 | | [mononuclear cell differentiation](http://amigo.geneontology.org/amigo/term/GO:1903131) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&list=upload_1&organism=Homo%20sapiens) | 19.62 | 2.14 | + | 1.84E-05 | 6.30E-04 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 24.07 | 2.24 | + | 2.91E-07 | 1.43E-05 | | [T cell activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002286) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002286&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002286&list=upload_1&organism=Homo%20sapiens) | 4.39 | 3.19 | + | 3.70E-04 | 8.36E-03 | | [lymphocyte activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002285) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002285&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002285&list=upload_1&organism=Homo%20sapiens) | 7.70 | 2.86 | + | 3.98E-05 | 1.23E-03 | | [leukocyte activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002366) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002366&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002366&list=upload_1&organism=Homo%20sapiens) | 11.31 | 2.65 | + | 9.16E-06 | 3.29E-04 | | [cell activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002263) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002263&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002263&list=upload_1&organism=Homo%20sapiens) | 11.55 | 2.60 | + | 1.14E-05 | 3.99E-04 | | [immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002252) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002252&list=upload_1&organism=Homo%20sapiens) | 28.28 | 1.87 | + | 4.81E-05 | 1.46E-03 | | [telomere maintenance via semi-conservative replication](http://amigo.geneontology.org/amigo/term/GO:0032201) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032201&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032201&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.12E-02 | | [positive regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032075) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032075&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032075&list=upload_1&organism=Homo%20sapiens) | .42 | 9.50 | + | 2.47E-03 | 4.12E-02 | | [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) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 123.85 | 2.27 | + | 6.09E-36 | 3.08E-33 | | [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) | [382](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 191.00 | 2.00 | + | 2.53E-39 | 1.65E-36 | | [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) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 232.17 | 1.87 | + | 2.28E-39 | 1.55E-36 | | [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) | [375](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 187.87 | 2.00 | + | 3.36E-38 | 1.95E-35 | | [regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032069) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&list=upload_1&organism=Homo%20sapiens) | 1.32 | 5.29 | + | 9.66E-04 | 1.90E-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) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&list=upload_1&organism=Homo%20sapiens) | 61.38 | 1.52 | + | 1.84E-04 | 4.64E-03 | | [regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0050790) | [2373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&reflist=1) | [233](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 142.80 | 1.63 | + | 7.03E-13 | 7.45E-11 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 186.19 | 1.55 | + | 1.85E-13 | 2.01E-11 | | [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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&list=upload_1&organism=Homo%20sapiens) | 35.44 | 1.66 | + | 3.72E-04 | 8.38E-03 | | [positive regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0043085) | [1194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&reflist=1) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 71.85 | 1.73 | + | 2.50E-08 | 1.49E-06 | | [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) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 95.68 | 1.66 | + | 1.78E-09 | 1.24E-07 | | [mismatch repair](http://amigo.geneontology.org/amigo/term/GO:0006298) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&list=upload_1&organism=Homo%20sapiens) | 2.05 | 9.29 | + | 3.48E-11 | 2.93E-09 | | [double-strand break repair via nonhomologous end joining](http://amigo.geneontology.org/amigo/term/GO:0006303) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006303&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006303&list=upload_1&organism=Homo%20sapiens) | 2.59 | 9.27 | + | 9.29E-14 | 1.03E-11 | | [replication fork protection](http://amigo.geneontology.org/amigo/term/GO:0048478) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048478&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048478&list=upload_1&organism=Homo%20sapiens) | .54 | 9.23 | + | 7.60E-04 | 1.55E-02 | | [negative regulation of DNA-templated DNA replication](http://amigo.geneontology.org/amigo/term/GO:2000104) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000104&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000104&list=upload_1&organism=Homo%20sapiens) | .90 | 7.75 | + | 1.50E-04 | 3.89E-03 | | [negative regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0008156) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008156&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008156&list=upload_1&organism=Homo%20sapiens) | 1.93 | 6.75 | + | 7.91E-07 | 3.58E-05 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 8.18 | 5.38 | + | 8.27E-17 | 1.19E-14 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090329&list=upload_1&organism=Homo%20sapiens) | 3.43 | 6.41 | + | 2.82E-10 | 2.18E-08 | | [negative regulation of glial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0034351) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034351&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034351&list=upload_1&organism=Homo%20sapiens) | .54 | 9.23 | + | 7.60E-04 | 1.55E-02 | | [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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 54.04 | 2.11 | + | 1.59E-12 | 1.62E-10 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [177](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 88.34 | 2.00 | + | 5.16E-17 | 7.56E-15 | | [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) | [180](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 90.15 | 2.00 | + | 3.87E-17 | 5.78E-15 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 99.53 | 1.90 | + | 5.57E-16 | 7.52E-14 | | [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) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 55.24 | 2.08 | + | 2.73E-12 | 2.67E-10 | | [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) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&list=upload_1&organism=Homo%20sapiens) | 61.50 | 1.97 | + | 2.80E-11 | 2.39E-09 | | [regulation of glial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0034350) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034350&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034350&list=upload_1&organism=Homo%20sapiens) | .66 | 7.55 | + | 1.51E-03 | 2.76E-02 | | [positive regulation of peptidyl-serine phosphorylation of STAT protein](http://amigo.geneontology.org/amigo/term/GO:0033141) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033141&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033141&list=upload_1&organism=Homo%20sapiens) | 1.20 | 9.14 | + | 5.57E-07 | 2.61E-05 | | [positive regulation of peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0033138) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033138&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033138&list=upload_1&organism=Homo%20sapiens) | 6.62 | 3.47 | + | 1.60E-06 | 6.96E-05 | | [positive regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001934) | [748](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&list=upload_1&organism=Homo%20sapiens) | 45.01 | 1.78 | + | 3.53E-06 | 1.39E-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) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 66.50 | 1.85 | + | 5.14E-10 | 3.86E-08 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 75.10 | 1.85 | + | 3.88E-11 | 3.25E-09 | | [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) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 84.49 | 1.81 | + | 1.30E-11 | 1.13E-09 | | [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) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 84.55 | 1.81 | + | 1.34E-11 | 1.15E-09 | | [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) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 94.06 | 1.95 | + | 1.60E-16 | 2.24E-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) | [285](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&list=upload_1&organism=Homo%20sapiens) | 155.68 | 1.83 | + | 1.56E-22 | 2.99E-20 | | [positive regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042327) | [826](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&list=upload_1&organism=Homo%20sapiens) | 49.71 | 1.73 | + | 3.48E-06 | 1.39E-04 | | [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) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&list=upload_1&organism=Homo%20sapiens) | 54.82 | 1.77 | + | 2.94E-07 | 1.44E-05 | | [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) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&list=upload_1&organism=Homo%20sapiens) | 54.82 | 1.77 | + | 2.94E-07 | 1.44E-05 | | [positive regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031401) | [1019](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 61.32 | 1.89 | + | 5.71E-10 | 4.24E-08 | | [positive regulation of protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051247) | [1515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&reflist=1) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 91.17 | 1.88 | + | 4.68E-14 | 5.31E-12 | | [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) | [405](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 213.15 | 1.90 | + | 3.07E-37 | 1.61E-34 | | [regulation of peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0033135) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033135&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033135&list=upload_1&organism=Homo%20sapiens) | 8.61 | 3.02 | + | 3.38E-06 | 1.36E-04 | | [regulation of peptidyl-serine phosphorylation of STAT protein](http://amigo.geneontology.org/amigo/term/GO:0033139) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033139&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033139&list=upload_1&organism=Homo%20sapiens) | 1.38 | 7.95 | + | 1.61E-06 | 6.96E-05 | | [DNA unwinding involved in DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006268) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&list=upload_1&organism=Homo%20sapiens) | 1.32 | 9.06 | + | 1.81E-07 | 9.38E-06 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 5.54 | 6.32 | + | 2.28E-15 | 2.86E-13 | | [regulation of DNA-templated DNA replication initiation](http://amigo.geneontology.org/amigo/term/GO:0030174) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&list=upload_1&organism=Homo%20sapiens) | .90 | 8.86 | + | 2.40E-05 | 7.95E-04 | | [interstrand cross-link repair](http://amigo.geneontology.org/amigo/term/GO:0036297) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036297&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036297&list=upload_1&organism=Homo%20sapiens) | 2.47 | 8.51 | + | 1.14E-11 | 9.92E-10 | | [foregut morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0007440) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007440&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007440&list=upload_1&organism=Homo%20sapiens) | .60 | 8.31 | + | 1.09E-03 | 2.09E-02 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 134.62 | 1.51 | + | 1.30E-08 | 8.06E-07 | | [digestive tract morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048546) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&list=upload_1&organism=Homo%20sapiens) | 2.89 | 3.81 | + | 4.26E-04 | 9.39E-03 | | [tube development](http://amigo.geneontology.org/amigo/term/GO:0035295) | [885](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035295&list=upload_1&organism=Homo%20sapiens) | 53.26 | 1.52 | + | 4.62E-04 | 1.01E-02 | | [telomeric loop disassembly](http://amigo.geneontology.org/amigo/term/GO:0090657) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090657&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090657&list=upload_1&organism=Homo%20sapiens) | .60 | 8.31 | + | 1.09E-03 | 2.08E-02 | | [transcription-coupled nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006283) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006283&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006283&list=upload_1&organism=Homo%20sapiens) | .60 | 8.31 | + | 1.09E-03 | 2.08E-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) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000727&list=upload_1&organism=Homo%20sapiens) | .72 | 8.31 | + | 3.40E-04 | 7.76E-03 | | [mitotic intra-S DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0031573) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031573&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031573&list=upload_1&organism=Homo%20sapiens) | 1.02 | 7.82 | + | 4.78E-05 | 1.45E-03 | | [mitotic DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0044773) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044773&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044773&list=upload_1&organism=Homo%20sapiens) | 4.87 | 4.92 | + | 3.58E-09 | 2.38E-07 | | [DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000077) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000077&list=upload_1&organism=Homo%20sapiens) | 6.32 | 4.91 | + | 2.09E-11 | 1.79E-09 | | [DNA integrity checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0031570) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031570&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031570&list=upload_1&organism=Homo%20sapiens) | 6.80 | 5.15 | + | 3.38E-13 | 3.64E-11 | | [cell cycle checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000075) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000075&list=upload_1&organism=Homo%20sapiens) | 9.45 | 4.13 | + | 5.29E-12 | 4.88E-10 | | [intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:0035556) | [1511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&list=upload_1&organism=Homo%20sapiens) | 90.93 | 1.91 | + | 4.98E-15 | 6.01E-13 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [378](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 294.09 | 1.29 | + | 1.32E-07 | 6.95E-06 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [399](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 314.79 | 1.27 | + | 2.09E-07 | 1.06E-05 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 321.47 | 1.28 | + | 5.89E-08 | 3.27E-06 | | [negative regulation of cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901988) | [224](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901988&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901988&list=upload_1&organism=Homo%20sapiens) | 13.48 | 3.49 | + | 6.42E-12 | 5.85E-10 | | [negative regulation of cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0010948) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010948&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010948&list=upload_1&organism=Homo%20sapiens) | 16.37 | 3.67 | + | 1.09E-15 | 1.46E-13 | | [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) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045786&list=upload_1&organism=Homo%20sapiens) | 21.60 | 3.29 | + | 3.60E-16 | 4.95E-14 | | [signal transduction in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:0042770) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042770&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042770&list=upload_1&organism=Homo%20sapiens) | 8.12 | 4.55 | + | 1.59E-12 | 1.61E-10 | | [mitotic DNA integrity checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0044774) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044774&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044774&list=upload_1&organism=Homo%20sapiens) | 5.12 | 4.89 | + | 1.93E-09 | 1.33E-07 | | [mitotic cell cycle checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0007093) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007093&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007093&list=upload_1&organism=Homo%20sapiens) | 7.64 | 3.79 | + | 1.39E-08 | 8.57E-07 | | [negative regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045930) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045930&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045930&list=upload_1&organism=Homo%20sapiens) | 12.82 | 3.04 | + | 1.13E-08 | 7.05E-07 | | [regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0007346) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 29.67 | 2.56 | + | 4.49E-12 | 4.22E-10 | | [DNA replication checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0000076) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000076&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000076&list=upload_1&organism=Homo%20sapiens) | 1.02 | 7.82 | + | 4.78E-05 | 1.45E-03 | | [phosphorylation of RNA polymerase II C-terminal domain](http://amigo.geneontology.org/amigo/term/GO:0070816) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070816&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070816&list=upload_1&organism=Homo%20sapiens) | .66 | 7.55 | + | 1.51E-03 | 2.77E-02 | | [regulation of transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0006357) | [2606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&reflist=1) | [259](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 156.82 | 1.65 | + | 5.51E-15 | 6.59E-13 | | [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) | 207.85 | 1.63 | + | 1.80E-19 | 3.04E-17 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [456](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 292.16 | 1.56 | + | 7.54E-24 | 1.69E-21 | | [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) | 207.97 | 1.63 | + | 2.49E-19 | 4.11E-17 | | [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) | [341](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 208.52 | 1.64 | + | 9.51E-20 | 1.62E-17 | | [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) | [402](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 236.98 | 1.70 | + | 6.42E-27 | 1.90E-24 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 250.52 | 1.68 | + | 5.87E-28 | 1.96E-25 | | [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) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 225.79 | 1.68 | + | 2.46E-24 | 5.85E-22 | | [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) | [418](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 246.85 | 1.69 | + | 3.26E-28 | 1.14E-25 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 43.27 | 2.22 | + | 8.24E-12 | 7.39E-10 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 159.95 | 1.52 | + | 1.48E-10 | 1.19E-08 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 173.49 | 1.54 | + | 2.05E-12 | 2.06E-10 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 235.90 | 1.41 | + | 1.13E-10 | 9.26E-09 | | [organonitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901564) | [5013](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&reflist=1) | [405](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 301.67 | 1.34 | + | 1.38E-10 | 1.12E-08 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 55.24 | 1.95 | + | 4.59E-10 | 3.49E-08 | | [phosphate-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006796) | [1855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&reflist=1) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 111.63 | 1.50 | + | 4.04E-07 | 1.94E-05 | | [phosphorus metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006793) | [1881](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&reflist=1) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006793&list=upload_1&organism=Homo%20sapiens) | 113.19 | 1.49 | + | 6.17E-07 | 2.84E-05 | | [lung epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060487) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&list=upload_1&organism=Homo%20sapiens) | 1.50 | 7.31 | + | 3.04E-06 | 1.25E-04 | | [lung cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060479) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&list=upload_1&organism=Homo%20sapiens) | 1.50 | 7.31 | + | 3.04E-06 | 1.24E-04 | | [lung development](http://amigo.geneontology.org/amigo/term/GO:0030324) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&list=upload_1&organism=Homo%20sapiens) | 10.95 | 2.37 | + | 2.01E-04 | 4.99E-03 | | [respiratory system development](http://amigo.geneontology.org/amigo/term/GO:0060541) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&list=upload_1&organism=Homo%20sapiens) | 12.40 | 2.26 | + | 1.76E-04 | 4.48E-03 | | [respiratory tube development](http://amigo.geneontology.org/amigo/term/GO:0030323) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&list=upload_1&organism=Homo%20sapiens) | 11.19 | 2.32 | + | 2.36E-04 | 5.75E-03 | | [epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030855) | [620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&list=upload_1&organism=Homo%20sapiens) | 37.31 | 1.77 | + | 3.38E-05 | 1.07E-03 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 64.51 | 1.67 | + | 7.52E-07 | 3.43E-05 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 103.87 | 1.52 | + | 5.07E-07 | 2.39E-05 | | [lung epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060428) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060428&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060428&list=upload_1&organism=Homo%20sapiens) | 2.23 | 4.94 | + | 6.10E-05 | 1.78E-03 | | [protein localization to chromosome, telomeric region](http://amigo.geneontology.org/amigo/term/GO:0070198) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070198&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070198&list=upload_1&organism=Homo%20sapiens) | .96 | 7.27 | + | 2.05E-04 | 5.07E-03 | | [protein localization to chromosome](http://amigo.geneontology.org/amigo/term/GO:0034502) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034502&list=upload_1&organism=Homo%20sapiens) | 4.51 | 5.32 | + | 1.00E-09 | 7.18E-08 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 41.76 | 1.99 | + | 3.31E-08 | 1.95E-06 | | [protein localization](http://amigo.geneontology.org/amigo/term/GO:0008104) | [1919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&reflist=1) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&list=upload_1&organism=Homo%20sapiens) | 115.48 | 1.49 | + | 4.70E-07 | 2.26E-05 | | [cellular macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0070727) | [1925](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&list=upload_1&organism=Homo%20sapiens) | 115.84 | 1.50 | + | 2.84E-07 | 1.41E-05 | | [cellular localization](http://amigo.geneontology.org/amigo/term/GO:0051641) | [2655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&reflist=1) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&list=upload_1&organism=Homo%20sapiens) | 159.77 | 1.40 | + | 7.68E-07 | 3.49E-05 | | [localization](http://amigo.geneontology.org/amigo/term/GO:0051179) | [4566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&reflist=1) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&list=upload_1&organism=Homo%20sapiens) | 274.77 | 1.27 | + | 1.29E-06 | 5.69E-05 | | [macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0033036) | [2345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&reflist=1) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&list=upload_1&organism=Homo%20sapiens) | 141.12 | 1.40 | + | 3.89E-06 | 1.52E-04 | | [isotype switching](http://amigo.geneontology.org/amigo/term/GO:0045190) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045190&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045190&list=upload_1&organism=Homo%20sapiens) | 1.38 | 7.22 | + | 9.32E-06 | 3.32E-04 | | [somatic recombination of immunoglobulin genes involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002204) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002204&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002204&list=upload_1&organism=Homo%20sapiens) | 1.38 | 7.22 | + | 9.32E-06 | 3.32E-04 | | [somatic recombination of immunoglobulin gene segments](http://amigo.geneontology.org/amigo/term/GO:0016447) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016447&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016447&list=upload_1&organism=Homo%20sapiens) | 1.87 | 6.97 | + | 5.94E-07 | 2.75E-05 | | [somatic diversification of immune receptors via germline recombination within a single locus](http://amigo.geneontology.org/amigo/term/GO:0002562) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002562&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002562&list=upload_1&organism=Homo%20sapiens) | 2.47 | 5.67 | + | 1.63E-06 | 7.03E-05 | | [somatic cell DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0016444) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016444&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016444&list=upload_1&organism=Homo%20sapiens) | 2.47 | 5.67 | + | 1.63E-06 | 7.01E-05 | | [somatic diversification of immunoglobulins involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002208) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002208&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002208&list=upload_1&organism=Homo%20sapiens) | 1.62 | 6.15 | + | 2.85E-05 | 9.27E-04 | | [immunoglobulin production involved in immunoglobulin-mediated immune response](http://amigo.geneontology.org/amigo/term/GO:0002381) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002381&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002381&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.61 | + | 1.09E-03 | 2.09E-02 | | [B cell mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0019724) | [196](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019724&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019724&list=upload_1&organism=Homo%20sapiens) | 11.79 | 2.03 | + | 1.93E-03 | 3.35E-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) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002460&list=upload_1&organism=Homo%20sapiens) | 15.95 | 1.94 | + | 9.22E-04 | 1.84E-02 | | [adaptive immune response](http://amigo.geneontology.org/amigo/term/GO:0002250) | [659](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002250&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002250&list=upload_1&organism=Homo%20sapiens) | 39.66 | 1.56 | + | 1.33E-03 | 2.46E-02 | | [lymphocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002449) | [257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002449&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002449&list=upload_1&organism=Homo%20sapiens) | 15.47 | 1.88 | + | 2.71E-03 | 4.40E-02 | | [leukocyte mediated immunity](http://amigo.geneontology.org/amigo/term/GO:0002443) | [310](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002443&list=upload_1&organism=Homo%20sapiens) | 18.66 | 1.82 | + | 2.00E-03 | 3.47E-02 | | [B cell activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002312) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002312&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002312&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.56 | + | 4.02E-04 | 8.93E-03 | | [B cell activation](http://amigo.geneontology.org/amigo/term/GO:0042113) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&list=upload_1&organism=Homo%20sapiens) | 11.49 | 3.05 | + | 6.18E-08 | 3.43E-06 | | [regulation of sister chromatid cohesion](http://amigo.geneontology.org/amigo/term/GO:0007063) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007063&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007063&list=upload_1&organism=Homo%20sapiens) | 1.26 | 7.12 | + | 2.87E-05 | 9.32E-04 | | [positive regulation of transcription elongation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0032968) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032968&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032968&list=upload_1&organism=Homo%20sapiens) | 3.01 | 6.98 | + | 2.07E-10 | 1.66E-08 | | [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) | [177](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045944&list=upload_1&organism=Homo%20sapiens) | 75.76 | 2.34 | + | 2.01E-23 | 4.20E-21 | | [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) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 103.20 | 2.13 | + | 2.41E-24 | 5.80E-22 | | [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) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 103.20 | 2.13 | + | 2.41E-24 | 5.89E-22 | | [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) | [221](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 103.57 | 2.13 | + | 1.65E-24 | 4.17E-22 | | [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) | [235](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 111.21 | 2.11 | + | 9.06E-26 | 2.49E-23 | | [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) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 123.24 | 2.14 | + | 6.88E-30 | 2.57E-27 | | [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) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 125.59 | 2.13 | + | 6.85E-30 | 2.62E-27 | | [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) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 116.93 | 2.16 | + | 6.10E-29 | 2.17E-26 | | [positive regulation of DNA-templated transcription, elongation](http://amigo.geneontology.org/amigo/term/GO:0032786) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032786&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032786&list=upload_1&organism=Homo%20sapiens) | 3.61 | 6.92 | + | 4.56E-12 | 4.25E-10 | | [regulation of DNA-templated transcription elongation](http://amigo.geneontology.org/amigo/term/GO:0032784) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032784&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032784&list=upload_1&organism=Homo%20sapiens) | 6.20 | 5.16 | + | 3.24E-12 | 3.08E-10 | | [regulation of transcription elongation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0034243) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034243&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034243&list=upload_1&organism=Homo%20sapiens) | 5.18 | 5.41 | + | 2.94E-11 | 2.49E-09 | | [regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay](http://amigo.geneontology.org/amigo/term/GO:2000622) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000622&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000622&list=upload_1&organism=Homo%20sapiens) | .72 | 6.92 | + | 2.04E-03 | 3.53E-02 | | [regulation of mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0061013) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061013&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061013&list=upload_1&organism=Homo%20sapiens) | 10.89 | 3.03 | + | 1.62E-07 | 8.47E-06 | | [regulation of cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0031329) | [786](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&list=upload_1&organism=Homo%20sapiens) | 47.30 | 2.22 | + | 8.13E-13 | 8.50E-11 | | [regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009894) | [987](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&list=upload_1&organism=Homo%20sapiens) | 59.40 | 2.07 | + | 7.30E-13 | 7.68E-11 | | [regulation of mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903311) | [301](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&list=upload_1&organism=Homo%20sapiens) | 18.11 | 2.43 | + | 4.72E-07 | 2.25E-05 | | [base-excision repair, AP site formation](http://amigo.geneontology.org/amigo/term/GO:0006285) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006285&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006285&list=upload_1&organism=Homo%20sapiens) | .72 | 6.92 | + | 2.04E-03 | 3.52E-02 | | [negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay](http://amigo.geneontology.org/amigo/term/GO:1900152) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900152&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900152&list=upload_1&organism=Homo%20sapiens) | .72 | 6.92 | + | 2.04E-03 | 3.52E-02 | | [negative regulation of mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902373) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902373&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902373&list=upload_1&organism=Homo%20sapiens) | 4.03 | 3.72 | + | 5.17E-05 | 1.55E-03 | | [negative regulation of mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903312) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903312&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903312&list=upload_1&organism=Homo%20sapiens) | 5.54 | 3.07 | + | 1.35E-04 | 3.58E-03 | | [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) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 86.36 | 2.04 | + | 1.49E-17 | 2.26E-15 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 69.26 | 1.93 | + | 4.64E-12 | 4.30E-10 | | [negative regulation of RNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902369) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902369&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902369&list=upload_1&organism=Homo%20sapiens) | 4.75 | 3.37 | + | 8.33E-05 | 2.36E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 14.56 | 2.27 | + | 5.59E-05 | 1.66E-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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009895&list=upload_1&organism=Homo%20sapiens) | 19.62 | 2.04 | + | 8.23E-05 | 2.34E-03 | | [positive regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034250) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034250&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034250&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.59 | + | 3.38E-05 | 1.07E-03 | | [regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034248) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&list=upload_1&organism=Homo%20sapiens) | 28.22 | 2.34 | + | 3.36E-09 | 2.25E-07 | | [regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0006417) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&list=upload_1&organism=Homo%20sapiens) | 24.67 | 2.07 | + | 5.44E-06 | 2.05E-04 | | [regulation of cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000112) | [493](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&list=upload_1&organism=Homo%20sapiens) | 29.67 | 2.12 | + | 2.01E-07 | 1.03E-05 | | [post-transcriptional regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010608) | [498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010608&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010608&list=upload_1&organism=Homo%20sapiens) | 29.97 | 2.10 | + | 2.37E-07 | 1.20E-05 | | [regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay](http://amigo.geneontology.org/amigo/term/GO:1900151) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900151&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900151&list=upload_1&organism=Homo%20sapiens) | 1.56 | 5.75 | + | 1.10E-04 | 3.00E-03 | | [regulation of mRNA stability](http://amigo.geneontology.org/amigo/term/GO:0043488) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&list=upload_1&organism=Homo%20sapiens) | 9.81 | 2.96 | + | 1.38E-06 | 6.06E-05 | | [regulation of RNA stability](http://amigo.geneontology.org/amigo/term/GO:0043487) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&list=upload_1&organism=Homo%20sapiens) | 10.53 | 2.85 | + | 1.80E-06 | 7.68E-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) | [315](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 221.27 | 1.42 | + | 1.37E-10 | 1.12E-08 | | [telomere capping](http://amigo.geneontology.org/amigo/term/GO:0016233) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016233&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016233&list=upload_1&organism=Homo%20sapiens) | 1.02 | 6.84 | + | 2.75E-04 | 6.52E-03 | | [hematopoietic stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060218) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060218&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060218&list=upload_1&organism=Homo%20sapiens) | 1.20 | 6.65 | + | 1.18E-04 | 3.16E-03 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 11.01 | 2.63 | + | 1.41E-05 | 4.92E-04 | | [response to X-ray](http://amigo.geneontology.org/amigo/term/GO:0010165) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010165&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010165&list=upload_1&organism=Homo%20sapiens) | 1.87 | 6.43 | + | 3.15E-06 | 1.28E-04 | | [response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0010212) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&list=upload_1&organism=Homo%20sapiens) | 8.67 | 5.08 | + | 4.70E-16 | 6.42E-14 | | [regulation of T-helper 2 cell cytokine production](http://amigo.geneontology.org/amigo/term/GO:2000551) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000551&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000551&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.40E-02 | | [regulation of cytokine production](http://amigo.geneontology.org/amigo/term/GO:0001817) | [742](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&list=upload_1&organism=Homo%20sapiens) | 44.65 | 1.52 | + | 1.43E-03 | 2.63E-02 | | [regulation of multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0051239) | [2750](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&reflist=1) | [246](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 165.49 | 1.49 | + | 7.89E-10 | 5.73E-08 | | [regulation of production of molecular mediator of immune response](http://amigo.geneontology.org/amigo/term/GO:0002700) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002700&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002700&list=upload_1&organism=Homo%20sapiens) | 11.37 | 2.02 | + | 2.60E-03 | 4.28E-02 | | [regulation of immune effector process](http://amigo.geneontology.org/amigo/term/GO:0002697) | [386](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002697&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002697&list=upload_1&organism=Homo%20sapiens) | 23.23 | 1.77 | + | 9.75E-04 | 1.92E-02 | | [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) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 91.47 | 1.62 | + | 4.12E-08 | 2.33E-06 | | [regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050776) | [935](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&list=upload_1&organism=Homo%20sapiens) | 56.27 | 1.69 | + | 3.21E-06 | 1.30E-04 | | [negative regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051974) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051974&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051974&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.39E-02 | | [negative regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051348) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&list=upload_1&organism=Homo%20sapiens) | 16.55 | 1.99 | + | 4.40E-04 | 9.69E-03 | | [negative regulation of catalytic activity](http://amigo.geneontology.org/amigo/term/GO:0043086) | [781](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043086&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043086&list=upload_1&organism=Homo%20sapiens) | 47.00 | 1.57 | + | 2.81E-04 | 6.65E-03 | | [negative regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0044092) | [1150](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 69.20 | 1.65 | + | 8.73E-07 | 3.92E-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) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 55.06 | 1.93 | + | 1.61E-09 | 1.13E-07 | | [negative regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000279) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000279&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000279&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.57 | + | 1.10E-04 | 3.00E-03 | | [negative regulation of macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010558) | [1533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&reflist=1) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 92.25 | 2.03 | + | 1.76E-18 | 2.77E-16 | | [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) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 97.73 | 1.97 | + | 5.17E-18 | 8.03E-16 | | [negative regulation of cellular biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0031327) | [1594](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&reflist=1) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 95.92 | 2.00 | + | 1.69E-18 | 2.68E-16 | | [regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000278) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&list=upload_1&organism=Homo%20sapiens) | 7.52 | 3.72 | + | 3.51E-08 | 2.05E-06 | | [regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051972) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&list=upload_1&organism=Homo%20sapiens) | 3.01 | 3.66 | + | 5.74E-04 | 1.21E-02 | | [UV-damage excision repair](http://amigo.geneontology.org/amigo/term/GO:0070914) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070914&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070914&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.39E-02 | | [cellular response to UV](http://amigo.geneontology.org/amigo/term/GO:0034644) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034644&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034644&list=upload_1&organism=Homo%20sapiens) | 5.42 | 3.69 | + | 3.41E-06 | 1.36E-04 | | [cellular response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0071482) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&list=upload_1&organism=Homo%20sapiens) | 6.98 | 3.29 | + | 3.50E-06 | 1.39E-04 | | [cellular response to radiation](http://amigo.geneontology.org/amigo/term/GO:0071478) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 10.95 | 4.02 | + | 5.11E-13 | 5.45E-11 | | [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) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 19.62 | 2.96 | + | 8.67E-12 | 7.68E-10 | | [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) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&list=upload_1&organism=Homo%20sapiens) | 19.62 | 2.96 | + | 8.67E-12 | 7.64E-10 | | [positive regulation of astrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0048711) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048711&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048711&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.38E-02 | | [regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050767) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&list=upload_1&organism=Homo%20sapiens) | 22.45 | 1.78 | + | 1.13E-03 | 2.15E-02 | | [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) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 83.23 | 1.75 | + | 4.23E-10 | 3.24E-08 | | [regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0050793) | [2489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&reflist=1) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 149.78 | 1.60 | + | 2.75E-12 | 2.68E-10 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 30.87 | 1.91 | + | 8.93E-06 | 3.22E-04 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 95.14 | 1.77 | + | 7.43E-12 | 6.69E-10 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 13.90 | 2.01 | + | 1.02E-03 | 2.00E-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) | 80.58 | 1.66 | + | 4.72E-08 | 2.64E-06 | | [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) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 91.17 | 1.61 | + | 5.40E-08 | 3.01E-06 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 18.53 | 2.16 | + | 2.06E-05 | 6.97E-04 | | [positive regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045597) | [884](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 53.20 | 1.95 | + | 8.99E-10 | 6.47E-08 | | [positive regulation of DNA-directed DNA polymerase activity](http://amigo.geneontology.org/amigo/term/GO:1900264) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900264&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900264&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.38E-02 | | [regulation of DNA-directed DNA polymerase activity](http://amigo.geneontology.org/amigo/term/GO:1900262) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900262&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900262&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.38E-02 | | [positive regulation of DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000573) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000573&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000573&list=upload_1&organism=Homo%20sapiens) | 4.51 | 3.32 | + | 1.55E-04 | 4.01E-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) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 18.35 | 3.87 | + | 1.99E-19 | 3.31E-17 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051347&list=upload_1&organism=Homo%20sapiens) | 35.50 | 1.83 | + | 1.07E-05 | 3.74E-04 | | [hepatocyte apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0097284) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097284&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097284&list=upload_1&organism=Homo%20sapiens) | .78 | 6.39 | + | 2.69E-03 | 4.37E-02 | | [epithelial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1904019) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904019&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904019&list=upload_1&organism=Homo%20sapiens) | 3.13 | 3.20 | + | 2.42E-03 | 4.07E-02 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 62.16 | 2.01 | + | 2.43E-12 | 2.39E-10 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 64.63 | 2.00 | + | 2.16E-12 | 2.15E-10 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 66.68 | 1.96 | + | 3.07E-12 | 2.95E-10 | | [mRNA transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0042789) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042789&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042789&list=upload_1&organism=Homo%20sapiens) | 2.71 | 6.28 | + | 3.84E-08 | 2.19E-06 | | [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) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006366&list=upload_1&organism=Homo%20sapiens) | 21.42 | 3.73 | + | 6.13E-21 | 1.07E-18 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 36.89 | 3.06 | + | 5.72E-23 | 1.13E-20 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 36.95 | 3.06 | + | 6.41E-23 | 1.26E-20 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 37.55 | 3.09 | + | 7.93E-24 | 1.75E-21 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 98.39 | 2.08 | + | 1.42E-21 | 2.50E-19 | | [mRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0009299) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009299&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009299&list=upload_1&organism=Homo%20sapiens) | 3.07 | 5.86 | + | 3.59E-08 | 2.07E-06 | | [mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016071) | [607](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&list=upload_1&organism=Homo%20sapiens) | 36.53 | 2.11 | + | 1.05E-08 | 6.56E-07 | | [regulation of telomere maintenance in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:1904505) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904505&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904505&list=upload_1&organism=Homo%20sapiens) | .96 | 6.23 | + | 1.12E-03 | 2.13E-02 | | [positive regulation of transcription initiation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0060261) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060261&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060261&list=upload_1&organism=Homo%20sapiens) | 3.55 | 6.20 | + | 4.79E-10 | 3.63E-08 | | [positive regulation of DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:2000144) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000144&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000144&list=upload_1&organism=Homo%20sapiens) | 3.97 | 5.54 | + | 2.66E-09 | 1.80E-07 | | [regulation of DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:2000142) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000142&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000142&list=upload_1&organism=Homo%20sapiens) | 4.63 | 4.96 | + | 6.65E-09 | 4.31E-07 | | [regulation of transcription initiation by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0060260) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060260&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060260&list=upload_1&organism=Homo%20sapiens) | 4.03 | 5.70 | + | 7.28E-10 | 5.36E-08 | | [regulation of fibroblast apoptotic process](http://amigo.geneontology.org/amigo/term/GO:2000269) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000269&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000269&list=upload_1&organism=Homo%20sapiens) | 1.14 | 6.12 | + | 4.73E-04 | 1.03E-02 | | [positive regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035066) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&list=upload_1&organism=Homo%20sapiens) | 2.23 | 5.84 | + | 2.95E-06 | 1.22E-04 | | [regulation of histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0035065) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035065&list=upload_1&organism=Homo%20sapiens) | 4.09 | 3.91 | + | 1.73E-05 | 5.96E-04 | | [regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031056) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031056&list=upload_1&organism=Homo%20sapiens) | 10.89 | 3.31 | + | 6.37E-09 | 4.15E-07 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000756&list=upload_1&organism=Homo%20sapiens) | 4.63 | 3.67 | + | 1.95E-05 | 6.65E-04 | | [regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901983) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901983&list=upload_1&organism=Homo%20sapiens) | 5.36 | 3.36 | + | 3.12E-05 | 1.00E-03 | | [positive regulation of peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:2000758) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&list=upload_1&organism=Homo%20sapiens) | 2.59 | 5.41 | + | 2.58E-06 | 1.08E-04 | | [positive regulation of protein acetylation](http://amigo.geneontology.org/amigo/term/GO:1901985) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901985&list=upload_1&organism=Homo%20sapiens) | 3.19 | 4.70 | + | 4.85E-06 | 1.83E-04 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 6.44 | 4.19 | + | 7.27E-09 | 4.67E-07 | | [type I interferon signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0060337) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060337&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060337&list=upload_1&organism=Homo%20sapiens) | 2.53 | 5.54 | + | 2.06E-06 | 8.76E-05 | | [cytokine-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0019221) | [366](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019221&list=upload_1&organism=Homo%20sapiens) | 22.03 | 1.95 | + | 1.29E-04 | 3.45E-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) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 130.83 | 1.32 | + | 2.72E-04 | 6.50E-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) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 42.97 | 2.05 | + | 3.15E-09 | 2.12E-07 | | [response to cytokine](http://amigo.geneontology.org/amigo/term/GO:0034097) | [808](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&list=upload_1&organism=Homo%20sapiens) | 48.62 | 2.04 | + | 4.05E-10 | 3.12E-08 | | [cellular response to type I interferon](http://amigo.geneontology.org/amigo/term/GO:0071357) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071357&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071357&list=upload_1&organism=Homo%20sapiens) | 2.65 | 5.29 | + | 3.23E-06 | 1.30E-04 | | [response to type I interferon](http://amigo.geneontology.org/amigo/term/GO:0034340) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034340&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034340&list=upload_1&organism=Homo%20sapiens) | 3.13 | 4.79 | + | 3.99E-06 | 1.54E-04 | | [innate immune response](http://amigo.geneontology.org/amigo/term/GO:0045087) | [832](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&list=upload_1&organism=Homo%20sapiens) | 50.07 | 1.48 | + | 1.57E-03 | 2.85E-02 | | [defense response to other organism](http://amigo.geneontology.org/amigo/term/GO:0098542) | [1068](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098542&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098542&list=upload_1&organism=Homo%20sapiens) | 64.27 | 1.48 | + | 3.26E-04 | 7.48E-03 | | [response to other organism](http://amigo.geneontology.org/amigo/term/GO:0051707) | [1429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&list=upload_1&organism=Homo%20sapiens) | 85.99 | 1.55 | + | 2.20E-06 | 9.36E-05 | | [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) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&list=upload_1&organism=Homo%20sapiens) | 96.40 | 1.62 | + | 1.40E-08 | 8.55E-07 | | [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) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&list=upload_1&organism=Homo%20sapiens) | 86.17 | 1.55 | + | 1.32E-06 | 5.82E-05 | | [response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009607) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&reflist=1) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009607&list=upload_1&organism=Homo%20sapiens) | 88.94 | 1.53 | + | 3.13E-06 | 1.27E-04 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [224](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 148.58 | 1.51 | + | 2.11E-09 | 1.45E-07 | | [defense response](http://amigo.geneontology.org/amigo/term/GO:0006952) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&reflist=1) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&list=upload_1&organism=Homo%20sapiens) | 88.94 | 1.45 | + | 5.27E-05 | 1.57E-03 | | [response to follicle-stimulating hormone](http://amigo.geneontology.org/amigo/term/GO:0032354) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032354&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032354&list=upload_1&organism=Homo%20sapiens) | 1.08 | 5.54 | + | 1.84E-03 | 3.22E-02 | | [response to gonadotropin](http://amigo.geneontology.org/amigo/term/GO:0034698) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034698&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034698&list=upload_1&organism=Homo%20sapiens) | 1.75 | 4.58 | + | 9.29E-04 | 1.85E-02 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 46.16 | 1.97 | + | 7.19E-09 | 4.64E-07 | | [positive regulation of erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045648) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045648&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045648&list=upload_1&organism=Homo%20sapiens) | 1.87 | 5.36 | + | 7.45E-05 | 2.15E-03 | | [positive regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045639) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 6.02 | 2.66 | + | 8.58E-04 | 1.73E-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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 12.04 | 2.24 | + | 2.52E-04 | 6.12E-03 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 23.95 | 2.42 | + | 8.18E-09 | 5.21E-07 | | [regulation of erythrocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045646) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045646&list=upload_1&organism=Homo%20sapiens) | 2.71 | 4.43 | + | 6.95E-05 | 2.03E-03 | | [natural killer cell activation involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002323) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002323&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002323&list=upload_1&organism=Homo%20sapiens) | 1.50 | 5.32 | + | 4.09E-04 | 9.06E-03 | | [natural killer cell activation](http://amigo.geneontology.org/amigo/term/GO:0030101) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030101&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030101&list=upload_1&organism=Homo%20sapiens) | 3.97 | 3.27 | + | 4.75E-04 | 1.03E-02 | | [positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:1901522) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901522&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901522&list=upload_1&organism=Homo%20sapiens) | 1.32 | 5.29 | + | 9.66E-04 | 1.91E-02 | | [negative regulation of anoikis](http://amigo.geneontology.org/amigo/term/GO:2000811) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000811&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000811&list=upload_1&organism=Homo%20sapiens) | 1.14 | 5.25 | + | 2.30E-03 | 3.89E-02 | | [regulation of anoikis](http://amigo.geneontology.org/amigo/term/GO:2000209) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000209&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000209&list=upload_1&organism=Homo%20sapiens) | 1.56 | 5.75 | + | 1.10E-04 | 3.00E-03 | | [cellular response to gamma radiation](http://amigo.geneontology.org/amigo/term/GO:0071480) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071480&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071480&list=upload_1&organism=Homo%20sapiens) | 1.75 | 5.16 | + | 2.17E-04 | 5.32E-03 | | [response to gamma radiation](http://amigo.geneontology.org/amigo/term/GO:0010332) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010332&list=upload_1&organism=Homo%20sapiens) | 3.37 | 6.53 | + | 2.15E-10 | 1.71E-08 | | [cellular response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0071479) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&list=upload_1&organism=Homo%20sapiens) | 4.51 | 5.54 | + | 2.23E-10 | 1.75E-08 | | [nuclear migration](http://amigo.geneontology.org/amigo/term/GO:0007097) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007097&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007097&list=upload_1&organism=Homo%20sapiens) | 1.38 | 5.06 | + | 1.20E-03 | 2.25E-02 | | [nucleus localization](http://amigo.geneontology.org/amigo/term/GO:0051647) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051647&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051647&list=upload_1&organism=Homo%20sapiens) | 1.75 | 4.58 | + | 9.29E-04 | 1.86E-02 | | [organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051640) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051640&list=upload_1&organism=Homo%20sapiens) | 30.87 | 1.75 | + | 2.07E-04 | 5.12E-03 | | [intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0046907) | [1360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&reflist=1) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&list=upload_1&organism=Homo%20sapiens) | 81.84 | 1.41 | + | 4.60E-04 | 1.00E-02 | | [establishment of localization in cell](http://amigo.geneontology.org/amigo/term/GO:0051649) | [1752](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&list=upload_1&organism=Homo%20sapiens) | 105.43 | 1.41 | + | 4.92E-05 | 1.49E-03 | | [establishment of localization](http://amigo.geneontology.org/amigo/term/GO:0051234) | [3997](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&reflist=1) | [302](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&list=upload_1&organism=Homo%20sapiens) | 240.53 | 1.26 | + | 3.16E-05 | 1.01E-03 | | [transport](http://amigo.geneontology.org/amigo/term/GO:0006810) | [3840](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&reflist=1) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&list=upload_1&organism=Homo%20sapiens) | 231.08 | 1.23 | + | 2.85E-04 | 6.71E-03 | | [establishment of organelle localization](http://amigo.geneontology.org/amigo/term/GO:0051656) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051656&list=upload_1&organism=Homo%20sapiens) | 22.81 | 1.93 | + | 1.10E-04 | 2.99E-03 | | [neuronal stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0097150) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097150&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097150&list=upload_1&organism=Homo%20sapiens) | 1.38 | 5.06 | + | 1.20E-03 | 2.25E-02 | | [stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:0019827) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019827&list=upload_1&organism=Homo%20sapiens) | 6.86 | 3.35 | + | 2.71E-06 | 1.13E-04 | | [maintenance of cell number](http://amigo.geneontology.org/amigo/term/GO:0098727) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098727&list=upload_1&organism=Homo%20sapiens) | 7.10 | 3.24 | + | 4.49E-06 | 1.71E-04 | | [cellular response to gonadotropin stimulus](http://amigo.geneontology.org/amigo/term/GO:0071371) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071371&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071371&list=upload_1&organism=Homo%20sapiens) | 1.20 | 4.99 | + | 2.85E-03 | 4.57E-02 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 29.43 | 2.21 | + | 3.74E-08 | 2.15E-06 | | [positive regulation of amyloid-beta formation](http://amigo.geneontology.org/amigo/term/GO:1902004) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902004&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902004&list=upload_1&organism=Homo%20sapiens) | 1.20 | 4.99 | + | 2.85E-03 | 4.56E-02 | | [regulation of amyloid-beta formation](http://amigo.geneontology.org/amigo/term/GO:1902003) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902003&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902003&list=upload_1&organism=Homo%20sapiens) | 2.17 | 4.15 | + | 8.24E-04 | 1.67E-02 | | [regulation of amyloid precursor protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902991) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902991&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902991&list=upload_1&organism=Homo%20sapiens) | 2.59 | 3.86 | + | 6.98E-04 | 1.44E-02 | | [positive regulation of amyloid precursor protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1902993) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902993&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902993&list=upload_1&organism=Homo%20sapiens) | 1.56 | 4.47 | + | 2.17E-03 | 3.69E-02 | | [B cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0042100) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042100&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042100&list=upload_1&organism=Homo%20sapiens) | 3.13 | 4.79 | + | 3.99E-06 | 1.55E-04 | | [lymphocyte proliferation](http://amigo.geneontology.org/amigo/term/GO:0046651) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046651&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046651&list=upload_1&organism=Homo%20sapiens) | 7.40 | 2.97 | + | 2.33E-05 | 7.77E-04 | | [mononuclear cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0032943) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032943&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032943&list=upload_1&organism=Homo%20sapiens) | 7.64 | 2.88 | + | 3.59E-05 | 1.12E-03 | | [leukocyte proliferation](http://amigo.geneontology.org/amigo/term/GO:0070661) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070661&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070661&list=upload_1&organism=Homo%20sapiens) | 8.73 | 2.75 | + | 3.11E-05 | 1.00E-03 | | [cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0008283) | [718](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008283&list=upload_1&organism=Homo%20sapiens) | 43.21 | 1.97 | + | 3.53E-08 | 2.05E-06 | | [histone H2A ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0033522) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033522&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033522&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.75 | + | 7.66E-04 | 1.56E-02 | | [histone ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016574) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016574&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016574&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.97 | + | 3.12E-04 | 7.24E-03 | | [protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016567) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016567&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016567&list=upload_1&organism=Homo%20sapiens) | 41.16 | 1.51 | + | 2.77E-03 | 4.45E-02 | | [protein modification by small protein conjugation](http://amigo.geneontology.org/amigo/term/GO:0032446) | [753](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032446&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032446&list=upload_1&organism=Homo%20sapiens) | 45.31 | 1.59 | + | 2.89E-04 | 6.79E-03 | | [protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:0070647) | [898](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070647&reflist=1) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070647&list=upload_1&organism=Homo%20sapiens) | 54.04 | 1.59 | + | 7.15E-05 | 2.07E-03 | | [histone modification](http://amigo.geneontology.org/amigo/term/GO:0016570) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016570&list=upload_1&organism=Homo%20sapiens) | 21.96 | 2.19 | + | 2.55E-06 | 1.07E-04 | | [intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0042771) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042771&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042771&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.67 | + | 4.00E-04 | 8.89E-03 | | [intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0072332) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072332&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072332&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.86 | + | 1.18E-04 | 3.18E-03 | | [signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0072331) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072331&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072331&list=upload_1&organism=Homo%20sapiens) | 5.54 | 3.25 | + | 4.56E-05 | 1.39E-03 | | [intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097193) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&list=upload_1&organism=Homo%20sapiens) | 9.81 | 3.06 | + | 4.91E-07 | 2.34E-05 | | [apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097190) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&list=upload_1&organism=Homo%20sapiens) | 19.02 | 2.68 | + | 3.46E-09 | 2.31E-07 | | [intrinsic apoptotic signaling pathway in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:0008630) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&list=upload_1&organism=Homo%20sapiens) | 4.45 | 4.27 | + | 9.58E-07 | 4.28E-05 | | [positive regulation of muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:1901863) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901863&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901863&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.18E-02 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071459&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.17E-02 | | [regulation of DNA methylation](http://amigo.geneontology.org/amigo/term/GO:0044030) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044030&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.17E-02 | | [positive regulation of purine nucleotide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1900373) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900373&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900373&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.17E-02 | | [regulation of small molecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0062012) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062012&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062012&list=upload_1&organism=Homo%20sapiens) | 20.04 | 2.05 | + | 6.07E-05 | 1.78E-03 | | [positive regulation of small molecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0062013) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062013&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062013&list=upload_1&organism=Homo%20sapiens) | 8.85 | 2.37 | + | 6.18E-04 | 1.29E-02 | | [positive regulation of nucleotide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0030810) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030810&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030810&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.16E-02 | | [regulation of nucleotide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0030808) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030808&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030808&list=upload_1&organism=Homo%20sapiens) | 2.47 | 3.65 | + | 1.81E-03 | 3.17E-02 | | [regulation of purine nucleotide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1900371) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900371&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900371&list=upload_1&organism=Homo%20sapiens) | 2.41 | 3.74 | + | 1.56E-03 | 2.84E-02 | | [positive regulation of histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0031065) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031065&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031065&list=upload_1&organism=Homo%20sapiens) | 1.50 | 4.65 | + | 1.80E-03 | 3.16E-02 | | [positive regulation of protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0090312) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090312&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090312&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.29 | + | 1.34E-03 | 2.48E-02 | | [regulation of protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0090311) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090311&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090311&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.48 | + | 2.81E-04 | 6.65E-03 | | [regulation of histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0031063) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031063&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031063&list=upload_1&organism=Homo%20sapiens) | 2.71 | 4.06 | + | 2.65E-04 | 6.34E-03 | | [regulation of autophagy of mitochondrion](http://amigo.geneontology.org/amigo/term/GO:1903146) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903146&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903146&list=upload_1&organism=Homo%20sapiens) | 2.17 | 4.62 | + | 2.09E-04 | 5.16E-03 | | [regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010506) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&list=upload_1&organism=Homo%20sapiens) | 20.76 | 2.17 | + | 6.71E-06 | 2.48E-04 | | [regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010821) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&list=upload_1&organism=Homo%20sapiens) | 9.15 | 3.17 | + | 3.96E-07 | 1.91E-05 | | [positive regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0045740) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045740&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045740&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.57 | + | 1.10E-04 | 3.00E-03 | | [histone deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0016578) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016578&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016578&list=upload_1&organism=Homo%20sapiens) | 2.65 | 4.53 | + | 5.78E-05 | 1.71E-03 | | [proteolysis](http://amigo.geneontology.org/amigo/term/GO:0006508) | [1266](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006508&list=upload_1&organism=Homo%20sapiens) | 76.19 | 1.46 | + | 1.81E-04 | 4.58E-03 | | [positive regulation of chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0051984) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051984&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051984&list=upload_1&organism=Homo%20sapiens) | 1.56 | 4.47 | + | 2.17E-03 | 3.70E-02 | | [regulation of chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0051983) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051983&list=upload_1&organism=Homo%20sapiens) | 7.88 | 2.79 | + | 5.41E-05 | 1.61E-03 | | [response to exogenous dsRNA](http://amigo.geneontology.org/amigo/term/GO:0043330) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043330&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043330&list=upload_1&organism=Homo%20sapiens) | 2.95 | 4.41 | + | 3.66E-05 | 1.14E-03 | | [response to dsRNA](http://amigo.geneontology.org/amigo/term/GO:0043331) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043331&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043331&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.86 | + | 1.18E-04 | 3.17E-03 | | [mitotic G2 DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0007095) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007095&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007095&list=upload_1&organism=Homo%20sapiens) | 2.05 | 4.40 | + | 5.81E-04 | 1.22E-02 | | [mitotic G2/M transition checkpoint](http://amigo.geneontology.org/amigo/term/GO:0044818) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044818&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044818&list=upload_1&organism=Homo%20sapiens) | 3.01 | 4.32 | + | 4.37E-05 | 1.34E-03 | | [negative regulation of G2/M transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0010972) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010972&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010972&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.48 | + | 2.81E-04 | 6.64E-03 | | [regulation of G2/M transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0010389) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010389&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010389&list=upload_1&organism=Homo%20sapiens) | 5.90 | 3.22 | + | 3.16E-05 | 1.01E-03 | | [regulation of cell cycle G2/M phase transition](http://amigo.geneontology.org/amigo/term/GO:1902749) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902749&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902749&list=upload_1&organism=Homo%20sapiens) | 6.62 | 3.02 | + | 4.41E-05 | 1.35E-03 | | [regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901990) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901990&list=upload_1&organism=Homo%20sapiens) | 19.98 | 2.60 | + | 5.43E-09 | 3.55E-07 | | [negative regulation of cell cycle G2/M phase transition](http://amigo.geneontology.org/amigo/term/GO:1902750) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902750&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902750&list=upload_1&organism=Homo%20sapiens) | 3.85 | 3.38 | + | 3.67E-04 | 8.31E-03 | | [negative regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901991) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901991&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901991&list=upload_1&organism=Homo%20sapiens) | 9.99 | 3.00 | + | 6.87E-07 | 3.15E-05 | | [RNA polymerase II preinitiation complex assembly](http://amigo.geneontology.org/amigo/term/GO:0051123) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051123&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051123&list=upload_1&organism=Homo%20sapiens) | 3.43 | 4.37 | + | 1.02E-05 | 3.60E-04 | | [transcription initiation at RNA polymerase II promoter](http://amigo.geneontology.org/amigo/term/GO:0006367) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006367&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006367&list=upload_1&organism=Homo%20sapiens) | 4.75 | 4.21 | + | 6.04E-07 | 2.79E-05 | | [DNA-templated transcription initiation](http://amigo.geneontology.org/amigo/term/GO:0006352) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006352&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006352&list=upload_1&organism=Homo%20sapiens) | 6.86 | 3.21 | + | 8.26E-06 | 3.00E-04 | | [transcription preinitiation complex assembly](http://amigo.geneontology.org/amigo/term/GO:0070897) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070897&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070897&list=upload_1&organism=Homo%20sapiens) | 4.27 | 3.74 | + | 2.74E-05 | 8.97E-04 | | [protein-DNA complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065004) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065004&list=upload_1&organism=Homo%20sapiens) | 12.04 | 2.74 | + | 1.18E-06 | 5.22E-05 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 76.43 | 1.40 | + | 9.05E-04 | 1.82E-02 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 85.63 | 1.42 | + | 2.00E-04 | 4.98E-03 | | [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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&list=upload_1&organism=Homo%20sapiens) | 14.02 | 3.07 | + | 1.64E-09 | 1.15E-07 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051570&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.31 | + | 2.60E-03 | 4.29E-02 | | [regulation of histone methylation](http://amigo.geneontology.org/amigo/term/GO:0031060) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031060&list=upload_1&organism=Homo%20sapiens) | 5.05 | 2.77 | + | 1.25E-03 | 2.34E-02 | | [regulation of cardiocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1905207) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905207&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905207&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.31 | + | 2.60E-03 | 4.28E-02 | | [branched-chain amino acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0009081) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009081&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009081&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.31 | + | 2.60E-03 | 4.28E-02 | | [positive regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032206) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&list=upload_1&organism=Homo%20sapiens) | 3.97 | 4.28 | + | 3.41E-06 | 1.36E-04 | | [positive regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001252) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 6.38 | 3.92 | + | 8.01E-08 | 4.33E-06 | | [positive regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0010638) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&list=upload_1&organism=Homo%20sapiens) | 30.57 | 2.09 | + | 2.00E-07 | 1.02E-05 | | [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) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 63.43 | 1.81 | + | 7.70E-09 | 4.93E-07 | | [negative regulation of cytokine production involved in immune response](http://amigo.geneontology.org/amigo/term/GO:0002719) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002719&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002719&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.27 | + | 6.94E-04 | 1.44E-02 | | [negative regulation of production of molecular mediator of immune response](http://amigo.geneontology.org/amigo/term/GO:0002701) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002701&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002701&list=upload_1&organism=Homo%20sapiens) | 2.83 | 3.89 | + | 3.65E-04 | 8.27E-03 | | [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) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 54.28 | 1.79 | + | 2.50E-07 | 1.26E-05 | | [negative regulation of immune system process](http://amigo.geneontology.org/amigo/term/GO:0002683) | [434](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002683&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002683&list=upload_1&organism=Homo%20sapiens) | 26.12 | 1.65 | + | 2.59E-03 | 4.28E-02 | | [positive regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902895) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&list=upload_1&organism=Homo%20sapiens) | 2.83 | 4.24 | + | 9.90E-05 | 2.76E-03 | | [positive regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000630) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&list=upload_1&organism=Homo%20sapiens) | 3.19 | 4.08 | + | 7.29E-05 | 2.11E-03 | | [regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000628) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 4.45 | 3.37 | + | 1.36E-04 | 3.60E-03 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 3.79 | 3.69 | + | 9.75E-05 | 2.73E-03 | | [reciprocal meiotic recombination](http://amigo.geneontology.org/amigo/term/GO:0007131) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007131&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007131&list=upload_1&organism=Homo%20sapiens) | 3.37 | 4.15 | + | 3.25E-05 | 1.03E-03 | | [meiosis I](http://amigo.geneontology.org/amigo/term/GO:0007127) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007127&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007127&list=upload_1&organism=Homo%20sapiens) | 7.70 | 3.12 | + | 5.03E-06 | 1.89E-04 | | [meiosis I cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0061982) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061982&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061982&list=upload_1&organism=Homo%20sapiens) | 7.82 | 3.32 | + | 7.17E-07 | 3.28E-05 | | [meiotic cell cycle process](http://amigo.geneontology.org/amigo/term/GO:1903046) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903046&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903046&list=upload_1&organism=Homo%20sapiens) | 11.43 | 2.71 | + | 3.03E-06 | 1.25E-04 | | [reproductive process](http://amigo.geneontology.org/amigo/term/GO:0022414) | [1437](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&reflist=1) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022414&list=upload_1&organism=Homo%20sapiens) | 86.48 | 1.50 | + | 1.17E-05 | 4.09E-04 | | [reproduction](http://amigo.geneontology.org/amigo/term/GO:0000003) | [1447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&reflist=1) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000003&list=upload_1&organism=Homo%20sapiens) | 87.08 | 1.49 | + | 1.62E-05 | 5.58E-04 | | [meiotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051321) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051321&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051321&list=upload_1&organism=Homo%20sapiens) | 15.10 | 2.91 | + | 4.23E-09 | 2.80E-07 | | [meiotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0140013) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140013&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140013&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.59 | + | 3.38E-05 | 1.07E-03 | | [nuclear division](http://amigo.geneontology.org/amigo/term/GO:0000280) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000280&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000280&list=upload_1&organism=Homo%20sapiens) | 19.44 | 2.47 | + | 9.30E-08 | 4.96E-06 | | [organelle fission](http://amigo.geneontology.org/amigo/term/GO:0048285) | [349](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048285&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048285&list=upload_1&organism=Homo%20sapiens) | 21.00 | 2.38 | + | 1.47E-07 | 7.69E-06 | | [reciprocal homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0140527) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140527&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140527&list=upload_1&organism=Homo%20sapiens) | 3.37 | 4.15 | + | 3.25E-05 | 1.03E-03 | | [homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0035825) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035825&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035825&list=upload_1&organism=Homo%20sapiens) | 3.79 | 4.75 | + | 4.98E-07 | 2.37E-05 | | [somitogenesis](http://amigo.geneontology.org/amigo/term/GO:0001756) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001756&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001756&list=upload_1&organism=Homo%20sapiens) | 3.85 | 4.15 | + | 9.07E-06 | 3.26E-04 | | [anatomical structure formation involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048646) | [941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&reflist=1) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&list=upload_1&organism=Homo%20sapiens) | 56.63 | 1.70 | + | 2.45E-06 | 1.03E-04 | | [chordate embryonic development](http://amigo.geneontology.org/amigo/term/GO:0043009) | [655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043009&list=upload_1&organism=Homo%20sapiens) | 39.42 | 2.03 | + | 2.20E-08 | 1.33E-06 | | [embryo development ending in birth or egg hatching](http://amigo.geneontology.org/amigo/term/GO:0009792) | [677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009792&list=upload_1&organism=Homo%20sapiens) | 40.74 | 1.99 | + | 3.77E-08 | 2.16E-06 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 63.73 | 1.79 | + | 1.78E-08 | 1.08E-06 | | [segmentation](http://amigo.geneontology.org/amigo/term/GO:0035282) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035282&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035282&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.88 | + | 1.80E-04 | 4.57E-03 | | [somite development](http://amigo.geneontology.org/amigo/term/GO:0061053) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061053&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061053&list=upload_1&organism=Homo%20sapiens) | 4.93 | 3.85 | + | 3.53E-06 | 1.39E-04 | | [anterior/posterior pattern specification](http://amigo.geneontology.org/amigo/term/GO:0009952) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009952&list=upload_1&organism=Homo%20sapiens) | 13.12 | 2.36 | + | 4.13E-05 | 1.27E-03 | | [regulation of intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1902253) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902253&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902253&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.15 | + | 1.59E-03 | 2.89E-02 | | [regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001242) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001242&list=upload_1&organism=Homo%20sapiens) | 10.05 | 2.19 | + | 1.30E-03 | 2.43E-02 | | [regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001233) | [364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001233&list=upload_1&organism=Homo%20sapiens) | 21.90 | 2.05 | + | 2.05E-05 | 6.97E-04 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.56 | + | 1.24E-03 | 2.32E-02 | | [positive regulation of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0045070) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045070&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045070&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.15 | + | 1.59E-03 | 2.89E-02 | | [regulation of viral process](http://amigo.geneontology.org/amigo/term/GO:0050792) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&list=upload_1&organism=Homo%20sapiens) | 9.87 | 2.43 | + | 1.88E-04 | 4.72E-03 | | [regulation of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0045069) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045069&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045069&list=upload_1&organism=Homo%20sapiens) | 5.24 | 3.25 | + | 7.45E-05 | 2.15E-03 | | [regulation of viral life cycle](http://amigo.geneontology.org/amigo/term/GO:1903900) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903900&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903900&list=upload_1&organism=Homo%20sapiens) | 8.55 | 2.34 | + | 9.60E-04 | 1.90E-02 | | [mitotic G1 DNA damage checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0031571) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031571&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031571&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.15 | + | 1.59E-03 | 2.89E-02 | | [mitotic G1/S transition checkpoint signaling](http://amigo.geneontology.org/amigo/term/GO:0044819) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044819&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044819&list=upload_1&organism=Homo%20sapiens) | 1.99 | 4.03 | + | 1.88E-03 | 3.28E-02 | | [negative regulation of G1/S transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:2000134) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000134&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000134&list=upload_1&organism=Homo%20sapiens) | 4.51 | 2.88 | + | 1.35E-03 | 2.50E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000045&list=upload_1&organism=Homo%20sapiens) | 9.87 | 2.53 | + | 8.65E-05 | 2.43E-03 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 11.55 | 2.34 | + | 1.63E-04 | 4.19E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902807&list=upload_1&organism=Homo%20sapiens) | 5.05 | 2.97 | + | 4.53E-04 | 9.94E-03 | | [positive regulation of mitochondrial membrane permeability](http://amigo.geneontology.org/amigo/term/GO:0035794) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035794&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035794&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.15 | + | 1.59E-03 | 2.88E-02 | | [membrane organization](http://amigo.geneontology.org/amigo/term/GO:0061024) | [851](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061024&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061024&list=upload_1&organism=Homo%20sapiens) | 51.21 | 1.44 | + | 2.83E-03 | 4.54E-02 | | [positive regulation of membrane permeability](http://amigo.geneontology.org/amigo/term/GO:1905710) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905710&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905710&list=upload_1&organism=Homo%20sapiens) | 2.17 | 3.69 | + | 3.00E-03 | 4.78E-02 | | [negative regulation of telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:1904357) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904357&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904357&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.15 | + | 3.09E-03 | 4.91E-02 | | [regulation of telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:1904356) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904356&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904356&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.22 | + | 8.86E-04 | 1.78E-02 | | [negative regulation of cardiac muscle hypertrophy](http://amigo.geneontology.org/amigo/term/GO:0010614) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010614&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010614&list=upload_1&organism=Homo%20sapiens) | 1.68 | 4.15 | + | 3.09E-03 | 4.90E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043502&list=upload_1&organism=Homo%20sapiens) | 4.81 | 3.12 | + | 2.87E-04 | 6.74E-03 | | [aortic valve morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003180) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003180&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003180&list=upload_1&organism=Homo%20sapiens) | 1.93 | 4.15 | + | 1.59E-03 | 2.88E-02 | | [aortic valve development](http://amigo.geneontology.org/amigo/term/GO:0003176) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003176&list=upload_1&organism=Homo%20sapiens) | 2.23 | 4.49 | + | 2.52E-04 | 6.13E-03 | | [semi-lunar valve development](http://amigo.geneontology.org/amigo/term/GO:1905314) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905314&list=upload_1&organism=Homo%20sapiens) | 2.47 | 4.05 | + | 5.07E-04 | 1.08E-02 | | [heart valve development](http://amigo.geneontology.org/amigo/term/GO:0003170) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003170&list=upload_1&organism=Homo%20sapiens) | 3.91 | 3.58 | + | 1.30E-04 | 3.45E-03 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 33.40 | 2.01 | + | 5.87E-07 | 2.73E-05 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 54.70 | 1.59 | + | 5.93E-05 | 1.74E-03 | | [heart valve morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003179) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003179&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003179&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.32 | + | 1.14E-03 | 2.15E-02 | | [regulation of cellular respiration](http://amigo.geneontology.org/amigo/term/GO:0043457) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043457&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043457&list=upload_1&organism=Homo%20sapiens) | 2.95 | 4.07 | + | 1.39E-04 | 3.65E-03 | | [regulation of generation of precursor metabolites and energy](http://amigo.geneontology.org/amigo/term/GO:0043467) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043467&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043467&list=upload_1&organism=Homo%20sapiens) | 7.94 | 2.64 | + | 1.55E-04 | 4.02E-03 | | [negative regulation of double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:2000780) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000780&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000780&list=upload_1&organism=Homo%20sapiens) | 1.99 | 4.03 | + | 1.88E-03 | 3.29E-02 | | [negative regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0045738) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045738&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045738&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.27 | + | 6.94E-04 | 1.44E-02 | | [regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006282) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&list=upload_1&organism=Homo%20sapiens) | 12.76 | 4.31 | + | 4.60E-17 | 6.81E-15 | | [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) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000779&list=upload_1&organism=Homo%20sapiens) | 8.12 | 3.69 | + | 1.34E-08 | 8.30E-07 | | [regulation of keratinocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045616) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045616&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045616&list=upload_1&organism=Homo%20sapiens) | 2.29 | 3.94 | + | 1.14E-03 | 2.16E-02 | | [regulation of epidermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045604) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045604&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045604&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.15 | + | 1.65E-03 | 2.96E-02 | | [regulation of epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030856) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&list=upload_1&organism=Homo%20sapiens) | 9.15 | 2.51 | + | 1.85E-04 | 4.67E-03 | | [negative regulation of fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048147) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048147&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048147&list=upload_1&organism=Homo%20sapiens) | 2.05 | 3.91 | + | 2.21E-03 | 3.76E-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) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 42.91 | 1.77 | + | 6.58E-06 | 2.43E-04 | | [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) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 100.74 | 1.59 | + | 3.47E-08 | 2.04E-06 | | [regulation of fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048145) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&list=upload_1&organism=Homo%20sapiens) | 5.36 | 3.36 | + | 3.12E-05 | 1.00E-03 | | [establishment of mitotic spindle orientation](http://amigo.geneontology.org/amigo/term/GO:0000132) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000132&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000132&list=upload_1&organism=Homo%20sapiens) | 2.05 | 3.91 | + | 2.21E-03 | 3.75E-02 | | [establishment of spindle orientation](http://amigo.geneontology.org/amigo/term/GO:0051294) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051294&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051294&list=upload_1&organism=Homo%20sapiens) | 2.47 | 4.05 | + | 5.07E-04 | 1.09E-02 | | [establishment of spindle localization](http://amigo.geneontology.org/amigo/term/GO:0051293) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051293&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051293&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.32 | + | 1.14E-03 | 2.15E-02 | | [microtubule cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0000226) | [547](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000226&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000226&list=upload_1&organism=Homo%20sapiens) | 32.92 | 1.67 | + | 4.69E-04 | 1.02E-02 | | [cytoskeleton organization](http://amigo.geneontology.org/amigo/term/GO:0007010) | [1240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&reflist=1) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007010&list=upload_1&organism=Homo%20sapiens) | 74.62 | 1.49 | + | 7.52E-05 | 2.16E-03 | | [microtubule-based process](http://amigo.geneontology.org/amigo/term/GO:0007017) | [809](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007017&list=upload_1&organism=Homo%20sapiens) | 48.68 | 1.52 | + | 7.93E-04 | 1.61E-02 | | [spindle localization](http://amigo.geneontology.org/amigo/term/GO:0051653) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051653&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051653&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.05 | + | 2.09E-03 | 3.60E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902850&list=upload_1&organism=Homo%20sapiens) | 7.76 | 2.96 | + | 1.61E-05 | 5.56E-04 | | [monoubiquitinated protein deubiquitination](http://amigo.geneontology.org/amigo/term/GO:0035520) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035520&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035520&list=upload_1&organism=Homo%20sapiens) | 2.05 | 3.91 | + | 2.21E-03 | 3.75E-02 | | [chromosome condensation](http://amigo.geneontology.org/amigo/term/GO:0030261) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030261&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030261&list=upload_1&organism=Homo%20sapiens) | 2.59 | 3.86 | + | 6.98E-04 | 1.44E-02 | | [DNA-templated transcription elongation](http://amigo.geneontology.org/amigo/term/GO:0006354) | [185](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006354&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006354&list=upload_1&organism=Homo%20sapiens) | 11.13 | 3.86 | + | 2.88E-12 | 2.79E-10 | | [mRNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0048255) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.86 | + | 1.18E-04 | 3.17E-03 | | [RNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0043489) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&list=upload_1&organism=Homo%20sapiens) | 3.91 | 3.58 | + | 1.30E-04 | 3.46E-03 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035019&list=upload_1&organism=Homo%20sapiens) | 3.37 | 3.86 | + | 1.18E-04 | 3.16E-03 | | [regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060251) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.80 | + | 2.58E-03 | 4.28E-02 | | [fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048144) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048144&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048144&list=upload_1&organism=Homo%20sapiens) | 2.17 | 3.69 | + | 3.00E-03 | 4.78E-02 | | [regulation of double-strand break repair via homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0010569) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010569&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010569&list=upload_1&organism=Homo%20sapiens) | 4.33 | 3.69 | + | 3.17E-05 | 1.01E-03 | | [regulation of DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0000018) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000018&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000018&list=upload_1&organism=Homo%20sapiens) | 8.00 | 3.37 | + | 3.41E-07 | 1.66E-05 | | [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) | 2.71 | 3.69 | + | 9.44E-04 | 1.88E-02 | | [protein monoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0006513) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006513&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006513&list=upload_1&organism=Homo%20sapiens) | 4.69 | 3.62 | + | 2.25E-05 | 7.53E-04 | | [glandular epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002067) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002067&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002067&list=upload_1&organism=Homo%20sapiens) | 3.91 | 3.58 | + | 1.30E-04 | 3.47E-03 | | [columnar/cuboidal epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0002065) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002065&list=upload_1&organism=Homo%20sapiens) | 6.32 | 2.85 | + | 2.00E-04 | 4.97E-03 | | [regulation of T-helper cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045622) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045622&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045622&list=upload_1&organism=Homo%20sapiens) | 2.53 | 3.56 | + | 2.09E-03 | 3.59E-02 | | [regulation of CD4-positive, alpha-beta T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0043370) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043370&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043370&list=upload_1&organism=Homo%20sapiens) | 3.31 | 3.32 | + | 1.14E-03 | 2.15E-02 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050863&list=upload_1&organism=Homo%20sapiens) | 22.69 | 2.07 | + | 1.09E-05 | 3.82E-04 | | [regulation of lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0051249) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051249&list=upload_1&organism=Homo%20sapiens) | 35.57 | 1.83 | + | 1.50E-05 | 5.19E-04 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 41.16 | 1.72 | + | 2.79E-05 | 9.11E-04 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 44.59 | 1.70 | + | 2.03E-05 | 6.91E-04 | | [regulation of alpha-beta T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0046637) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046637&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046637&list=upload_1&organism=Homo%20sapiens) | 4.33 | 2.77 | + | 2.71E-03 | 4.40E-02 | | [regulation of T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045580) | [179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045580&list=upload_1&organism=Homo%20sapiens) | 10.77 | 2.69 | + | 7.03E-06 | 2.59E-04 | | [regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045619) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 12.64 | 2.61 | + | 3.65E-06 | 1.44E-04 | | [regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902105) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 19.02 | 2.37 | + | 7.75E-07 | 3.51E-05 | | [regulation of miRNA-mediated gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060964) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&list=upload_1&organism=Homo%20sapiens) | 2.53 | 3.56 | + | 2.09E-03 | 3.59E-02 | | [regulation of post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:1900368) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.78 | + | 8.13E-04 | 1.65E-02 | | [regulation of post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060147) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&list=upload_1&organism=Homo%20sapiens) | 2.71 | 3.69 | + | 9.44E-04 | 1.88E-02 | | [regulation of gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0060966) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&list=upload_1&organism=Homo%20sapiens) | 2.77 | 3.61 | + | 1.09E-03 | 2.09E-02 | | [peptidyl-threonine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018107) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018107&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018107&list=upload_1&organism=Homo%20sapiens) | 4.21 | 3.56 | + | 7.95E-05 | 2.27E-03 | | [peptidyl-threonine modification](http://amigo.geneontology.org/amigo/term/GO:0018210) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018210&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018210&list=upload_1&organism=Homo%20sapiens) | 4.75 | 3.16 | + | 2.55E-04 | 6.15E-03 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 53.08 | 1.94 | + | 2.03E-09 | 1.39E-07 | | [cardiac ventricle morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003208) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003208&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003208&list=upload_1&organism=Homo%20sapiens) | 4.21 | 3.56 | + | 7.95E-05 | 2.26E-03 | | [cardiac chamber development](http://amigo.geneontology.org/amigo/term/GO:0003205) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003205&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003205&list=upload_1&organism=Homo%20sapiens) | 10.11 | 2.28 | + | 7.11E-04 | 1.46E-02 | | [cardiac chamber morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003206) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003206&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003206&list=upload_1&organism=Homo%20sapiens) | 7.46 | 2.68 | + | 1.88E-04 | 4.73E-03 | | [heart morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0003007) | [249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003007&list=upload_1&organism=Homo%20sapiens) | 14.98 | 2.27 | + | 4.06E-05 | 1.25E-03 | | [animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009887) | [1003](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&reflist=1) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&list=upload_1&organism=Homo%20sapiens) | 60.36 | 1.66 | + | 3.49E-06 | 1.38E-04 | | [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) | 3.13 | 3.52 | + | 7.62E-04 | 1.55E-02 | | [response to dexamethasone](http://amigo.geneontology.org/amigo/term/GO:0071548) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.40 | + | 2.75E-03 | 4.43E-02 | | [response to glucocorticoid](http://amigo.geneontology.org/amigo/term/GO:0051384) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&list=upload_1&organism=Homo%20sapiens) | 8.61 | 2.32 | + | 1.03E-03 | 2.00E-02 | | [response to corticosteroid](http://amigo.geneontology.org/amigo/term/GO:0031960) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&list=upload_1&organism=Homo%20sapiens) | 9.99 | 2.20 | + | 1.24E-03 | 2.32E-02 | | [response to steroid hormone](http://amigo.geneontology.org/amigo/term/GO:0048545) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 17.09 | 2.34 | + | 4.40E-06 | 1.68E-04 | | [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) | 50.73 | 1.85 | + | 6.85E-08 | 3.76E-06 | | [response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901654) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&list=upload_1&organism=Homo%20sapiens) | 12.40 | 2.02 | + | 2.24E-03 | 3.80E-02 | | [negative regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000378) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000378&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000378&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.40 | + | 2.75E-03 | 4.43E-02 | | [DNA damage response, signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:0030330) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030330&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030330&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.40 | + | 2.75E-03 | 4.42E-02 | | [regulation of telomere maintenance via telomerase](http://amigo.geneontology.org/amigo/term/GO:0032210) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032210&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032210&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.39 | + | 9.98E-04 | 1.96E-02 | | [positive regulation of double-strand break repair](http://amigo.geneontology.org/amigo/term/GO:2000781) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000781&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000781&list=upload_1&organism=Homo%20sapiens) | 5.36 | 3.36 | + | 3.12E-05 | 1.00E-03 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&list=upload_1&organism=Homo%20sapiens) | 7.82 | 4.09 | + | 5.13E-10 | 3.87E-08 | | [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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&list=upload_1&organism=Homo%20sapiens) | 10.11 | 3.96 | + | 8.74E-12 | 7.66E-10 | | [positive regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048584) | [2223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&reflist=1) | [214](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 133.78 | 1.60 | + | 4.37E-11 | 3.64E-09 | | [negative regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0032091) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032091&list=upload_1&organism=Homo%20sapiens) | 5.66 | 3.36 | + | 1.91E-05 | 6.53E-04 | | [negative regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051100) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 9.81 | 2.85 | + | 3.79E-06 | 1.49E-04 | | [regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051098) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&list=upload_1&organism=Homo%20sapiens) | 22.51 | 2.53 | + | 2.61E-09 | 1.77E-07 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 12.10 | 2.48 | + | 2.15E-05 | 7.28E-04 | | [neuroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0007405) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007405&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007405&list=upload_1&organism=Homo%20sapiens) | 3.01 | 3.32 | + | 1.88E-03 | 3.29E-02 | | [generation of neurons](http://amigo.geneontology.org/amigo/term/GO:0048699) | [1134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048699&list=upload_1&organism=Homo%20sapiens) | 68.24 | 1.45 | + | 4.71E-04 | 1.02E-02 | | [neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0022008) | [1290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&list=upload_1&organism=Homo%20sapiens) | 77.63 | 1.47 | + | 1.01E-04 | 2.80E-03 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 131.85 | 1.47 | + | 1.74E-07 | 9.04E-06 | | [cellular senescence](http://amigo.geneontology.org/amigo/term/GO:0090398) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090398&list=upload_1&organism=Homo%20sapiens) | 3.61 | 3.32 | + | 6.89E-04 | 1.43E-02 | | [regulation of stem cell population maintenance](http://amigo.geneontology.org/amigo/term/GO:2000036) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000036&list=upload_1&organism=Homo%20sapiens) | 4.21 | 3.32 | + | 2.54E-04 | 6.16E-03 | | [protein destabilization](http://amigo.geneontology.org/amigo/term/GO:0031648) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031648&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031648&list=upload_1&organism=Homo%20sapiens) | 3.01 | 3.32 | + | 1.88E-03 | 3.28E-02 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 20.04 | 2.84 | + | 4.97E-11 | 4.12E-09 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000082&list=upload_1&organism=Homo%20sapiens) | 5.12 | 3.32 | + | 5.79E-05 | 1.70E-03 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044772&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.79 | + | 3.92E-06 | 1.53E-04 | | [cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:0044770) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044770&list=upload_1&organism=Homo%20sapiens) | 11.01 | 2.81 | + | 1.52E-06 | 6.61E-05 | | [cell cycle G1/S phase transition](http://amigo.geneontology.org/amigo/term/GO:0044843) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044843&list=upload_1&organism=Homo%20sapiens) | 5.24 | 3.44 | + | 2.40E-05 | 7.96E-04 | | [centrosome cycle](http://amigo.geneontology.org/amigo/term/GO:0007098) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007098&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007098&list=upload_1&organism=Homo%20sapiens) | 5.42 | 3.32 | + | 3.55E-05 | 1.11E-03 | | [microtubule organizing center organization](http://amigo.geneontology.org/amigo/term/GO:0031023) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031023&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031023&list=upload_1&organism=Homo%20sapiens) | 6.38 | 3.29 | + | 9.28E-06 | 3.31E-04 | | [organelle transport along microtubule](http://amigo.geneontology.org/amigo/term/GO:0072384) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072384&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072384&list=upload_1&organism=Homo%20sapiens) | 4.87 | 3.28 | + | 1.08E-04 | 2.95E-03 | | [transport along microtubule](http://amigo.geneontology.org/amigo/term/GO:0010970) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010970&list=upload_1&organism=Homo%20sapiens) | 9.69 | 2.27 | + | 9.85E-04 | 1.94E-02 | | [cytoskeleton-dependent intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0030705) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030705&list=upload_1&organism=Homo%20sapiens) | 11.98 | 2.09 | + | 1.19E-03 | 2.23E-02 | | [positive regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010822) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010822&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010822&list=upload_1&organism=Homo%20sapiens) | 4.57 | 3.28 | + | 1.76E-04 | 4.48E-03 | | [histone H4 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043967) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043967&list=upload_1&organism=Homo%20sapiens) | 3.67 | 3.27 | + | 7.82E-04 | 1.59E-02 | | [histone acetylation](http://amigo.geneontology.org/amigo/term/GO:0016573) | [126](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016573&list=upload_1&organism=Homo%20sapiens) | 7.58 | 2.64 | + | 2.27E-04 | 5.54E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018393&list=upload_1&organism=Homo%20sapiens) | 7.94 | 2.90 | + | 2.22E-05 | 7.43E-04 | | [peptidyl-lysine acetylation](http://amigo.geneontology.org/amigo/term/GO:0018394) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018394&list=upload_1&organism=Homo%20sapiens) | 8.12 | 2.83 | + | 3.03E-05 | 9.82E-04 | | [protein acetylation](http://amigo.geneontology.org/amigo/term/GO:0006473) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006473&list=upload_1&organism=Homo%20sapiens) | 9.33 | 2.68 | + | 3.15E-05 | 1.01E-03 | | [protein acylation](http://amigo.geneontology.org/amigo/term/GO:0043543) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043543&list=upload_1&organism=Homo%20sapiens) | 11.73 | 2.22 | + | 3.85E-04 | 8.62E-03 | | [peptidyl-lysine modification](http://amigo.geneontology.org/amigo/term/GO:0018205) | [311](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018205&list=upload_1&organism=Homo%20sapiens) | 18.72 | 2.03 | + | 1.48E-04 | 3.87E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006475&list=upload_1&organism=Homo%20sapiens) | 8.06 | 2.85 | + | 2.74E-05 | 8.97E-04 | | [histone H3 acetylation](http://amigo.geneontology.org/amigo/term/GO:0043966) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043966&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043966&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.22 | + | 8.86E-04 | 1.78E-02 | | [cellular response to virus](http://amigo.geneontology.org/amigo/term/GO:0098586) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&list=upload_1&organism=Homo%20sapiens) | 5.30 | 3.21 | + | 8.43E-05 | 2.38E-03 | | [response to virus](http://amigo.geneontology.org/amigo/term/GO:0009615) | [357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&list=upload_1&organism=Homo%20sapiens) | 21.48 | 2.19 | + | 3.33E-06 | 1.34E-04 | | [G2/M transition of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0000086) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000086&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000086&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.15 | + | 1.65E-03 | 2.95E-02 | | [cell cycle G2/M phase transition](http://amigo.geneontology.org/amigo/term/GO:0044839) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044839&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044839&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.22 | + | 8.86E-04 | 1.78E-02 | | [negative regulation of epithelial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1904036) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904036&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904036&list=upload_1&organism=Homo%20sapiens) | 3.49 | 3.15 | + | 1.65E-03 | 2.95E-02 | | [regulation of epithelial cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1904035) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904035&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904035&list=upload_1&organism=Homo%20sapiens) | 5.90 | 3.39 | + | 1.03E-05 | 3.63E-04 | | [regulation of embryonic development](http://amigo.geneontology.org/amigo/term/GO:0045995) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045995&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045995&list=upload_1&organism=Homo%20sapiens) | 5.42 | 3.14 | + | 1.07E-04 | 2.95E-03 | | [homologous chromosome pairing at meiosis](http://amigo.geneontology.org/amigo/term/GO:0007129) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007129&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007129&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.14 | + | 2.74E-03 | 4.43E-02 | | [chromosome organization involved in meiotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0070192) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070192&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070192&list=upload_1&organism=Homo%20sapiens) | 4.63 | 3.24 | + | 2.00E-04 | 4.98E-03 | | [homologous chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0045143) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045143&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045143&list=upload_1&organism=Homo%20sapiens) | 3.91 | 3.32 | + | 4.18E-04 | 9.24E-03 | | [meiotic chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0045132) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045132&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045132&list=upload_1&organism=Homo%20sapiens) | 6.02 | 2.99 | + | 1.17E-04 | 3.16E-03 | | [nuclear chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0098813) | [234](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098813&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098813&list=upload_1&organism=Homo%20sapiens) | 14.08 | 2.63 | + | 8.02E-07 | 3.61E-05 | | [chromosome segregation](http://amigo.geneontology.org/amigo/term/GO:0007059) | [291](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007059&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007059&list=upload_1&organism=Homo%20sapiens) | 17.51 | 2.80 | + | 1.83E-09 | 1.27E-07 | | [peptidyl-serine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018105) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018105&list=upload_1&organism=Homo%20sapiens) | 11.19 | 3.13 | + | 3.48E-08 | 2.04E-06 | | [peptidyl-serine modification](http://amigo.geneontology.org/amigo/term/GO:0018209) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018209&list=upload_1&organism=Homo%20sapiens) | 12.40 | 2.82 | + | 3.08E-07 | 1.50E-05 | | [regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0051101) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 7.46 | 3.08 | + | 9.17E-06 | 3.28E-04 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 4.87 | 3.08 | + | 3.22E-04 | 7.42E-03 | | [positive regulation of fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048146) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048146&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048146&list=upload_1&organism=Homo%20sapiens) | 3.25 | 3.08 | + | 3.08E-03 | 4.90E-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) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 57.11 | 1.59 | + | 3.51E-05 | 1.10E-03 | | [protein autoubiquitination](http://amigo.geneontology.org/amigo/term/GO:0051865) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051865&list=upload_1&organism=Homo%20sapiens) | 4.63 | 3.02 | + | 5.92E-04 | 1.25E-02 | | [modulation by host of symbiont process](http://amigo.geneontology.org/amigo/term/GO:0051851) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&list=upload_1&organism=Homo%20sapiens) | 4.99 | 3.00 | + | 4.05E-04 | 8.98E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 6.80 | 2.79 | + | 1.68E-04 | 4.30E-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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 15.71 | 2.16 | + | 1.04E-04 | 2.89E-03 | | [response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0046686) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&list=upload_1&organism=Homo%20sapiens) | 3.67 | 3.00 | + | 2.35E-03 | 3.96E-02 | | [animal organ regeneration](http://amigo.geneontology.org/amigo/term/GO:0031100) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031100&list=upload_1&organism=Homo%20sapiens) | 4.03 | 2.98 | + | 1.59E-03 | 2.88E-02 | | [regeneration](http://amigo.geneontology.org/amigo/term/GO:0031099) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&list=upload_1&organism=Homo%20sapiens) | 9.27 | 2.27 | + | 1.37E-03 | 2.53E-02 | | [T cell differentiation in thymus](http://amigo.geneontology.org/amigo/term/GO:0033077) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033077&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033077&list=upload_1&organism=Homo%20sapiens) | 3.79 | 2.90 | + | 2.93E-03 | 4.68E-02 | | [myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002573) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&list=upload_1&organism=Homo%20sapiens) | 8.06 | 2.85 | + | 2.74E-05 | 8.99E-04 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 15.89 | 2.58 | + | 2.81E-07 | 1.40E-05 | | [DNA modification](http://amigo.geneontology.org/amigo/term/GO:0006304) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006304&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006304&list=upload_1&organism=Homo%20sapiens) | 6.02 | 2.82 | + | 3.24E-04 | 7.45E-03 | | [regulation of circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0042752) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.77 | + | 1.27E-04 | 3.40E-03 | | [actomyosin structure organization](http://amigo.geneontology.org/amigo/term/GO:0031032) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031032&list=upload_1&organism=Homo%20sapiens) | 6.86 | 2.77 | + | 1.86E-04 | 4.68E-03 | | [positive regulation of DNA recombination](http://amigo.geneontology.org/amigo/term/GO:0045911) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045911&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045911&list=upload_1&organism=Homo%20sapiens) | 4.33 | 2.77 | + | 2.71E-03 | 4.40E-02 | | [mitotic spindle organization](http://amigo.geneontology.org/amigo/term/GO:0007052) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007052&list=upload_1&organism=Homo%20sapiens) | 5.84 | 2.74 | + | 6.42E-04 | 1.34E-02 | | [regulation of blood vessel endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0043535) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&list=upload_1&organism=Homo%20sapiens) | 5.48 | 2.74 | + | 9.42E-04 | 1.88E-02 | | [regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030334) | [929](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 55.91 | 1.43 | + | 2.64E-03 | 4.34E-02 | | [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) | 62.22 | 1.40 | + | 2.82E-03 | 4.52E-02 | | [regulation of glucose metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010906) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010906&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010906&list=upload_1&organism=Homo%20sapiens) | 6.26 | 2.72 | + | 4.84E-04 | 1.04E-02 | | [regulation of cellular carbohydrate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010675) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010675&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010675&list=upload_1&organism=Homo%20sapiens) | 9.51 | 2.10 | + | 3.12E-03 | 4.94E-02 | | [epithelial to mesenchymal transition](http://amigo.geneontology.org/amigo/term/GO:0001837) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001837&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001837&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.70 | + | 2.25E-03 | 3.80E-02 | | [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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040029&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.68 | + | 2.74E-04 | 6.53E-03 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006325) | [585](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&list=upload_1&organism=Homo%20sapiens) | 35.20 | 2.58 | + | 1.55E-14 | 1.80E-12 | | [cellular response to monosaccharide stimulus](http://amigo.geneontology.org/amigo/term/GO:0071326) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071326&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071326&list=upload_1&organism=Homo%20sapiens) | 4.87 | 2.67 | + | 2.47E-03 | 4.12E-02 | | [response to carbohydrate](http://amigo.geneontology.org/amigo/term/GO:0009743) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009743&list=upload_1&organism=Homo%20sapiens) | 10.89 | 2.20 | + | 7.04E-04 | 1.45E-02 | | [response to monosaccharide](http://amigo.geneontology.org/amigo/term/GO:0034284) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&list=upload_1&organism=Homo%20sapiens) | 9.27 | 2.27 | + | 1.37E-03 | 2.53E-02 | | [nucleosome organization](http://amigo.geneontology.org/amigo/term/GO:0034728) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034728&list=upload_1&organism=Homo%20sapiens) | 7.52 | 2.66 | + | 2.06E-04 | 5.11E-03 | | [chromatin remodeling](http://amigo.geneontology.org/amigo/term/GO:0006338) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&list=upload_1&organism=Homo%20sapiens) | 19.44 | 2.78 | + | 5.65E-10 | 4.22E-08 | | [neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0051402) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051402&list=upload_1&organism=Homo%20sapiens) | 5.66 | 2.65 | + | 1.26E-03 | 2.35E-02 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 8.30 | 2.65 | + | 1.07E-04 | 2.94E-03 | | [rhythmic process](http://amigo.geneontology.org/amigo/term/GO:0048511) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 16.37 | 2.38 | + | 3.18E-06 | 1.29E-04 | | [multicellular organism growth](http://amigo.geneontology.org/amigo/term/GO:0035264) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035264&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035264&list=upload_1&organism=Homo%20sapiens) | 5.30 | 2.64 | + | 1.85E-03 | 3.24E-02 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 24.85 | 1.97 | + | 2.49E-05 | 8.21E-04 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 24.85 | 1.97 | + | 2.49E-05 | 8.23E-04 | | [B cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030183) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030183&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030183&list=upload_1&organism=Homo%20sapiens) | 7.94 | 2.64 | + | 1.55E-04 | 4.01E-03 | | [mitotic sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0000070) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000070&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000070&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.63 | + | 3.31E-04 | 7.58E-03 | | [mitotic nuclear division](http://amigo.geneontology.org/amigo/term/GO:0140014) | [173](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140014&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.31 | + | 4.72E-04 | 1.02E-02 | | [sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0000819) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000819&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000819&list=upload_1&organism=Homo%20sapiens) | 8.91 | 2.58 | + | 1.50E-04 | 3.89E-03 | | [nuclear-transcribed mRNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0000956) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000956&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000956&list=upload_1&organism=Homo%20sapiens) | 6.14 | 2.61 | + | 1.03E-03 | 2.00E-02 | | [RNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006401) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&list=upload_1&organism=Homo%20sapiens) | 9.75 | 2.26 | + | 1.03E-03 | 2.00E-02 | | [cellular macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044265) | [785](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&list=upload_1&organism=Homo%20sapiens) | 47.24 | 1.76 | + | 2.93E-06 | 1.21E-04 | | [macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009057) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&list=upload_1&organism=Homo%20sapiens) | 59.52 | 1.70 | + | 1.11E-06 | 4.90E-05 | | [nucleobase-containing compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0034655) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034655&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034655&list=upload_1&organism=Homo%20sapiens) | 17.09 | 2.16 | + | 4.39E-05 | 1.35E-03 | | [cellular nitrogen compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044270) | [330](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044270&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044270&list=upload_1&organism=Homo%20sapiens) | 19.86 | 2.06 | + | 5.59E-05 | 1.66E-03 | | [heterocycle catabolic process](http://amigo.geneontology.org/amigo/term/GO:0046700) | [324](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046700&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046700&list=upload_1&organism=Homo%20sapiens) | 19.50 | 2.05 | + | 7.81E-05 | 2.23E-03 | | [aromatic compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:0019439) | [346](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019439&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019439&list=upload_1&organism=Homo%20sapiens) | 20.82 | 1.92 | + | 2.22E-04 | 5.42E-03 | | [organic cyclic compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901361) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901361&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901361&list=upload_1&organism=Homo%20sapiens) | 22.51 | 1.91 | + | 1.56E-04 | 4.01E-03 | | [tissue remodeling](http://amigo.geneontology.org/amigo/term/GO:0048771) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048771&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048771&list=upload_1&organism=Homo%20sapiens) | 6.14 | 2.61 | + | 1.03E-03 | 1.99E-02 | | [activation of cysteine-type endopeptidase activity involved in apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006919) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006919&list=upload_1&organism=Homo%20sapiens) | 4.99 | 2.60 | + | 2.99E-03 | 4.76E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043281&list=upload_1&organism=Homo%20sapiens) | 12.52 | 2.00 | + | 2.37E-03 | 3.98E-02 | | [regulation of cysteine-type endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:2000116) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000116&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000116&list=upload_1&organism=Homo%20sapiens) | 14.38 | 2.02 | + | 7.93E-04 | 1.61E-02 | | [regulation of endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:0052548) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052548&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052548&list=upload_1&organism=Homo%20sapiens) | 25.40 | 1.69 | + | 1.59E-03 | 2.89E-02 | | [regulation of peptidase activity](http://amigo.geneontology.org/amigo/term/GO:0052547) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052547&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0052547&list=upload_1&organism=Homo%20sapiens) | 27.20 | 1.69 | + | 1.14E-03 | 2.16E-02 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 44.71 | 1.70 | + | 2.79E-05 | 9.11E-04 | | [positive regulation of cysteine-type endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:2001056) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001056&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001056&list=upload_1&organism=Homo%20sapiens) | 8.91 | 2.25 | + | 1.98E-03 | 3.43E-02 | | [positive regulation of endopeptidase activity](http://amigo.geneontology.org/amigo/term/GO:0010950) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010950&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010950&list=upload_1&organism=Homo%20sapiens) | 10.47 | 2.20 | + | 9.56E-04 | 1.89E-02 | | [positive regulation of peptidase activity](http://amigo.geneontology.org/amigo/term/GO:0010952) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010952&list=upload_1&organism=Homo%20sapiens) | 11.61 | 2.24 | + | 3.42E-04 | 7.80E-03 | | [positive regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0045862) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045862&list=upload_1&organism=Homo%20sapiens) | 22.45 | 2.00 | + | 3.90E-05 | 1.21E-03 | | [cellular response to insulin stimulus](http://amigo.geneontology.org/amigo/term/GO:0032869) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&list=upload_1&organism=Homo%20sapiens) | 8.85 | 2.60 | + | 1.43E-04 | 3.74E-03 | | [response to insulin](http://amigo.geneontology.org/amigo/term/GO:0032868) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032868&list=upload_1&organism=Homo%20sapiens) | 12.82 | 2.26 | + | 1.30E-04 | 3.45E-03 | | [response to peptide hormone](http://amigo.geneontology.org/amigo/term/GO:0043434) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&list=upload_1&organism=Homo%20sapiens) | 21.84 | 2.15 | + | 4.37E-06 | 1.68E-04 | | [response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901652) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&list=upload_1&organism=Homo%20sapiens) | 26.78 | 2.17 | + | 2.67E-07 | 1.34E-05 | | [cellular response to peptide hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071375) | [241](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071375&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071375&list=upload_1&organism=Homo%20sapiens) | 14.50 | 2.34 | + | 1.86E-05 | 6.36E-04 | | [cellular response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901653) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&list=upload_1&organism=Homo%20sapiens) | 18.23 | 2.30 | + | 3.06E-06 | 1.25E-04 | | [protein stabilization](http://amigo.geneontology.org/amigo/term/GO:0050821) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&list=upload_1&organism=Homo%20sapiens) | 13.12 | 2.59 | + | 2.87E-06 | 1.19E-04 | | [negative regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043524) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043524&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043524&list=upload_1&organism=Homo%20sapiens) | 9.33 | 2.57 | + | 1.07E-04 | 2.95E-03 | | [regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043523) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043523&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043523&list=upload_1&organism=Homo%20sapiens) | 13.12 | 2.29 | + | 8.51E-05 | 2.40E-03 | | [regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901214) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&list=upload_1&organism=Homo%20sapiens) | 19.56 | 1.94 | + | 3.22E-04 | 7.42E-03 | | [negative regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901215) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&list=upload_1&organism=Homo%20sapiens) | 13.24 | 2.11 | + | 4.79E-04 | 1.03E-02 | | [regulation of mitotic sister chromatid separation](http://amigo.geneontology.org/amigo/term/GO:0010965) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010965&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010965&list=upload_1&organism=Homo%20sapiens) | 5.90 | 2.54 | + | 1.82E-03 | 3.19E-02 | | [regulation of chromosome separation](http://amigo.geneontology.org/amigo/term/GO:1905818) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905818&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905818&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.69 | + | 3.64E-04 | 8.27E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 7.88 | 2.54 | + | 4.99E-04 | 1.07E-02 | | [positive regulation of leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1902107) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902107&list=upload_1&organism=Homo%20sapiens) | 11.01 | 2.27 | + | 3.94E-04 | 8.81E-03 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 11.01 | 2.27 | + | 3.94E-04 | 8.80E-03 | | [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) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 58.19 | 1.53 | + | 1.69E-04 | 4.32E-03 | | [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) | 25.33 | 1.82 | + | 3.49E-04 | 7.93E-03 | | [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) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&list=upload_1&organism=Homo%20sapiens) | 28.22 | 1.77 | + | 2.42E-04 | 5.90E-03 | | [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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&list=upload_1&organism=Homo%20sapiens) | 29.25 | 1.78 | + | 2.03E-04 | 5.03E-03 | | [liver development](http://amigo.geneontology.org/amigo/term/GO:0001889) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&list=upload_1&organism=Homo%20sapiens) | 7.88 | 2.54 | + | 4.99E-04 | 1.07E-02 | | [gland development](http://amigo.geneontology.org/amigo/term/GO:0048732) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&list=upload_1&organism=Homo%20sapiens) | 25.40 | 2.13 | + | 1.65E-06 | 7.08E-05 | | [hepaticobiliary system development](http://amigo.geneontology.org/amigo/term/GO:0061008) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&list=upload_1&organism=Homo%20sapiens) | 8.06 | 2.60 | + | 3.00E-04 | 7.01E-03 | | [positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0090100) | [118](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090100&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090100&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.53 | + | 1.04E-03 | 2.00E-02 | | [positive regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009967) | [1528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&reflist=1) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 91.95 | 1.50 | + | 5.75E-06 | 2.15E-04 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 102.36 | 1.41 | + | 7.68E-05 | 2.20E-03 | | [positive regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010647) | [1696](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&reflist=1) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 102.06 | 1.41 | + | 7.46E-05 | 2.15E-03 | | [positive regulation of mitotic cell cycle phase transition](http://amigo.geneontology.org/amigo/term/GO:1901992) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901992&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901992&list=upload_1&organism=Homo%20sapiens) | 5.54 | 2.53 | + | 2.67E-03 | 4.37E-02 | | [positive regulation of mitotic cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045931) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&list=upload_1&organism=Homo%20sapiens) | 7.28 | 3.16 | + | 6.45E-06 | 2.39E-04 | | [fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045444) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045444&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045444&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.49 | + | 1.13E-03 | 2.15E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050680&list=upload_1&organism=Homo%20sapiens) | 8.42 | 2.49 | + | 3.97E-04 | 8.84E-03 | | [regulation of epithelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0050678) | [369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&list=upload_1&organism=Homo%20sapiens) | 22.21 | 2.03 | + | 3.47E-05 | 1.09E-03 | | [regulation of sister chromatid segregation](http://amigo.geneontology.org/amigo/term/GO:0033045) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033045&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033045&list=upload_1&organism=Homo%20sapiens) | 6.44 | 2.48 | + | 2.35E-03 | 3.96E-02 | | [negative regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071901) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071901&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071901&list=upload_1&organism=Homo%20sapiens) | 6.86 | 2.48 | + | 1.67E-03 | 2.97E-02 | | [negative regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001933) | [322](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001933&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001933&list=upload_1&organism=Homo%20sapiens) | 19.38 | 1.86 | + | 1.10E-03 | 2.09E-02 | | [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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 30.27 | 1.82 | + | 8.36E-05 | 2.37E-03 | | [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) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 62.71 | 1.72 | + | 2.62E-07 | 1.32E-05 | | [negative regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042326) | [365](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042326&list=upload_1&organism=Homo%20sapiens) | 21.96 | 1.78 | + | 1.47E-03 | 2.71E-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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045936&list=upload_1&organism=Homo%20sapiens) | 25.40 | 1.65 | + | 3.05E-03 | 4.84E-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) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010563&list=upload_1&organism=Homo%20sapiens) | 25.46 | 1.69 | + | 1.62E-03 | 2.92E-02 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 47.12 | 1.70 | + | 1.62E-05 | 5.58E-04 | | [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) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045859&list=upload_1&organism=Homo%20sapiens) | 40.20 | 1.74 | + | 2.31E-05 | 7.69E-04 | | [regulation of protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0071900) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071900&list=upload_1&organism=Homo%20sapiens) | 23.53 | 1.95 | + | 5.79E-05 | 1.71E-03 | | [regulation of cyclin-dependent protein serine/threonine kinase activity](http://amigo.geneontology.org/amigo/term/GO:0000079) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000079&list=upload_1&organism=Homo%20sapiens) | 6.92 | 2.46 | + | 1.75E-03 | 3.10E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904029&list=upload_1&organism=Homo%20sapiens) | 7.10 | 2.39 | + | 2.05E-03 | 3.53E-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) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001701&list=upload_1&organism=Homo%20sapiens) | 23.77 | 2.40 | + | 1.45E-08 | 8.86E-07 | | [negative regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903707) | [111](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903707&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903707&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.40 | + | 2.84E-03 | 4.55E-02 | | [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) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&list=upload_1&organism=Homo%20sapiens) | 55.54 | 1.75 | + | 5.03E-07 | 2.38E-05 | | [positive regulation of proteasomal protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901800) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901800&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901800&list=upload_1&organism=Homo%20sapiens) | 7.16 | 2.37 | + | 2.17E-03 | 3.70E-02 | | [regulation of proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:1903050) | [228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&list=upload_1&organism=Homo%20sapiens) | 13.72 | 1.97 | + | 2.35E-03 | 3.96E-02 | | [regulation of protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0042176) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&list=upload_1&organism=Homo%20sapiens) | 22.09 | 1.86 | + | 4.68E-04 | 1.02E-02 | | [positive regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009896) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009896&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009896&list=upload_1&organism=Homo%20sapiens) | 30.87 | 1.78 | + | 1.03E-04 | 2.86E-03 | | [positive regulation of NF-kappaB transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051092) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051092&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051092&list=upload_1&organism=Homo%20sapiens) | 9.39 | 2.34 | + | 5.24E-04 | 1.12E-02 | | [positive regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051091) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&list=upload_1&organism=Homo%20sapiens) | 16.13 | 2.36 | + | 7.89E-06 | 2.89E-04 | | [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) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&list=upload_1&organism=Homo%20sapiens) | 26.36 | 2.20 | + | 1.92E-07 | 9.93E-06 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 13.24 | 2.34 | + | 4.63E-05 | 1.41E-03 | | [regulation of proteasomal ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0032434) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&list=upload_1&organism=Homo%20sapiens) | 8.55 | 2.34 | + | 9.60E-04 | 1.90E-02 | | [regulation of cellular ketone metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010565) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010565&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010565&list=upload_1&organism=Homo%20sapiens) | 8.12 | 2.34 | + | 1.30E-03 | 2.43E-02 | | [cellular response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0071456) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071456&list=upload_1&organism=Homo%20sapiens) | 7.70 | 2.34 | + | 1.78E-03 | 3.15E-02 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 16.67 | 2.04 | + | 2.74E-04 | 6.52E-03 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 17.45 | 1.95 | + | 5.93E-04 | 1.25E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 19.20 | 1.93 | + | 4.43E-04 | 9.73E-03 | | [cellular response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0071453) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&list=upload_1&organism=Homo%20sapiens) | 9.21 | 2.28 | + | 1.32E-03 | 2.46E-02 | | [cellular response to tumor necrosis factor](http://amigo.geneontology.org/amigo/term/GO:0071356) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.33 | + | 3.13E-04 | 7.26E-03 | | [response to tumor necrosis factor](http://amigo.geneontology.org/amigo/term/GO:0034612) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&list=upload_1&organism=Homo%20sapiens) | 12.16 | 2.14 | + | 7.36E-04 | 1.51E-02 | | [cellular response to starvation](http://amigo.geneontology.org/amigo/term/GO:0009267) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&list=upload_1&organism=Homo%20sapiens) | 10.71 | 2.33 | + | 3.13E-04 | 7.25E-03 | | [cellular response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031669) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&list=upload_1&organism=Homo%20sapiens) | 13.60 | 2.21 | + | 1.78E-04 | 4.52E-03 | | [response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031667) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&list=upload_1&organism=Homo%20sapiens) | 28.28 | 1.98 | + | 5.75E-06 | 2.16E-04 | | [response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0009991) | [500](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&list=upload_1&organism=Homo%20sapiens) | 30.09 | 1.96 | + | 4.38E-06 | 1.68E-04 | | [cellular response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0031668) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&list=upload_1&organism=Homo%20sapiens) | 15.41 | 2.14 | + | 1.53E-04 | 3.96E-03 | | [cellular response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0071496) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&list=upload_1&organism=Homo%20sapiens) | 19.56 | 1.94 | + | 3.22E-04 | 7.43E-03 | | [response to starvation](http://amigo.geneontology.org/amigo/term/GO:0042594) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&list=upload_1&organism=Homo%20sapiens) | 12.94 | 2.24 | + | 2.13E-04 | 5.23E-03 | | [cell division](http://amigo.geneontology.org/amigo/term/GO:0051301) | [514](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051301&list=upload_1&organism=Homo%20sapiens) | 30.93 | 2.33 | + | 5.93E-10 | 4.38E-08 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&list=upload_1&organism=Homo%20sapiens) | 13.78 | 2.32 | + | 3.86E-05 | 1.20E-03 | | [cellular response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0034599) | [222](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&list=upload_1&organism=Homo%20sapiens) | 13.36 | 2.32 | + | 5.22E-05 | 1.56E-03 | | [cellular response to chemical stress](http://amigo.geneontology.org/amigo/term/GO:0062197) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&list=upload_1&organism=Homo%20sapiens) | 16.43 | 2.31 | + | 9.53E-06 | 3.38E-04 | | [response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0006979) | [367](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 22.09 | 1.95 | + | 1.31E-04 | 3.48E-03 | | [regulation of ossification](http://amigo.geneontology.org/amigo/term/GO:0030278) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030278&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030278&list=upload_1&organism=Homo%20sapiens) | 7.34 | 2.32 | + | 2.59E-03 | 4.29E-02 | | [positive regulation of mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903313) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903313&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903313&list=upload_1&organism=Homo%20sapiens) | 7.34 | 2.32 | + | 2.59E-03 | 4.28E-02 | | [response to interferon-gamma](http://amigo.geneontology.org/amigo/term/GO:0034341) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&list=upload_1&organism=Homo%20sapiens) | 7.82 | 2.30 | + | 2.02E-03 | 3.51E-02 | | [cellular response to steroid hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071383) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 9.15 | 2.30 | + | 1.28E-03 | 2.39E-02 | | [cellular response to lipid](http://amigo.geneontology.org/amigo/term/GO:0071396) | [519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&list=upload_1&organism=Homo%20sapiens) | 31.23 | 1.95 | + | 4.03E-06 | 1.56E-04 | | [regulation of macroautophagy](http://amigo.geneontology.org/amigo/term/GO:0016241) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&list=upload_1&organism=Homo%20sapiens) | 9.63 | 2.28 | + | 9.48E-04 | 1.88E-02 | | [cardiac muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0048738) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048738&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048738&list=upload_1&organism=Homo%20sapiens) | 10.95 | 2.28 | + | 3.75E-04 | 8.45E-03 | | [striated muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0014706) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014706&list=upload_1&organism=Homo%20sapiens) | 11.31 | 2.30 | + | 2.60E-04 | 6.24E-03 | | [muscle tissue development](http://amigo.geneontology.org/amigo/term/GO:0060537) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060537&list=upload_1&organism=Homo%20sapiens) | 19.62 | 1.89 | + | 5.38E-04 | 1.14E-02 | | [cellular response to xenobiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0071466) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071466&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071466&list=upload_1&organism=Homo%20sapiens) | 11.01 | 2.27 | + | 3.94E-04 | 8.82E-03 | | [response to xenobiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009410) | [423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 25.46 | 2.67 | + | 8.51E-12 | 7.58E-10 | | [response to glucose](http://amigo.geneontology.org/amigo/term/GO:0009749) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&list=upload_1&organism=Homo%20sapiens) | 8.49 | 2.24 | + | 2.76E-03 | 4.44E-02 | | [response to nutrient](http://amigo.geneontology.org/amigo/term/GO:0007584) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&list=upload_1&organism=Homo%20sapiens) | 8.97 | 2.23 | + | 2.05E-03 | 3.54E-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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&list=upload_1&organism=Homo%20sapiens) | 11.67 | 2.23 | + | 3.62E-04 | 8.24E-03 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 18.84 | 1.96 | + | 2.62E-04 | 6.28E-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) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&list=upload_1&organism=Homo%20sapiens) | 19.92 | 1.86 | + | 8.50E-04 | 1.72E-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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&list=upload_1&organism=Homo%20sapiens) | 12.28 | 2.12 | + | 8.00E-04 | 1.62E-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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&list=upload_1&organism=Homo%20sapiens) | 13.90 | 2.01 | + | 1.02E-03 | 2.00E-02 | | [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) | 10.89 | 2.20 | + | 7.04E-04 | 1.45E-02 | | [regulation of RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0043484) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&list=upload_1&organism=Homo%20sapiens) | 10.89 | 2.20 | + | 7.04E-04 | 1.45E-02 | | [regulation of cell division](http://amigo.geneontology.org/amigo/term/GO:0051302) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051302&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051302&list=upload_1&organism=Homo%20sapiens) | 11.37 | 2.20 | + | 5.51E-04 | 1.17E-02 | | [viral process](http://amigo.geneontology.org/amigo/term/GO:0016032) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&list=upload_1&organism=Homo%20sapiens) | 15.10 | 2.18 | + | 8.67E-05 | 2.44E-03 | | [muscle cell development](http://amigo.geneontology.org/amigo/term/GO:0055001) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055001&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055001&list=upload_1&organism=Homo%20sapiens) | 9.63 | 2.18 | + | 1.78E-03 | 3.15E-02 | | [muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0042692) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042692&list=upload_1&organism=Homo%20sapiens) | 16.13 | 2.11 | + | 1.37E-04 | 3.60E-03 | | [muscle structure development](http://amigo.geneontology.org/amigo/term/GO:0061061) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&list=upload_1&organism=Homo%20sapiens) | 30.03 | 1.80 | + | 1.15E-04 | 3.13E-03 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 103.81 | 1.47 | + | 4.10E-06 | 1.58E-04 | | [peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018108) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&list=upload_1&organism=Homo%20sapiens) | 10.11 | 2.18 | + | 1.37E-03 | 2.53E-02 | | [peptidyl-tyrosine modification](http://amigo.geneontology.org/amigo/term/GO:0018212) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&list=upload_1&organism=Homo%20sapiens) | 10.23 | 2.15 | + | 1.53E-03 | 2.79E-02 | | [regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001236) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&list=upload_1&organism=Homo%20sapiens) | 9.27 | 2.16 | + | 2.55E-03 | 4.24E-02 | | [negative regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043409) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043409&list=upload_1&organism=Homo%20sapiens) | 10.23 | 2.15 | + | 1.53E-03 | 2.79E-02 | | [regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043408) | [672](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&list=upload_1&organism=Homo%20sapiens) | 40.44 | 1.51 | + | 2.60E-03 | 4.27E-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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045664&list=upload_1&organism=Homo%20sapiens) | 11.73 | 2.13 | + | 1.01E-03 | 1.97E-02 | | [negative regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050777) | [188](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050777&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050777&list=upload_1&organism=Homo%20sapiens) | 11.31 | 2.12 | + | 1.38E-03 | 2.55E-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) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&list=upload_1&organism=Homo%20sapiens) | 30.27 | 2.08 | + | 2.95E-07 | 1.44E-05 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&list=upload_1&organism=Homo%20sapiens) | 31.05 | 2.09 | + | 2.28E-07 | 1.16E-05 | | [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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 35.08 | 2.05 | + | 7.11E-08 | 3.87E-06 | | [negative regulation of cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034249) | [192](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034249&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034249&list=upload_1&organism=Homo%20sapiens) | 11.55 | 2.08 | + | 1.61E-03 | 2.90E-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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048872&list=upload_1&organism=Homo%20sapiens) | 15.47 | 2.07 | + | 2.85E-04 | 6.71E-03 | | [homeostatic process](http://amigo.geneontology.org/amigo/term/GO:0042592) | [1424](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&reflist=1) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042592&list=upload_1&organism=Homo%20sapiens) | 85.69 | 1.39 | + | 5.96E-04 | 1.25E-02 | | [learning or memory](http://amigo.geneontology.org/amigo/term/GO:0007611) | [275](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007611&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007611&list=upload_1&organism=Homo%20sapiens) | 16.55 | 2.05 | + | 2.58E-04 | 6.22E-03 | | [behavior](http://amigo.geneontology.org/amigo/term/GO:0007610) | [606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007610&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007610&list=upload_1&organism=Homo%20sapiens) | 36.47 | 1.70 | + | 1.65E-04 | 4.24E-03 | | [cognition](http://amigo.geneontology.org/amigo/term/GO:0050890) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050890&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050890&list=upload_1&organism=Homo%20sapiens) | 19.08 | 1.89 | + | 6.73E-04 | 1.40E-02 | | [positive regulation of intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0032388) | [203](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032388&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032388&list=upload_1&organism=Homo%20sapiens) | 12.22 | 2.05 | + | 2.10E-03 | 3.60E-02 | | [regulation of intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0032386) | [342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032386&list=upload_1&organism=Homo%20sapiens) | 20.58 | 1.75 | + | 2.30E-03 | 3.89E-02 | | [regulation of localization](http://amigo.geneontology.org/amigo/term/GO:0032879) | [2104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&reflist=1) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032879&list=upload_1&organism=Homo%20sapiens) | 126.61 | 1.32 | + | 4.57E-04 | 1.00E-02 | | [regulation of cellular localization](http://amigo.geneontology.org/amigo/term/GO:0060341) | [962](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&list=upload_1&organism=Homo%20sapiens) | 57.89 | 1.64 | + | 8.34E-06 | 3.02E-04 | | [positive regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051050) | [919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&list=upload_1&organism=Homo%20sapiens) | 55.30 | 1.43 | + | 2.56E-03 | 4.26E-02 | | [striated muscle cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0051146) | [204](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051146&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051146&list=upload_1&organism=Homo%20sapiens) | 12.28 | 2.04 | + | 2.14E-03 | 3.66E-02 | | [negative regulation of transcription by RNA polymerase II](http://amigo.geneontology.org/amigo/term/GO:0000122) | [974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&reflist=1) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 58.61 | 2.03 | + | 6.07E-12 | 5.56E-10 | | [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) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 79.62 | 2.00 | + | 2.80E-15 | 3.46E-13 | | [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) | [159](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 79.74 | 1.99 | + | 3.03E-15 | 3.72E-13 | | [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) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 79.86 | 2.00 | + | 1.84E-15 | 2.38E-13 | | [negative regulation of cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:2000113) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000113&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000113&list=upload_1&organism=Homo%20sapiens) | 11.43 | 2.01 | + | 2.72E-03 | 4.39E-02 | | [humoral immune response](http://amigo.geneontology.org/amigo/term/GO:0006959) | [339](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006959&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006959&list=upload_1&organism=Homo%20sapiens) | 20.40 | 2.01 | + | 7.54E-05 | 2.16E-03 | | [cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0045165) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&list=upload_1&organism=Homo%20sapiens) | 15.04 | 1.99 | + | 9.55E-04 | 1.89E-02 | | [positive regulation of T cell activation](http://amigo.geneontology.org/amigo/term/GO:0050870) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 15.22 | 1.97 | + | 1.04E-03 | 2.00E-02 | | [positive regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903039) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 16.61 | 1.99 | + | 4.57E-04 | 1.00E-02 | | [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) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903037&list=upload_1&organism=Homo%20sapiens) | 22.21 | 1.85 | + | 4.86E-04 | 1.05E-02 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&list=upload_1&organism=Homo%20sapiens) | 29.13 | 1.65 | + | 1.62E-03 | 2.91E-02 | | [regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0030155) | [789](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 47.48 | 1.73 | + | 6.30E-06 | 2.34E-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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 19.50 | 1.95 | + | 3.15E-04 | 7.29E-03 | | [positive regulation of cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0045785) | [488](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 29.37 | 1.87 | + | 3.03E-05 | 9.81E-04 | | [regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031396) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&list=upload_1&organism=Homo%20sapiens) | 12.70 | 1.97 | + | 2.61E-03 | 4.29E-02 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&list=upload_1&organism=Homo%20sapiens) | 15.22 | 2.23 | + | 4.90E-05 | 1.48E-03 | | [tissue homeostasis](http://amigo.geneontology.org/amigo/term/GO:0001894) | [245](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001894&list=upload_1&organism=Homo%20sapiens) | 14.74 | 1.97 | + | 1.36E-03 | 2.52E-02 | | [anatomical structure homeostasis](http://amigo.geneontology.org/amigo/term/GO:0060249) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060249&list=upload_1&organism=Homo%20sapiens) | 18.23 | 2.03 | + | 1.99E-04 | 4.97E-03 | | [non-membrane-bounded organelle assembly](http://amigo.geneontology.org/amigo/term/GO:0140694) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&list=upload_1&organism=Homo%20sapiens) | 19.02 | 1.95 | + | 4.18E-04 | 9.25E-03 | | [positive regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031349) | [296](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031349&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031349&list=upload_1&organism=Homo%20sapiens) | 17.81 | 1.91 | + | 7.21E-04 | 1.48E-02 | | [regulation of defense response](http://amigo.geneontology.org/amigo/term/GO:0031347) | [642](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&list=upload_1&organism=Homo%20sapiens) | 38.63 | 1.66 | + | 2.48E-04 | 6.02E-03 | | [inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0006954) | [540](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006954&list=upload_1&organism=Homo%20sapiens) | 32.50 | 1.88 | + | 1.00E-05 | 3.55E-04 | | [positive regulation of cellular catabolic process](http://amigo.geneontology.org/amigo/term/GO:0031331) | [411](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031331&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031331&list=upload_1&organism=Homo%20sapiens) | 24.73 | 1.86 | + | 1.98E-04 | 4.95E-03 | | [RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0008380) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&list=upload_1&organism=Homo%20sapiens) | 22.15 | 1.85 | + | 4.77E-04 | 1.03E-02 | | [RNA processing](http://amigo.geneontology.org/amigo/term/GO:0006396) | [868](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&list=upload_1&organism=Homo%20sapiens) | 52.23 | 1.47 | + | 1.50E-03 | 2.75E-02 | | [establishment of protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0072594) | [334](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&list=upload_1&organism=Homo%20sapiens) | 20.10 | 1.84 | + | 9.07E-04 | 1.82E-02 | | [establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:0045184) | [1267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&reflist=1) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045184&list=upload_1&organism=Homo%20sapiens) | 76.25 | 1.47 | + | 1.13E-04 | 3.07E-03 | | [kidney development](http://amigo.geneontology.org/amigo/term/GO:0001822) | [299](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001822&list=upload_1&organism=Homo%20sapiens) | 17.99 | 1.83 | + | 1.72E-03 | 3.05E-02 | | [renal system development](http://amigo.geneontology.org/amigo/term/GO:0072001) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072001&list=upload_1&organism=Homo%20sapiens) | 18.53 | 1.78 | + | 2.90E-03 | 4.63E-02 | | [urogenital system development](http://amigo.geneontology.org/amigo/term/GO:0001655) | [350](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001655&list=upload_1&organism=Homo%20sapiens) | 21.06 | 1.85 | + | 5.46E-04 | 1.16E-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) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 40.68 | 1.79 | + | 5.86E-06 | 2.18E-04 | | [regulation of inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0050727) | [372](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050727&list=upload_1&organism=Homo%20sapiens) | 22.39 | 1.79 | + | 1.12E-03 | 2.13E-02 | | [regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032101) | [973](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&list=upload_1&organism=Homo%20sapiens) | 58.55 | 1.55 | + | 9.92E-05 | 2.76E-03 | | [mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0006397) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&list=upload_1&organism=Homo%20sapiens) | 27.14 | 1.77 | + | 3.77E-04 | 8.47E-03 | | [positive regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:1904951) | [320](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&list=upload_1&organism=Homo%20sapiens) | 19.26 | 1.77 | + | 2.50E-03 | 4.15E-02 | | [positive regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:1903829) | [462](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903829&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903829&list=upload_1&organism=Homo%20sapiens) | 27.80 | 1.73 | + | 6.31E-04 | 1.31E-02 | | [regulation of protein localization](http://amigo.geneontology.org/amigo/term/GO:0032880) | [850](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&list=upload_1&organism=Homo%20sapiens) | 51.15 | 1.62 | + | 4.66E-05 | 1.42E-03 | | [regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:0070201) | [527](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&list=upload_1&organism=Homo%20sapiens) | 31.71 | 1.64 | + | 1.01E-03 | 1.97E-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) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 28.70 | 1.74 | + | 3.80E-04 | 8.52E-03 | | [response to growth factor](http://amigo.geneontology.org/amigo/term/GO:0070848) | [507](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 30.51 | 1.93 | + | 7.60E-06 | 2.78E-04 | | [regulation of protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0043254) | [412](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&list=upload_1&organism=Homo%20sapiens) | 24.79 | 1.69 | + | 1.94E-03 | 3.37E-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) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 57.23 | 1.54 | + | 1.93E-04 | 4.83E-03 | | [skeletal system development](http://amigo.geneontology.org/amigo/term/GO:0001501) | [515](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001501&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001501&list=upload_1&organism=Homo%20sapiens) | 30.99 | 1.68 | + | 6.26E-04 | 1.31E-02 | | [positive regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050778) | [590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050778&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050778&list=upload_1&organism=Homo%20sapiens) | 35.50 | 1.66 | + | 3.77E-04 | 8.48E-03 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 28.95 | 1.66 | + | 1.56E-03 | 2.85E-02 | | [tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048729) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&list=upload_1&organism=Homo%20sapiens) | 34.18 | 1.61 | + | 1.10E-03 | 2.10E-02 | | [cell morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0000902) | [713](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000902&list=upload_1&organism=Homo%20sapiens) | 42.91 | 1.61 | + | 2.73E-04 | 6.52E-03 | | [regulation of growth](http://amigo.geneontology.org/amigo/term/GO:0040008) | [627](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040008&list=upload_1&organism=Homo%20sapiens) | 37.73 | 1.59 | + | 1.01E-03 | 1.98E-02 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 46.64 | 1.59 | + | 2.59E-04 | 6.24E-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) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 62.22 | 1.54 | + | 6.97E-05 | 2.03E-03 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 49.53 | 1.55 | + | 2.99E-04 | 7.01E-03 | | [modification-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0019941) | [586](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019941&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019941&list=upload_1&organism=Homo%20sapiens) | 35.26 | 1.56 | + | 2.31E-03 | 3.90E-02 | | [modification-dependent macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0043632) | [598](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043632&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043632&list=upload_1&organism=Homo%20sapiens) | 35.99 | 1.64 | + | 5.63E-04 | 1.19E-02 | | [proteolysis involved in protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0051603) | [647](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051603&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051603&list=upload_1&organism=Homo%20sapiens) | 38.94 | 1.54 | + | 2.11E-03 | 3.62E-02 | | [protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:0030163) | [756](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030163&list=upload_1&organism=Homo%20sapiens) | 45.49 | 1.60 | + | 2.19E-04 | 5.36E-03 | | [organonitrogen compound catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901565) | [1112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901565&list=upload_1&organism=Homo%20sapiens) | 66.92 | 1.52 | + | 7.01E-05 | 2.04E-03 | | [cellular component morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0032989) | [604](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032989&list=upload_1&organism=Homo%20sapiens) | 36.35 | 1.54 | + | 2.68E-03 | 4.38E-02 | | [intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0006886) | [682](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&reflist=1) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&list=upload_1&organism=Homo%20sapiens) | 41.04 | 1.54 | + | 1.60E-03 | 2.88E-02 | | [protein transport](http://amigo.geneontology.org/amigo/term/GO:0015031) | [1179](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015031&list=upload_1&organism=Homo%20sapiens) | 70.95 | 1.48 | + | 1.43E-04 | 3.73E-03 | | [nitrogen compound transport](http://amigo.geneontology.org/amigo/term/GO:0071705) | [1589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&reflist=1) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&list=upload_1&organism=Homo%20sapiens) | 95.62 | 1.43 | + | 5.70E-05 | 1.69E-03 | | [organic substance transport](http://amigo.geneontology.org/amigo/term/GO:0071702) | [1964](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&reflist=1) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&list=upload_1&organism=Homo%20sapiens) | 118.19 | 1.29 | + | 2.15E-03 | 3.68E-02 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 54.34 | 1.53 | + | 3.11E-04 | 7.23E-03 | | [cell motility](http://amigo.geneontology.org/amigo/term/GO:0048870) | [1061](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&list=upload_1&organism=Homo%20sapiens) | 63.85 | 1.39 | + | 3.12E-03 | 4.94E-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) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 60.12 | 1.50 | + | 3.49E-04 | 7.94E-03 | | [developmental process involved in reproduction](http://amigo.geneontology.org/amigo/term/GO:0003006) | [947](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003006&list=upload_1&organism=Homo%20sapiens) | 56.99 | 1.49 | + | 5.43E-04 | 1.15E-02 | | [cell-cell signaling](http://amigo.geneontology.org/amigo/term/GO:0007267) | [1083](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007267&list=upload_1&organism=Homo%20sapiens) | 65.17 | 1.41 | + | 1.80E-03 | 3.17E-02 | | [detection of chemical stimulus involved in sensory perception of smell](http://amigo.geneontology.org/amigo/term/GO:0050911) | [443](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050911&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050911&list=upload_1&organism=Homo%20sapiens) | 26.66 | .30 | - | 5.19E-05 | 1.55E-03 | | [detection of chemical stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050907) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050907&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050907&list=upload_1&organism=Homo%20sapiens) | 29.43 | .37 | - | 2.58E-04 | 6.21E-03 | | [detection of stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050906) | [560](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050906&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050906&list=upload_1&organism=Homo%20sapiens) | 33.70 | .39 | - | 1.06E-04 | 2.93E-03 | | [detection of stimulus](http://amigo.geneontology.org/amigo/term/GO:0051606) | [686](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051606&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051606&list=upload_1&organism=Homo%20sapiens) | 41.28 | .53 | - | 1.63E-03 | 2.93E-02 | | [detection of chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0009593) | [526](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009593&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009593&list=upload_1&organism=Homo%20sapiens) | 31.65 | .38 | - | 1.42E-04 | 3.71E-03 | | [sensory perception of chemical stimulus](http://amigo.geneontology.org/amigo/term/GO:0007606) | [551](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007606&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007606&list=upload_1&organism=Homo%20sapiens) | 33.16 | .39 | - | 1.39E-04 | 3.66E-03 | | [sensory perception of smell](http://amigo.geneontology.org/amigo/term/GO:0007608) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007608&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007608&list=upload_1&organism=Homo%20sapiens) | 28.28 | .32 | - | 5.53E-05 | 1.64E-03 | | Unclassified | [2725](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=UNCLASSIFIED&list=upload_1&organism=Homo%20sapiens) | 163.98 | .24 | - | 1.56E-32 | 6.62E-30 | |

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