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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 | [571](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) out of 1011 |
| Unmapped IDs: | [0](http://pantherdb.org/tools/unmappedBinom.jsp?refList=1) | [451](http://pantherdb.org/tools/unmappedBinom.jsp?listName=upload_1) |
| Multiple mapping information: | 0 | [527](http://pantherdb.org/tools/multipleMap.jsp?&listName=upload_1) |

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

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| |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | |  | [Homo sapiens](http://pantherdb.org/tools/gxIdsList.do?reflist=1) (REF) | [upload\_1](http://pantherdb.org/tools/gxIdsList.do?list=upload_1&organism=Homo%20sapiens) ( [Hierarchy](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1)  NEW! [Tips](javascript:;)) | | | | | | | [GO biological process complete](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=categories) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=Homo%20sapiens) | [#](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=num) | [expected](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=exp) | [Fold Enrichment](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=foldEnrich) | [+/-](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=rep) | [raw P value](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=1&sortList=upload_1&sortField=pval) | [FDR](http://pantherdb.org/tools/compareToRefList.jsp?sortOrder=2&sortList=upload_1&sortField=fdr) | | [negative regulation of calcium ion export across plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1905913) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905913&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905913&list=upload_1&organism=Homo%20sapiens) | .20 | 20.36 | + | 2.87E-04 | 6.95E-03 | | [regulation of calcium ion export across plasma membrane](http://amigo.geneontology.org/amigo/term/GO:1905912) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905912&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905912&list=upload_1&organism=Homo%20sapiens) | .20 | 20.36 | + | 2.87E-04 | 6.94E-03 | | [regulation of metal ion transport](http://amigo.geneontology.org/amigo/term/GO:0010959) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010959&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010959&list=upload_1&organism=Homo%20sapiens) | 20.13 | 2.04 | + | 6.07E-05 | 1.78E-03 | | [regulation of ion transport](http://amigo.geneontology.org/amigo/term/GO:0043269) | [708](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043269&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043269&list=upload_1&organism=Homo%20sapiens) | 34.77 | 1.75 | + | 5.62E-05 | 1.66E-03 | | [regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051049) | [1766](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&reflist=1) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051049&list=upload_1&organism=Homo%20sapiens) | 86.72 | 1.56 | + | 8.81E-07 | 4.18E-05 | | [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) | 103.31 | 1.62 | + | 2.33E-09 | 1.61E-07 | | [regulation of biological process](http://amigo.geneontology.org/amigo/term/GO:0050789) | [11806](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&reflist=1) | [724](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050789&list=upload_1&organism=Homo%20sapiens) | 579.72 | 1.25 | + | 5.23E-20 | 1.17E-17 | | [biological regulation](http://amigo.geneontology.org/amigo/term/GO:0065007) | [12544](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&reflist=1) | [753](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065007&list=upload_1&organism=Homo%20sapiens) | 615.96 | 1.22 | + | 7.92E-19 | 1.57E-16 | | [regulation of cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1904062) | [384](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904062&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904062&list=upload_1&organism=Homo%20sapiens) | 18.86 | 1.86 | + | 9.48E-04 | 1.89E-02 | | [regulation of ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034765) | [510](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034765&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034765&list=upload_1&organism=Homo%20sapiens) | 25.04 | 1.80 | + | 3.32E-04 | 7.83E-03 | | [regulation of transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034762) | [593](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034762&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034762&list=upload_1&organism=Homo%20sapiens) | 29.12 | 1.72 | + | 4.23E-04 | 9.55E-03 | | [regulation of cellular process](http://amigo.geneontology.org/amigo/term/GO:0050794) | [11187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&reflist=1) | [691](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050794&list=upload_1&organism=Homo%20sapiens) | 549.33 | 1.26 | + | 8.26E-19 | 1.62E-16 | | [negative regulation of cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1904063) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904063&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904063&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.70 | + | 2.06E-03 | 3.55E-02 | | [negative regulation of ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034766) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034766&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034766&list=upload_1&organism=Homo%20sapiens) | 5.16 | 2.72 | + | 1.35E-03 | 2.50E-02 | | [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) | [376](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048523&list=upload_1&organism=Homo%20sapiens) | 232.36 | 1.62 | + | 5.29E-23 | 1.54E-20 | | [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) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048519&list=upload_1&organism=Homo%20sapiens) | 260.94 | 1.58 | + | 4.00E-24 | 1.26E-21 | | [negative regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051051) | [435](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051051&list=upload_1&organism=Homo%20sapiens) | 21.36 | 1.87 | + | 3.73E-04 | 8.70E-03 | | [negative regulation of ion transport](http://amigo.geneontology.org/amigo/term/GO:0043271) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043271&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043271&list=upload_1&organism=Homo%20sapiens) | 7.61 | 2.50 | + | 7.62E-04 | 1.58E-02 | | [negative regulation of calcium ion transport](http://amigo.geneontology.org/amigo/term/GO:0051926) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051926&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051926&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.04 | + | 3.07E-03 | 4.86E-02 | | [miRNA transport](http://amigo.geneontology.org/amigo/term/GO:1990428) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990428&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990428&list=upload_1&organism=Homo%20sapiens) | .15 | 20.36 | + | 1.84E-03 | 3.23E-02 | | [RNA transport](http://amigo.geneontology.org/amigo/term/GO:0050658) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050658&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050658&list=upload_1&organism=Homo%20sapiens) | 8.25 | 3.03 | + | 4.06E-06 | 1.61E-04 | | [establishment of RNA localization](http://amigo.geneontology.org/amigo/term/GO:0051236) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051236&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051236&list=upload_1&organism=Homo%20sapiens) | 8.35 | 2.99 | + | 4.89E-06 | 1.90E-04 | | [establishment of localization](http://amigo.geneontology.org/amigo/term/GO:0051234) | [3997](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&reflist=1) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051234&list=upload_1&organism=Homo%20sapiens) | 196.27 | 1.35 | + | 4.81E-07 | 2.39E-05 | | [localization](http://amigo.geneontology.org/amigo/term/GO:0051179) | [4566](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&reflist=1) | [298](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051179&list=upload_1&organism=Homo%20sapiens) | 224.21 | 1.33 | + | 1.45E-07 | 7.93E-06 | | [RNA localization](http://amigo.geneontology.org/amigo/term/GO:0006403) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006403&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006403&list=upload_1&organism=Homo%20sapiens) | 9.33 | 3.32 | + | 4.77E-08 | 2.75E-06 | | [macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0033036) | [2345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&reflist=1) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033036&list=upload_1&organism=Homo%20sapiens) | 115.15 | 1.44 | + | 3.48E-06 | 1.42E-04 | | [nucleic acid transport](http://amigo.geneontology.org/amigo/term/GO:0050657) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050657&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050657&list=upload_1&organism=Homo%20sapiens) | 8.25 | 3.03 | + | 4.06E-06 | 1.61E-04 | | [nucleobase-containing compound transport](http://amigo.geneontology.org/amigo/term/GO:0015931) | [225](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015931&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015931&list=upload_1&organism=Homo%20sapiens) | 11.05 | 2.72 | + | 3.47E-06 | 1.42E-04 | | [nitrogen compound transport](http://amigo.geneontology.org/amigo/term/GO:0071705) | [1589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071705&list=upload_1&organism=Homo%20sapiens) | 78.03 | 1.45 | + | 1.56E-04 | 4.17E-03 | | [transport](http://amigo.geneontology.org/amigo/term/GO:0006810) | [3840](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&reflist=1) | [249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006810&list=upload_1&organism=Homo%20sapiens) | 188.56 | 1.32 | + | 4.76E-06 | 1.86E-04 | | [organic substance transport](http://amigo.geneontology.org/amigo/term/GO:0071702) | [1964](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&reflist=1) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071702&list=upload_1&organism=Homo%20sapiens) | 96.44 | 1.32 | + | 2.24E-03 | 3.83E-02 | | [regulation of G1 to G0 transition](http://amigo.geneontology.org/amigo/term/GO:1903450) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903450&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903450&list=upload_1&organism=Homo%20sapiens) | .20 | 20.36 | + | 2.87E-04 | 6.92E-03 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010564&list=upload_1&organism=Homo%20sapiens) | 35.11 | 1.85 | + | 8.47E-06 | 3.10E-04 | | [regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0051726) | [1122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051726&list=upload_1&organism=Homo%20sapiens) | 55.09 | 1.94 | + | 3.88E-10 | 2.94E-08 | | [cellular response to indole-3-methanol](http://amigo.geneontology.org/amigo/term/GO:0071681) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071681&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071681&list=upload_1&organism=Homo%20sapiens) | .25 | 16.29 | + | 4.98E-04 | 1.10E-02 | | [response to indole-3-methanol](http://amigo.geneontology.org/amigo/term/GO:0071680) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071680&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071680&list=upload_1&organism=Homo%20sapiens) | .29 | 16.97 | + | 8.11E-05 | 2.30E-03 | | [response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097305) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097305&list=upload_1&organism=Homo%20sapiens) | 12.47 | 2.49 | + | 1.31E-05 | 4.61E-04 | | [response to organic substance](http://amigo.geneontology.org/amigo/term/GO:0010033) | [2704](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&reflist=1) | [255](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010033&list=upload_1&organism=Homo%20sapiens) | 132.78 | 1.92 | + | 1.13E-23 | 3.46E-21 | | [response to chemical](http://amigo.geneontology.org/amigo/term/GO:0042221) | [4060](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&reflist=1) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042221&list=upload_1&organism=Homo%20sapiens) | 199.36 | 1.59 | + | 1.55E-17 | 2.70E-15 | | [response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0050896) | [8209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&reflist=1) | [534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050896&list=upload_1&organism=Homo%20sapiens) | 403.09 | 1.32 | + | 6.48E-16 | 9.86E-14 | | [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) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901700&list=upload_1&organism=Homo%20sapiens) | 76.16 | 2.07 | + | 5.34E-17 | 8.47E-15 | | [response to organonitrogen compound](http://amigo.geneontology.org/amigo/term/GO:0010243) | [968](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010243&list=upload_1&organism=Homo%20sapiens) | 47.53 | 2.25 | + | 1.16E-13 | 1.43E-11 | | [response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901698) | [1062](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&reflist=1) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901698&list=upload_1&organism=Homo%20sapiens) | 52.15 | 2.28 | + | 1.52E-15 | 2.23E-13 | | [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) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014070&list=upload_1&organism=Homo%20sapiens) | 43.16 | 2.55 | + | 1.72E-17 | 2.97E-15 | | [cellular response to alcohol](http://amigo.geneontology.org/amigo/term/GO:0097306) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097306&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097306&list=upload_1&organism=Homo%20sapiens) | 4.81 | 3.12 | + | 2.53E-04 | 6.20E-03 | | [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) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071310&list=upload_1&organism=Homo%20sapiens) | 99.48 | 1.99 | + | 1.48E-19 | 3.19E-17 | | [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) | [242](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070887&list=upload_1&organism=Homo%20sapiens) | 128.46 | 1.88 | + | 3.35E-21 | 8.33E-19 | | [cellular response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0051716) | [6569](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&reflist=1) | [440](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051716&list=upload_1&organism=Homo%20sapiens) | 322.56 | 1.36 | + | 4.99E-14 | 6.31E-12 | | [cellular process](http://amigo.geneontology.org/amigo/term/GO:0009987) | [15044](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&reflist=1) | [914](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009987&list=upload_1&organism=Homo%20sapiens) | 738.72 | 1.24 | + | 3.86E-41 | 8.65E-38 | | [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) | 52.00 | 2.21 | + | 4.44E-14 | 5.70E-12 | | [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) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071407&list=upload_1&organism=Homo%20sapiens) | 25.24 | 2.97 | + | 2.80E-15 | 4.03E-13 | | [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) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071417&list=upload_1&organism=Homo%20sapiens) | 28.38 | 2.33 | + | 3.25E-09 | 2.20E-07 | | [cellular response to nitrogen compound](http://amigo.geneontology.org/amigo/term/GO:1901699) | [641](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901699&list=upload_1&organism=Homo%20sapiens) | 31.48 | 2.41 | + | 2.83E-11 | 2.57E-09 | | [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) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071495&list=upload_1&organism=Homo%20sapiens) | 54.36 | 2.23 | + | 5.25E-15 | 7.29E-13 | | [response to endogenous stimulus](http://amigo.geneontology.org/amigo/term/GO:0009719) | [1371](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&reflist=1) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009719&list=upload_1&organism=Homo%20sapiens) | 67.32 | 2.20 | + | 6.53E-18 | 1.21E-15 | | [adenine transport](http://amigo.geneontology.org/amigo/term/GO:0015853) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015853&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015853&list=upload_1&organism=Homo%20sapiens) | .25 | 16.29 | + | 4.98E-04 | 1.10E-02 | | [purine nucleobase transport](http://amigo.geneontology.org/amigo/term/GO:0006863) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006863&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006863&list=upload_1&organism=Homo%20sapiens) | .44 | 9.05 | + | 2.43E-03 | 4.04E-02 | | [positive regulation of chronic inflammatory response](http://amigo.geneontology.org/amigo/term/GO:0002678) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002678&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002678&list=upload_1&organism=Homo%20sapiens) | .20 | 15.27 | + | 3.10E-03 | 4.90E-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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031347&list=upload_1&organism=Homo%20sapiens) | 31.52 | 1.87 | + | 1.53E-05 | 5.32E-04 | | [regulation of response to stress](http://amigo.geneontology.org/amigo/term/GO:0080134) | [1373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&reflist=1) | [128](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080134&list=upload_1&organism=Homo%20sapiens) | 67.42 | 1.90 | + | 2.59E-11 | 2.39E-09 | | [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) | [312](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048583&list=upload_1&organism=Homo%20sapiens) | 198.09 | 1.58 | + | 1.08E-16 | 1.66E-14 | | [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) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032101&list=upload_1&organism=Homo%20sapiens) | 47.78 | 1.67 | + | 1.80E-05 | 6.07E-04 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031349&list=upload_1&organism=Homo%20sapiens) | 14.53 | 2.20 | + | 9.53E-05 | 2.66E-03 | | [positive regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048584) | [2223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&reflist=1) | [189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048584&list=upload_1&organism=Homo%20sapiens) | 109.16 | 1.73 | + | 4.97E-13 | 5.69E-11 | | [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) | [473](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048518&list=upload_1&organism=Homo%20sapiens) | 309.55 | 1.53 | + | 1.12E-25 | 4.17E-23 | | [positive regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032103) | [455](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032103&list=upload_1&organism=Homo%20sapiens) | 22.34 | 1.92 | + | 1.40E-04 | 3.77E-03 | | [global gene silencing by mRNA cleavage](http://amigo.geneontology.org/amigo/term/GO:0098795) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098795&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098795&list=upload_1&organism=Homo%20sapiens) | .20 | 15.27 | + | 3.10E-03 | 4.90E-02 | | [post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0016441) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016441&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016441&list=upload_1&organism=Homo%20sapiens) | 1.92 | 5.22 | + | 7.50E-05 | 2.14E-03 | | [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) | [90](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010608&list=upload_1&organism=Homo%20sapiens) | 24.45 | 3.68 | + | 1.35E-23 | 4.08E-21 | | [regulation of gene expression](http://amigo.geneontology.org/amigo/term/GO:0010468) | [4855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&reflist=1) | [394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010468&list=upload_1&organism=Homo%20sapiens) | 238.40 | 1.65 | + | 3.19E-26 | 1.28E-23 | | [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) | [485](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060255&list=upload_1&organism=Homo%20sapiens) | 305.13 | 1.59 | + | 1.05E-30 | 7.50E-28 | | [regulation of metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019222) | [6754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&reflist=1) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019222&list=upload_1&organism=Homo%20sapiens) | 331.65 | 1.53 | + | 9.17E-29 | 5.33E-26 | | [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) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010629&list=upload_1&organism=Homo%20sapiens) | 44.29 | 2.53 | + | 1.92E-17 | 3.27E-15 | | [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) | [262](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010605&list=upload_1&organism=Homo%20sapiens) | 135.72 | 1.93 | + | 1.40E-24 | 4.68E-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) | [271](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009892&list=upload_1&organism=Homo%20sapiens) | 146.72 | 1.85 | + | 6.52E-23 | 1.86E-20 | | [telomerase holoenzyme complex assembly](http://amigo.geneontology.org/amigo/term/GO:1905323) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905323&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905323&list=upload_1&organism=Homo%20sapiens) | .20 | 15.27 | + | 3.10E-03 | 4.89E-02 | | [ribonucleoprotein complex assembly](http://amigo.geneontology.org/amigo/term/GO:0022618) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022618&list=upload_1&organism=Homo%20sapiens) | 9.87 | 6.08 | + | 2.94E-25 | 1.07E-22 | | [ribonucleoprotein complex biogenesis](http://amigo.geneontology.org/amigo/term/GO:0022613) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&reflist=1) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022613&list=upload_1&organism=Homo%20sapiens) | 22.05 | 4.90 | + | 1.46E-37 | 1.76E-34 | | [cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044085) | [2633](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&reflist=1) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044085&list=upload_1&organism=Homo%20sapiens) | 129.29 | 1.91 | + | 1.63E-22 | 4.57E-20 | | [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) | [416](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071840&list=upload_1&organism=Homo%20sapiens) | 281.22 | 1.48 | + | 9.11E-19 | 1.76E-16 | | [ribonucleoprotein complex subunit organization](http://amigo.geneontology.org/amigo/term/GO:0071826) | [209](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071826&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071826&list=upload_1&organism=Homo%20sapiens) | 10.26 | 6.04 | + | 6.10E-26 | 2.33E-23 | | [protein-containing complex organization](http://amigo.geneontology.org/amigo/term/GO:0043933) | [1423](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&reflist=1) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043933&list=upload_1&organism=Homo%20sapiens) | 69.87 | 2.18 | + | 4.76E-18 | 8.88E-16 | | [cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0016043) | [5523](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&reflist=1) | [377](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016043&list=upload_1&organism=Homo%20sapiens) | 271.20 | 1.39 | + | 1.46E-12 | 1.58E-10 | | [protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0065003) | [1270](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065003&list=upload_1&organism=Homo%20sapiens) | 62.36 | 2.13 | + | 3.82E-15 | 5.45E-13 | | [cellular component assembly](http://amigo.geneontology.org/amigo/term/GO:0022607) | [2394](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&reflist=1) | [200](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022607&list=upload_1&organism=Homo%20sapiens) | 117.55 | 1.70 | + | 4.21E-13 | 4.89E-11 | | [Langerhans cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0061520) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061520&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061520&list=upload_1&organism=Homo%20sapiens) | .20 | 15.27 | + | 3.10E-03 | 4.89E-02 | | [myeloid dendritic cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0043011) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043011&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043011&list=upload_1&organism=Homo%20sapiens) | 1.03 | 5.82 | + | 1.32E-03 | 2.46E-02 | | [myeloid dendritic cell activation](http://amigo.geneontology.org/amigo/term/GO:0001773) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001773&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001773&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.49E-02 | | [myeloid leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002274) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002274&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002274&list=upload_1&organism=Homo%20sapiens) | 7.27 | 2.61 | + | 3.17E-04 | 7.50E-03 | | [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) | 28.53 | 2.28 | + | 6.61E-09 | 4.34E-07 | | [cell activation](http://amigo.geneontology.org/amigo/term/GO:0001775) | [700](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&reflist=1) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001775&list=upload_1&organism=Homo%20sapiens) | 34.37 | 2.18 | + | 3.25E-09 | 2.19E-07 | | [immune system process](http://amigo.geneontology.org/amigo/term/GO:0002376) | [2429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&reflist=1) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002376&list=upload_1&organism=Homo%20sapiens) | 119.27 | 1.59 | + | 3.93E-10 | 2.96E-08 | | [mononuclear cell differentiation](http://amigo.geneontology.org/amigo/term/GO:1903131) | [326](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903131&list=upload_1&organism=Homo%20sapiens) | 16.01 | 2.56 | + | 2.65E-07 | 1.38E-05 | | [leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002521) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&reflist=1) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002521&list=upload_1&organism=Homo%20sapiens) | 19.64 | 2.39 | + | 3.11E-07 | 1.59E-05 | | [cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030154) | [3519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&reflist=1) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030154&list=upload_1&organism=Homo%20sapiens) | 172.80 | 1.49 | + | 5.24E-11 | 4.44E-09 | | [cellular developmental process](http://amigo.geneontology.org/amigo/term/GO:0048869) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&reflist=1) | [262](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048869&list=upload_1&organism=Homo%20sapiens) | 173.93 | 1.51 | + | 1.38E-11 | 1.32E-09 | | [developmental process](http://amigo.geneontology.org/amigo/term/GO:0032502) | [5677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&reflist=1) | [400](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032502&list=upload_1&organism=Homo%20sapiens) | 278.76 | 1.43 | + | 1.26E-15 | 1.86E-13 | | [hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:0030097) | [660](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&reflist=1) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030097&list=upload_1&organism=Homo%20sapiens) | 32.41 | 2.01 | + | 5.93E-07 | 2.90E-05 | | [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) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048534&list=upload_1&organism=Homo%20sapiens) | 34.86 | 1.95 | + | 9.24E-07 | 4.34E-05 | | [immune system development](http://amigo.geneontology.org/amigo/term/GO:0002520) | [757](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&reflist=1) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002520&list=upload_1&organism=Homo%20sapiens) | 37.17 | 1.91 | + | 8.52E-07 | 4.05E-05 | | [system development](http://amigo.geneontology.org/amigo/term/GO:0048731) | [3838](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&reflist=1) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048731&list=upload_1&organism=Homo%20sapiens) | 188.46 | 1.42 | + | 3.76E-09 | 2.52E-07 | | [anatomical structure development](http://amigo.geneontology.org/amigo/term/GO:0048856) | [5144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&reflist=1) | [360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048856&list=upload_1&organism=Homo%20sapiens) | 252.59 | 1.43 | + | 2.55E-13 | 3.03E-11 | | [multicellular organism development](http://amigo.geneontology.org/amigo/term/GO:0007275) | [4228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&reflist=1) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007275&list=upload_1&organism=Homo%20sapiens) | 207.61 | 1.46 | + | 6.00E-12 | 6.00E-10 | | [multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0032501) | [6581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&reflist=1) | [417](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032501&list=upload_1&organism=Homo%20sapiens) | 323.15 | 1.29 | + | 1.55E-09 | 1.10E-07 | | [animal organ development](http://amigo.geneontology.org/amigo/term/GO:0048513) | [3254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&reflist=1) | [244](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048513&list=upload_1&organism=Homo%20sapiens) | 159.78 | 1.53 | + | 3.12E-11 | 2.79E-09 | | [myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002573) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002573&list=upload_1&organism=Homo%20sapiens) | 6.58 | 2.74 | + | 2.76E-04 | 6.73E-03 | | [myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030099) | [264](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030099&list=upload_1&organism=Homo%20sapiens) | 12.96 | 2.08 | + | 6.82E-04 | 1.45E-02 | | [cellular response to actinomycin D](http://amigo.geneontology.org/amigo/term/GO:0072717) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072717&reflist=1) | [3](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072717&list=upload_1&organism=Homo%20sapiens) | .20 | 15.27 | + | 3.10E-03 | 4.88E-02 | | [cellular response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901653) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901653&list=upload_1&organism=Homo%20sapiens) | 14.88 | 2.82 | + | 1.53E-08 | 9.64E-07 | | [response to peptide](http://amigo.geneontology.org/amigo/term/GO:1901652) | [445](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901652&list=upload_1&organism=Homo%20sapiens) | 21.85 | 2.38 | + | 6.52E-08 | 3.73E-06 | | [CRD-mediated mRNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0070934) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070934&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070934&list=upload_1&organism=Homo%20sapiens) | .54 | 14.81 | + | 1.07E-06 | 4.95E-05 | | [mRNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0048255) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048255&list=upload_1&organism=Homo%20sapiens) | 2.75 | 5.45 | + | 7.97E-07 | 3.82E-05 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902373&list=upload_1&organism=Homo%20sapiens) | 3.29 | 4.86 | + | 1.27E-06 | 5.76E-05 | | [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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903312&list=upload_1&organism=Homo%20sapiens) | 4.52 | 5.09 | + | 3.03E-09 | 2.07E-07 | | [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) | [145](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051253&list=upload_1&organism=Homo%20sapiens) | 70.46 | 2.06 | + | 2.36E-15 | 3.43E-13 | | [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) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045934&list=upload_1&organism=Homo%20sapiens) | 76.70 | 2.02 | + | 8.98E-16 | 1.35E-13 | | [negative regulation of nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051172) | [2409](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&reflist=1) | [235](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051172&list=upload_1&organism=Homo%20sapiens) | 118.29 | 1.99 | + | 2.57E-23 | 7.60E-21 | | [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) | [455](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051171&list=upload_1&organism=Homo%20sapiens) | 280.33 | 1.62 | + | 4.14E-30 | 2.82E-27 | | [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) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019219&list=upload_1&organism=Homo%20sapiens) | 199.71 | 1.66 | + | 1.55E-21 | 4.05E-19 | | [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) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031323&list=upload_1&organism=Homo%20sapiens) | 277.29 | 1.63 | + | 6.16E-30 | 4.03E-27 | | [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) | [460](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080090&list=upload_1&organism=Homo%20sapiens) | 288.34 | 1.60 | + | 9.19E-29 | 5.15E-26 | | [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) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031324&list=upload_1&organism=Homo%20sapiens) | 111.17 | 2.01 | + | 1.75E-22 | 4.82E-20 | | [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) | [298](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051252&list=upload_1&organism=Homo%20sapiens) | 184.24 | 1.62 | + | 2.95E-17 | 4.81E-15 | | [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) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903311&list=upload_1&organism=Homo%20sapiens) | 14.78 | 3.18 | + | 6.45E-11 | 5.35E-09 | | [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) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010628&list=upload_1&organism=Homo%20sapiens) | 56.52 | 2.53 | + | 2.17E-22 | 5.86E-20 | | [positive regulation of macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0010604) | [3542](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&reflist=1) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010604&list=upload_1&organism=Homo%20sapiens) | 173.93 | 1.83 | + | 6.23E-27 | 2.71E-24 | | [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) | [338](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009893&list=upload_1&organism=Homo%20sapiens) | 189.44 | 1.78 | + | 4.64E-27 | 2.20E-24 | | [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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061013&list=upload_1&organism=Homo%20sapiens) | 8.89 | 3.26 | + | 1.80E-07 | 9.69E-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) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031329&list=upload_1&organism=Homo%20sapiens) | 38.60 | 2.23 | + | 6.95E-11 | 5.74E-09 | | [regulation of catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009894) | [987](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009894&list=upload_1&organism=Homo%20sapiens) | 48.47 | 2.04 | + | 1.93E-10 | 1.51E-08 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902369&list=upload_1&organism=Homo%20sapiens) | 3.88 | 4.38 | + | 2.06E-06 | 8.98E-05 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031330&list=upload_1&organism=Homo%20sapiens) | 11.88 | 2.69 | + | 1.94E-06 | 8.53E-05 | | [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) | 16.01 | 2.50 | + | 1.01E-06 | 4.70E-05 | | [regulation of mRNA stability](http://amigo.geneontology.org/amigo/term/GO:0043488) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043488&list=upload_1&organism=Homo%20sapiens) | 8.00 | 3.12 | + | 2.52E-06 | 1.07E-04 | | [regulation of RNA stability](http://amigo.geneontology.org/amigo/term/GO:0043487) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043487&list=upload_1&organism=Homo%20sapiens) | 8.59 | 3.03 | + | 2.69E-06 | 1.13E-04 | | [regulation of biological quality](http://amigo.geneontology.org/amigo/term/GO:0065008) | [3677](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&reflist=1) | [271](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065008&list=upload_1&organism=Homo%20sapiens) | 180.56 | 1.50 | + | 8.39E-12 | 8.22E-10 | | [RNA stabilization](http://amigo.geneontology.org/amigo/term/GO:0043489) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043489&list=upload_1&organism=Homo%20sapiens) | 3.19 | 5.01 | + | 9.01E-07 | 4.26E-05 | | [RISC complex assembly](http://amigo.geneontology.org/amigo/term/GO:0070922) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070922&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070922&list=upload_1&organism=Homo%20sapiens) | .44 | 13.58 | + | 3.60E-05 | 1.13E-03 | | [gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0031047) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031047&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031047&list=upload_1&organism=Homo%20sapiens) | 4.71 | 3.18 | + | 2.07E-04 | 5.23E-03 | | [mitochondrial ATP transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1990544) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990544&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990544&list=upload_1&organism=Homo%20sapiens) | .29 | 13.58 | + | 7.99E-04 | 1.65E-02 | | [ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0034220) | [891](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034220&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034220&list=upload_1&organism=Homo%20sapiens) | 43.75 | 1.55 | + | 7.20E-04 | 1.52E-02 | | [mitochondrial ADP transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0140021) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140021&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140021&list=upload_1&organism=Homo%20sapiens) | .29 | 13.58 | + | 7.99E-04 | 1.64E-02 | | [ADP transport](http://amigo.geneontology.org/amigo/term/GO:0015866) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015866&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0015866&list=upload_1&organism=Homo%20sapiens) | .44 | 9.05 | + | 2.43E-03 | 4.03E-02 | | [positive regulation of mRNA binding](http://amigo.geneontology.org/amigo/term/GO:1902416) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902416&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902416&list=upload_1&organism=Homo%20sapiens) | .39 | 12.73 | + | 2.09E-04 | 5.27E-03 | | [regulation of mRNA binding](http://amigo.geneontology.org/amigo/term/GO:1902415) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902415&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902415&list=upload_1&organism=Homo%20sapiens) | .49 | 12.22 | + | 5.53E-05 | 1.64E-03 | | [regulation of RNA binding](http://amigo.geneontology.org/amigo/term/GO:1905214) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905214&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905214&list=upload_1&organism=Homo%20sapiens) | .64 | 10.97 | + | 2.18E-05 | 7.21E-04 | | [regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051098) | [374](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051098&list=upload_1&organism=Homo%20sapiens) | 18.36 | 3.27 | + | 4.96E-14 | 6.32E-12 | | [regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0065009) | [3094](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&reflist=1) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0065009&list=upload_1&organism=Homo%20sapiens) | 151.93 | 1.67 | + | 9.10E-16 | 1.36E-13 | | [positive regulation of RNA binding](http://amigo.geneontology.org/amigo/term/GO:1905216) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905216&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905216&list=upload_1&organism=Homo%20sapiens) | .44 | 11.31 | + | 3.12E-04 | 7.41E-03 | | [positive regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051099) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051099&list=upload_1&organism=Homo%20sapiens) | 8.89 | 4.16 | + | 9.18E-12 | 8.95E-10 | | [positive regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0044093) | [1590](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&reflist=1) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044093&list=upload_1&organism=Homo%20sapiens) | 78.08 | 1.97 | + | 9.81E-15 | 1.34E-12 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900152&list=upload_1&organism=Homo%20sapiens) | .59 | 11.88 | + | 1.48E-05 | 5.17E-04 | | [positive regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0045727) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045727&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045727&list=upload_1&organism=Homo%20sapiens) | 7.17 | 4.88 | + | 6.85E-13 | 7.79E-11 | | [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) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031328&list=upload_1&organism=Homo%20sapiens) | 100.56 | 2.04 | + | 2.21E-21 | 5.69E-19 | | [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) | [292](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031325&list=upload_1&organism=Homo%20sapiens) | 153.30 | 1.90 | + | 4.97E-27 | 2.29E-24 | | [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) | [434](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048522&list=upload_1&organism=Homo%20sapiens) | 278.42 | 1.56 | + | 1.70E-24 | 5.55E-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) | [331](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031326&list=upload_1&organism=Homo%20sapiens) | 201.42 | 1.64 | + | 1.37E-20 | 3.21E-18 | | [regulation of biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009889) | [4163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&reflist=1) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009889&list=upload_1&organism=Homo%20sapiens) | 204.42 | 1.63 | + | 3.28E-20 | 7.56E-18 | | [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) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009891&list=upload_1&organism=Homo%20sapiens) | 102.48 | 2.02 | + | 3.14E-21 | 7.93E-19 | | [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) | [197](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010557&list=upload_1&organism=Homo%20sapiens) | 95.41 | 2.06 | + | 3.84E-21 | 9.26E-19 | | [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) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010556&list=upload_1&organism=Homo%20sapiens) | 193.37 | 1.67 | + | 3.71E-21 | 9.09E-19 | | [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) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051247&list=upload_1&organism=Homo%20sapiens) | 74.39 | 2.10 | + | 3.98E-17 | 6.43E-15 | | [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) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051173&list=upload_1&organism=Homo%20sapiens) | 155.86 | 1.86 | + | 3.09E-25 | 1.10E-22 | | [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) | [260](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051246&list=upload_1&organism=Homo%20sapiens) | 127.03 | 2.05 | + | 5.21E-28 | 2.73E-25 | | [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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034250&list=upload_1&organism=Homo%20sapiens) | 8.49 | 4.47 | + | 7.27E-13 | 8.14E-11 | | [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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034248&list=upload_1&organism=Homo%20sapiens) | 23.03 | 3.43 | + | 3.30E-19 | 6.72E-17 | | [regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0006417) | [410](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006417&list=upload_1&organism=Homo%20sapiens) | 20.13 | 3.68 | + | 1.56E-19 | 3.31E-17 | | [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) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000112&list=upload_1&organism=Homo%20sapiens) | 24.21 | 3.43 | + | 4.04E-20 | 9.17E-18 | | [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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900151&list=upload_1&organism=Homo%20sapiens) | 1.28 | 7.83 | + | 4.03E-06 | 1.61E-04 | | [negative regulation of cardiac muscle hypertrophy in response to stress](http://amigo.geneontology.org/amigo/term/GO:1903243) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903243&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903243&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.32E-02 | | [regulation of muscle system process](http://amigo.geneontology.org/amigo/term/GO:0090257) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090257&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090257&list=upload_1&organism=Homo%20sapiens) | 11.59 | 2.16 | + | 9.14E-04 | 1.83E-02 | | [regulation of system process](http://amigo.geneontology.org/amigo/term/GO:0044057) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044057&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044057&list=upload_1&organism=Homo%20sapiens) | 27.89 | 2.04 | + | 1.71E-06 | 7.62E-05 | | [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) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051239&list=upload_1&organism=Homo%20sapiens) | 135.04 | 1.75 | + | 6.98E-17 | 1.10E-14 | | [negative regulation of multicellular organismal process](http://amigo.geneontology.org/amigo/term/GO:0051241) | [1039](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&reflist=1) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051241&list=upload_1&organism=Homo%20sapiens) | 51.02 | 1.63 | + | 3.24E-05 | 1.03E-03 | | [negative regulation of cardiac muscle adaptation](http://amigo.geneontology.org/amigo/term/GO:0010616) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010616&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010616&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.29E-02 | | [negative regulation of response to stimulus](http://amigo.geneontology.org/amigo/term/GO:0048585) | [1620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&reflist=1) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048585&list=upload_1&organism=Homo%20sapiens) | 79.55 | 1.62 | + | 1.76E-07 | 9.48E-06 | | [trachea formation](http://amigo.geneontology.org/amigo/term/GO:0060440) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060440&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060440&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.31E-02 | | [animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009887) | [1003](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009887&list=upload_1&organism=Homo%20sapiens) | 49.25 | 1.62 | + | 6.00E-05 | 1.76E-03 | | [anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0009653) | [2237](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&reflist=1) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009653&list=upload_1&organism=Homo%20sapiens) | 109.85 | 1.56 | + | 2.01E-08 | 1.24E-06 | | [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) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048646&list=upload_1&organism=Homo%20sapiens) | 46.21 | 1.82 | + | 6.47E-07 | 3.14E-05 | | [respiratory system development](http://amigo.geneontology.org/amigo/term/GO:0060541) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060541&list=upload_1&organism=Homo%20sapiens) | 10.12 | 2.37 | + | 2.27E-04 | 5.66E-03 | | [common-partner SMAD protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0007182) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007182&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007182&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.31E-02 | | [protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0006468) | [719](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006468&list=upload_1&organism=Homo%20sapiens) | 35.31 | 1.87 | + | 4.06E-06 | 1.60E-04 | | [protein modification process](http://amigo.geneontology.org/amigo/term/GO:0036211) | [2658](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&reflist=1) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036211&list=upload_1&organism=Homo%20sapiens) | 130.52 | 1.31 | + | 3.99E-04 | 9.18E-03 | | [macromolecule modification](http://amigo.geneontology.org/amigo/term/GO:0043412) | [2883](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&reflist=1) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043412&list=upload_1&organism=Homo%20sapiens) | 141.57 | 1.29 | + | 4.41E-04 | 9.90E-03 | | [macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043170) | [5941](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&reflist=1) | [508](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043170&list=upload_1&organism=Homo%20sapiens) | 291.73 | 1.74 | + | 6.73E-44 | 1.76E-40 | | [organic substance metabolic process](http://amigo.geneontology.org/amigo/term/GO:0071704) | [7697](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&reflist=1) | [579](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071704&list=upload_1&organism=Homo%20sapiens) | 377.95 | 1.53 | + | 1.01E-35 | 1.06E-32 | | [metabolic process](http://amigo.geneontology.org/amigo/term/GO:0008152) | [8131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&reflist=1) | [604](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008152&list=upload_1&organism=Homo%20sapiens) | 399.26 | 1.51 | + | 1.03E-36 | 1.15E-33 | | [protein metabolic process](http://amigo.geneontology.org/amigo/term/GO:0019538) | [3920](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&reflist=1) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019538&list=upload_1&organism=Homo%20sapiens) | 192.49 | 1.64 | + | 2.08E-19 | 4.35E-17 | | [organonitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901564) | [5013](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&reflist=1) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901564&list=upload_1&organism=Homo%20sapiens) | 246.16 | 1.49 | + | 8.85E-17 | 1.37E-14 | | [nitrogen compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006807) | [6710](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&reflist=1) | [537](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006807&list=upload_1&organism=Homo%20sapiens) | 329.49 | 1.63 | + | 4.19E-39 | 6.58E-36 | | [primary metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044238) | [7228](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&reflist=1) | [549](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044238&list=upload_1&organism=Homo%20sapiens) | 354.92 | 1.55 | + | 7.97E-34 | 6.57E-31 | | [phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0016310) | [918](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016310&list=upload_1&organism=Homo%20sapiens) | 45.08 | 1.75 | + | 4.88E-06 | 1.90E-04 | | [phosphate-containing compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006796) | [1855](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&reflist=1) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006796&list=upload_1&organism=Homo%20sapiens) | 91.09 | 1.32 | + | 3.00E-03 | 4.78E-02 | | [cellular metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044237) | [6606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&reflist=1) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044237&list=upload_1&organism=Homo%20sapiens) | 324.38 | 1.64 | + | 1.28E-39 | 2.23E-36 | | [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) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007166&list=upload_1&organism=Homo%20sapiens) | 106.75 | 1.46 | + | 3.51E-06 | 1.43E-04 | | [signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007165) | [4887](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&reflist=1) | [310](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007165&list=upload_1&organism=Homo%20sapiens) | 239.97 | 1.29 | + | 9.20E-07 | 4.33E-05 | | [signaling](http://amigo.geneontology.org/amigo/term/GO:0023052) | [5231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&reflist=1) | [327](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023052&list=upload_1&organism=Homo%20sapiens) | 256.86 | 1.27 | + | 1.59E-06 | 7.07E-05 | | [cell communication](http://amigo.geneontology.org/amigo/term/GO:0007154) | [5342](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&reflist=1) | [338](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007154&list=upload_1&organism=Homo%20sapiens) | 262.31 | 1.29 | + | 2.83E-07 | 1.45E-05 | | [positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1902255) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902255&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902255&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.31E-02 | | [positive regulation of signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1901798) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901798&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901798&list=upload_1&organism=Homo%20sapiens) | 1.42 | 6.32 | + | 4.97E-05 | 1.50E-03 | | [regulation of signal transduction by p53 class mediator](http://amigo.geneontology.org/amigo/term/GO:1901796) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901796&list=upload_1&organism=Homo%20sapiens) | 5.11 | 3.72 | + | 4.41E-06 | 1.73E-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) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902531&list=upload_1&organism=Homo%20sapiens) | 84.51 | 1.79 | + | 2.06E-11 | 1.94E-09 | | [regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009966) | [2989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&reflist=1) | [236](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009966&list=upload_1&organism=Homo%20sapiens) | 146.77 | 1.61 | + | 4.55E-13 | 5.25E-11 | | [regulation of cell communication](http://amigo.geneontology.org/amigo/term/GO:0010646) | [3369](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&reflist=1) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010646&list=upload_1&organism=Homo%20sapiens) | 165.43 | 1.61 | + | 4.04E-15 | 5.70E-13 | | [regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023051) | [3381](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&reflist=1) | [267](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023051&list=upload_1&organism=Homo%20sapiens) | 166.02 | 1.61 | + | 6.22E-15 | 8.56E-13 | | [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) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902533&list=upload_1&organism=Homo%20sapiens) | 49.05 | 2.08 | + | 3.43E-11 | 3.02E-09 | | [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) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009967&list=upload_1&organism=Homo%20sapiens) | 75.03 | 1.91 | + | 9.65E-13 | 1.07E-10 | | [positive regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023056) | [1701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&reflist=1) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023056&list=upload_1&organism=Homo%20sapiens) | 83.53 | 1.88 | + | 2.31E-13 | 2.77E-11 | | [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) | [157](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010647&list=upload_1&organism=Homo%20sapiens) | 83.28 | 1.89 | + | 1.44E-13 | 1.73E-11 | | [positive regulation of intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001244) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001244&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001244&list=upload_1&organism=Homo%20sapiens) | 3.00 | 3.34 | + | 1.66E-03 | 2.99E-02 | | [positive regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001235) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001235&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001235&list=upload_1&organism=Homo%20sapiens) | 6.38 | 2.82 | + | 1.97E-04 | 5.05E-03 | | [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) | 17.87 | 2.52 | + | 1.54E-07 | 8.41E-06 | | [regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0042981) | [1468](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&reflist=1) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042981&list=upload_1&organism=Homo%20sapiens) | 72.08 | 2.12 | + | 2.63E-17 | 4.44E-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) | [158](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043067&list=upload_1&organism=Homo%20sapiens) | 73.56 | 2.15 | + | 3.07E-18 | 5.87E-16 | | [regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0010941) | [1654](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&reflist=1) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010941&list=upload_1&organism=Homo%20sapiens) | 81.22 | 2.14 | + | 5.47E-20 | 1.21E-17 | | [positive regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043065) | [503](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043065&list=upload_1&organism=Homo%20sapiens) | 24.70 | 2.59 | + | 9.93E-11 | 8.03E-09 | | [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) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043068&list=upload_1&organism=Homo%20sapiens) | 25.34 | 2.64 | + | 1.11E-11 | 1.07E-09 | | [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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010942&list=upload_1&organism=Homo%20sapiens) | 28.63 | 2.72 | + | 5.92E-14 | 7.43E-12 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902253&list=upload_1&organism=Homo%20sapiens) | 1.57 | 4.45 | + | 1.99E-03 | 3.46E-02 | | [cellular response to nicotine](http://amigo.geneontology.org/amigo/term/GO:0071316) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071316&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071316&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.31E-02 | | [corticosteroid receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0031958) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031958&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031958&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.30E-02 | | [intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030518) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030518&list=upload_1&organism=Homo%20sapiens) | 2.75 | 5.09 | + | 3.69E-06 | 1.49E-04 | | [intracellular receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030522) | [148](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030522&list=upload_1&organism=Homo%20sapiens) | 7.27 | 3.58 | + | 1.60E-07 | 8.70E-06 | | [steroid hormone mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0043401) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043401&list=upload_1&organism=Homo%20sapiens) | 3.78 | 3.97 | + | 2.28E-05 | 7.51E-04 | | [hormone-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0009755) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009755&list=upload_1&organism=Homo%20sapiens) | 6.43 | 2.95 | + | 7.67E-05 | 2.18E-03 | | [cellular response to hormone stimulus](http://amigo.geneontology.org/amigo/term/GO:0032870) | [489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032870&list=upload_1&organism=Homo%20sapiens) | 24.01 | 2.75 | + | 5.25E-12 | 5.31E-10 | | [response to hormone](http://amigo.geneontology.org/amigo/term/GO:0009725) | [767](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009725&list=upload_1&organism=Homo%20sapiens) | 37.66 | 2.47 | + | 4.21E-14 | 5.45E-12 | | [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) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071383&list=upload_1&organism=Homo%20sapiens) | 7.46 | 4.69 | + | 1.85E-12 | 1.93E-10 | | [cellular response to lipid](http://amigo.geneontology.org/amigo/term/GO:0071396) | [519](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071396&list=upload_1&organism=Homo%20sapiens) | 25.48 | 2.71 | + | 2.33E-12 | 2.42E-10 | | [response to lipid](http://amigo.geneontology.org/amigo/term/GO:0033993) | [843](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033993&list=upload_1&organism=Homo%20sapiens) | 41.39 | 2.25 | + | 6.26E-12 | 6.21E-10 | | [response to steroid hormone](http://amigo.geneontology.org/amigo/term/GO:0048545) | [284](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&reflist=1) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048545&list=upload_1&organism=Homo%20sapiens) | 13.95 | 3.30 | + | 3.49E-11 | 3.05E-09 | | [positive regulation of vascular associated smooth muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:1905461) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905461&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905461&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.30E-02 | | [regulation of smooth muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0034391) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034391&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034391&list=upload_1&organism=Homo%20sapiens) | 1.13 | 6.20 | + | 3.81E-04 | 8.85E-03 | | [regulation of muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0010660) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010660&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010660&list=upload_1&organism=Homo%20sapiens) | 3.34 | 4.49 | + | 6.27E-06 | 2.37E-04 | | [positive regulation of smooth muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0034393) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034393&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034393&list=upload_1&organism=Homo%20sapiens) | .59 | 10.18 | + | 1.18E-04 | 3.24E-03 | | [positive regulation of muscle cell apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0010661) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010661&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010661&list=upload_1&organism=Homo%20sapiens) | 1.28 | 7.05 | + | 2.44E-05 | 7.99E-04 | | [negative regulation of amyloid precursor protein biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0042985) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042985&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042985&list=upload_1&organism=Homo%20sapiens) | .34 | 11.64 | + | 1.21E-03 | 2.30E-02 | | [negative regulation of glycoprotein biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0010561) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010561&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010561&list=upload_1&organism=Homo%20sapiens) | .59 | 8.49 | + | 8.59E-04 | 1.74E-02 | | [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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000113&list=upload_1&organism=Homo%20sapiens) | 9.33 | 3.86 | + | 1.13E-10 | 9.04E-09 | | [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) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010558&list=upload_1&organism=Homo%20sapiens) | 75.28 | 2.13 | + | 4.16E-18 | 7.87E-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) | [165](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009890&list=upload_1&organism=Homo%20sapiens) | 79.74 | 2.07 | + | 1.13E-17 | 2.01E-15 | | [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) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031327&list=upload_1&organism=Homo%20sapiens) | 78.27 | 2.07 | + | 2.69E-17 | 4.48E-15 | | [negative regulation of glycoprotein metabolic process](http://amigo.geneontology.org/amigo/term/GO:1903019) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903019&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903019&list=upload_1&organism=Homo%20sapiens) | .74 | 8.15 | + | 3.07E-04 | 7.31E-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) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051248&list=upload_1&organism=Homo%20sapiens) | 51.17 | 2.23 | + | 2.92E-14 | 3.85E-12 | | [regulation of amyloid precursor protein biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0042984) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042984&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042984&list=upload_1&organism=Homo%20sapiens) | .69 | 7.27 | + | 1.49E-03 | 2.71E-02 | | [cell adhesion mediated by integrin](http://amigo.geneontology.org/amigo/term/GO:0033627) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033627&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033627&list=upload_1&organism=Homo%20sapiens) | 2.01 | 11.42 | + | 4.79E-15 | 6.71E-13 | | [cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0007155) | [969](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007155&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007155&list=upload_1&organism=Homo%20sapiens) | 47.58 | 1.56 | + | 3.84E-04 | 8.87E-03 | | [RNA secondary structure unwinding](http://amigo.geneontology.org/amigo/term/GO:0010501) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010501&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010501&list=upload_1&organism=Homo%20sapiens) | .44 | 11.31 | + | 3.12E-04 | 7.40E-03 | | [RNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016070) | [1635](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&reflist=1) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016070&list=upload_1&organism=Homo%20sapiens) | 80.28 | 2.50 | + | 4.05E-31 | 3.02E-28 | | [nucleic acid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0090304) | [2276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&reflist=1) | [249](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090304&list=upload_1&organism=Homo%20sapiens) | 111.76 | 2.23 | + | 9.51E-32 | 7.46E-29 | | [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) | [273](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006139&list=upload_1&organism=Homo%20sapiens) | 138.72 | 1.97 | + | 5.54E-27 | 2.48E-24 | | [organic cyclic compound metabolic process](http://amigo.geneontology.org/amigo/term/GO:1901360) | [3292](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&reflist=1) | [294](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901360&list=upload_1&organism=Homo%20sapiens) | 161.65 | 1.82 | + | 3.81E-24 | 1.22E-21 | | [heterocycle metabolic process](http://amigo.geneontology.org/amigo/term/GO:0046483) | [2999](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&reflist=1) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046483&list=upload_1&organism=Homo%20sapiens) | 147.26 | 1.91 | + | 6.08E-26 | 2.38E-23 | | [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) | [281](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006725&list=upload_1&organism=Homo%20sapiens) | 149.77 | 1.88 | + | 6.16E-25 | 2.10E-22 | | [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) | [375](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034641&list=upload_1&organism=Homo%20sapiens) | 175.45 | 2.14 | + | 1.77E-47 | 9.26E-44 | | [positive regulation of cytoplasmic translation](http://amigo.geneontology.org/amigo/term/GO:2000767) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000767&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000767&list=upload_1&organism=Homo%20sapiens) | .74 | 10.86 | + | 5.86E-06 | 2.23E-04 | | [regulation of cytoplasmic translation](http://amigo.geneontology.org/amigo/term/GO:2000765) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000765&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000765&list=upload_1&organism=Homo%20sapiens) | 1.42 | 7.02 | + | 8.87E-06 | 3.23E-04 | | [positive regulation by host of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0044829) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044829&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044829&list=upload_1&organism=Homo%20sapiens) | .49 | 10.18 | + | 4.51E-04 | 1.01E-02 | | [modulation by host of viral genome replication](http://amigo.geneontology.org/amigo/term/GO:0044827) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044827&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044827&list=upload_1&organism=Homo%20sapiens) | 1.08 | 6.48 | + | 3.04E-04 | 7.28E-03 | | [modulation by host of viral process](http://amigo.geneontology.org/amigo/term/GO:0044788) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044788&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044788&list=upload_1&organism=Homo%20sapiens) | 2.21 | 4.98 | + | 4.80E-05 | 1.45E-03 | | [modulation by host of symbiont process](http://amigo.geneontology.org/amigo/term/GO:0051851) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051851&list=upload_1&organism=Homo%20sapiens) | 4.08 | 5.40 | + | 2.67E-09 | 1.83E-07 | | [biological process involved in interaction with symbiont](http://amigo.geneontology.org/amigo/term/GO:0051702) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051702&list=upload_1&organism=Homo%20sapiens) | 5.55 | 4.87 | + | 3.10E-10 | 2.37E-08 | | [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) | [46](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044403&list=upload_1&organism=Homo%20sapiens) | 12.82 | 3.59 | + | 2.73E-12 | 2.80E-10 | | [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) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044419&list=upload_1&organism=Homo%20sapiens) | 78.66 | 2.12 | + | 7.70E-19 | 1.55E-16 | | [positive regulation by host of viral process](http://amigo.geneontology.org/amigo/term/GO:0044794) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044794&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044794&list=upload_1&organism=Homo%20sapiens) | 1.03 | 5.82 | + | 1.32E-03 | 2.46E-02 | | [positive regulation of transcription of nucleolar large rRNA by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:1901838) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901838&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901838&list=upload_1&organism=Homo%20sapiens) | .49 | 10.18 | + | 4.51E-04 | 1.01E-02 | | [positive regulation of transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0045943) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045943&list=upload_1&organism=Homo%20sapiens) | 1.67 | 4.79 | + | 6.40E-04 | 1.37E-02 | | [regulation of transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0006356) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006356&list=upload_1&organism=Homo%20sapiens) | 2.16 | 4.17 | + | 7.20E-04 | 1.52E-02 | | [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) | [255](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006355&list=upload_1&organism=Homo%20sapiens) | 169.60 | 1.50 | + | 3.76E-11 | 3.28E-09 | | [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) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903506&list=upload_1&organism=Homo%20sapiens) | 169.70 | 1.51 | + | 2.17E-11 | 2.03E-09 | | [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) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001141&list=upload_1&organism=Homo%20sapiens) | 170.14 | 1.50 | + | 3.00E-11 | 2.70E-09 | | [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) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045893&list=upload_1&organism=Homo%20sapiens) | 84.21 | 1.84 | + | 1.55E-12 | 1.66E-10 | | [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) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903508&list=upload_1&organism=Homo%20sapiens) | 84.21 | 1.84 | + | 1.55E-12 | 1.67E-10 | | [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) | [155](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902680&list=upload_1&organism=Homo%20sapiens) | 84.51 | 1.83 | + | 1.72E-12 | 1.81E-10 | | [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) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051254&list=upload_1&organism=Homo%20sapiens) | 90.74 | 1.83 | + | 3.23E-13 | 3.78E-11 | | [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) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045935&list=upload_1&organism=Homo%20sapiens) | 101.06 | 1.93 | + | 7.45E-18 | 1.36E-15 | | [regulation of transcription of nucleolar large rRNA by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:1901836) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901836&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901836&list=upload_1&organism=Homo%20sapiens) | .74 | 8.15 | + | 3.07E-04 | 7.30E-03 | | [regulation of ncRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0140747) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140747&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140747&list=upload_1&organism=Homo%20sapiens) | 1.13 | 5.31 | + | 1.95E-03 | 3.40E-02 | | [regulation of transforming growth factor beta activation](http://amigo.geneontology.org/amigo/term/GO:1901388) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901388&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901388&list=upload_1&organism=Homo%20sapiens) | .39 | 10.18 | + | 1.75E-03 | 3.10E-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) | [78](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001817&list=upload_1&organism=Homo%20sapiens) | 36.44 | 2.14 | + | 3.10E-09 | 2.11E-07 | | [regulation of helicase activity](http://amigo.geneontology.org/amigo/term/GO:0051095) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051095&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051095&list=upload_1&organism=Homo%20sapiens) | .59 | 10.18 | + | 1.18E-04 | 3.25E-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) | [184](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050790&list=upload_1&organism=Homo%20sapiens) | 116.52 | 1.58 | + | 1.73E-09 | 1.21E-07 | | [ribosomal large subunit assembly](http://amigo.geneontology.org/amigo/term/GO:0000027) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000027&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000027&list=upload_1&organism=Homo%20sapiens) | 1.28 | 10.18 | + | 1.25E-08 | 8.07E-07 | | [ribosome assembly](http://amigo.geneontology.org/amigo/term/GO:0042255) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042255&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042255&list=upload_1&organism=Homo%20sapiens) | 3.04 | 7.55 | + | 4.42E-12 | 4.50E-10 | | [ribosome biogenesis](http://amigo.geneontology.org/amigo/term/GO:0042254) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042254&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042254&list=upload_1&organism=Homo%20sapiens) | 14.88 | 4.84 | + | 5.54E-25 | 1.93E-22 | | [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) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140694&list=upload_1&organism=Homo%20sapiens) | 15.52 | 2.90 | + | 2.23E-09 | 1.55E-07 | | [organelle assembly](http://amigo.geneontology.org/amigo/term/GO:0070925) | [803](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070925&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070925&list=upload_1&organism=Homo%20sapiens) | 39.43 | 1.52 | + | 2.24E-03 | 3.83E-02 | | [organelle organization](http://amigo.geneontology.org/amigo/term/GO:0006996) | [3026](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&reflist=1) | [207](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006996&list=upload_1&organism=Homo%20sapiens) | 148.59 | 1.39 | + | 1.28E-06 | 5.78E-05 | | [ribosomal large subunit biogenesis](http://amigo.geneontology.org/amigo/term/GO:0042273) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042273&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042273&list=upload_1&organism=Homo%20sapiens) | 3.73 | 7.23 | + | 1.42E-13 | 1.73E-11 | | [siRNA processing](http://amigo.geneontology.org/amigo/term/GO:0030422) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030422&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030422&list=upload_1&organism=Homo%20sapiens) | .39 | 10.18 | + | 1.75E-03 | 3.10E-02 | | [small regulatory ncRNA processing](http://amigo.geneontology.org/amigo/term/GO:0070918) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070918&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070918&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.82 | + | 2.84E-04 | 6.90E-03 | | [ncRNA processing](http://amigo.geneontology.org/amigo/term/GO:0034470) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034470&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034470&list=upload_1&organism=Homo%20sapiens) | 20.28 | 3.45 | + | 2.90E-17 | 4.79E-15 | | [RNA processing](http://amigo.geneontology.org/amigo/term/GO:0006396) | [868](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&reflist=1) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006396&list=upload_1&organism=Homo%20sapiens) | 42.62 | 3.19 | + | 6.97E-30 | 4.37E-27 | | [gene expression](http://amigo.geneontology.org/amigo/term/GO:0010467) | [2314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&reflist=1) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010467&list=upload_1&organism=Homo%20sapiens) | 113.63 | 2.75 | + | 8.70E-60 | 1.36E-55 | | [ncRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0034660) | [536](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034660&reflist=1) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034660&list=upload_1&organism=Homo%20sapiens) | 26.32 | 3.12 | + | 1.13E-17 | 2.03E-15 | | [negative regulation of calcium ion-dependent exocytosis](http://amigo.geneontology.org/amigo/term/GO:0045955) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045955&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045955&list=upload_1&organism=Homo%20sapiens) | .39 | 10.18 | + | 1.75E-03 | 3.10E-02 | | [maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)](http://amigo.geneontology.org/amigo/term/GO:0000463) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000463&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000463&list=upload_1&organism=Homo%20sapiens) | .74 | 9.50 | + | 4.43E-05 | 1.35E-03 | | [maturation of LSU-rRNA](http://amigo.geneontology.org/amigo/term/GO:0000470) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000470&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000470&list=upload_1&organism=Homo%20sapiens) | 1.37 | 8.00 | + | 1.12E-06 | 5.15E-05 | | [rRNA processing](http://amigo.geneontology.org/amigo/term/GO:0006364) | [223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006364&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006364&list=upload_1&organism=Homo%20sapiens) | 10.95 | 4.93 | + | 2.47E-19 | 5.11E-17 | | [rRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016072) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016072&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016072&list=upload_1&organism=Homo%20sapiens) | 12.47 | 4.81 | + | 6.86E-21 | 1.63E-18 | | [negative regulation of ubiquitin protein ligase activity](http://amigo.geneontology.org/amigo/term/GO:1904667) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904667&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904667&list=upload_1&organism=Homo%20sapiens) | .64 | 9.40 | + | 1.66E-04 | 4.39E-03 | | [negative regulation of ubiquitin-protein transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051444) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051444&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051444&list=upload_1&organism=Homo%20sapiens) | 1.13 | 5.31 | + | 1.95E-03 | 3.40E-02 | | [negative regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031397) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031397&list=upload_1&organism=Homo%20sapiens) | 4.08 | 4.17 | + | 3.69E-06 | 1.49E-04 | | [negative regulation of protein modification by small protein conjugation or removal](http://amigo.geneontology.org/amigo/term/GO:1903321) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903321&list=upload_1&organism=Homo%20sapiens) | 4.66 | 4.07 | + | 1.37E-06 | 6.14E-05 | | [negative regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031400) | [503](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031400&list=upload_1&organism=Homo%20sapiens) | 24.70 | 2.15 | + | 1.10E-06 | 5.07E-05 | | [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) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031399&list=upload_1&organism=Homo%20sapiens) | 76.75 | 1.97 | + | 1.75E-14 | 2.37E-12 | | [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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903320&list=upload_1&organism=Homo%20sapiens) | 12.42 | 3.38 | + | 1.28E-10 | 1.01E-08 | | [regulation of protein ubiquitination](http://amigo.geneontology.org/amigo/term/GO:0031396) | [211](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031396&list=upload_1&organism=Homo%20sapiens) | 10.36 | 3.09 | + | 1.30E-07 | 7.13E-06 | | [regulation of transferase activity](http://amigo.geneontology.org/amigo/term/GO:0051338) | [915](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051338&list=upload_1&organism=Homo%20sapiens) | 44.93 | 2.05 | + | 8.55E-10 | 6.24E-08 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051348&list=upload_1&organism=Homo%20sapiens) | 13.50 | 2.00 | + | 1.35E-03 | 2.51E-02 | | [negative regulation of molecular function](http://amigo.geneontology.org/amigo/term/GO:0044092) | [1150](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&reflist=1) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044092&list=upload_1&organism=Homo%20sapiens) | 56.47 | 1.65 | + | 8.27E-06 | 3.04E-04 | | [ribosomal subunit export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0000054) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000054&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000054&list=upload_1&organism=Homo%20sapiens) | .64 | 9.40 | + | 1.66E-04 | 4.39E-03 | | [ribosome localization](http://amigo.geneontology.org/amigo/term/GO:0033750) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033750&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033750&list=upload_1&organism=Homo%20sapiens) | .64 | 9.40 | + | 1.66E-04 | 4.40E-03 | | [nuclear export](http://amigo.geneontology.org/amigo/term/GO:0051168) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051168&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051168&list=upload_1&organism=Homo%20sapiens) | 6.53 | 3.06 | + | 3.18E-05 | 1.02E-03 | | [nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0006913) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006913&list=upload_1&organism=Homo%20sapiens) | 12.18 | 2.71 | + | 1.19E-06 | 5.45E-05 | | [nuclear transport](http://amigo.geneontology.org/amigo/term/GO:0051169) | [248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051169&list=upload_1&organism=Homo%20sapiens) | 12.18 | 2.71 | + | 1.19E-06 | 5.43E-05 | | [intracellular transport](http://amigo.geneontology.org/amigo/term/GO:0046907) | [1360](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046907&list=upload_1&organism=Homo%20sapiens) | 66.78 | 1.45 | + | 3.99E-04 | 9.17E-03 | | [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) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051649&list=upload_1&organism=Homo%20sapiens) | 86.03 | 1.45 | + | 5.86E-05 | 1.73E-03 | | [cellular localization](http://amigo.geneontology.org/amigo/term/GO:0051641) | [2655](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&reflist=1) | [187](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051641&list=upload_1&organism=Homo%20sapiens) | 130.37 | 1.43 | + | 8.50E-07 | 4.05E-05 | | [ribosomal small subunit assembly](http://amigo.geneontology.org/amigo/term/GO:0000028) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000028&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000028&list=upload_1&organism=Homo%20sapiens) | .98 | 9.16 | + | 4.46E-06 | 1.75E-04 | | [ribosomal small subunit biogenesis](http://amigo.geneontology.org/amigo/term/GO:0042274) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042274&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042274&list=upload_1&organism=Homo%20sapiens) | 3.88 | 6.70 | + | 1.69E-12 | 1.80E-10 | | [positive regulation of T cell tolerance induction](http://amigo.geneontology.org/amigo/term/GO:0002666) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002666&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002666&list=upload_1&organism=Homo%20sapiens) | .44 | 9.05 | + | 2.43E-03 | 4.04E-02 | | [regulation of T cell tolerance induction](http://amigo.geneontology.org/amigo/term/GO:0002664) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002664&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002664&list=upload_1&organism=Homo%20sapiens) | .64 | 7.83 | + | 1.14E-03 | 2.21E-02 | | [regulation of tolerance induction](http://amigo.geneontology.org/amigo/term/GO:0002643) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002643&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002643&list=upload_1&organism=Homo%20sapiens) | .98 | 6.11 | + | 1.06E-03 | 2.08E-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) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002682&list=upload_1&organism=Homo%20sapiens) | 74.64 | 1.78 | + | 6.38E-10 | 4.70E-08 | | [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) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051240&list=upload_1&organism=Homo%20sapiens) | 74.39 | 1.96 | + | 7.30E-14 | 9.09E-12 | | [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) | [87](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002684&list=upload_1&organism=Homo%20sapiens) | 47.48 | 1.83 | + | 2.76E-07 | 1.43E-05 | | [embryonic foregut morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048617) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048617&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048617&list=upload_1&organism=Homo%20sapiens) | .44 | 9.05 | + | 2.43E-03 | 4.03E-02 | | [digestive tract morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048546) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048546&list=upload_1&organism=Homo%20sapiens) | 2.36 | 3.82 | + | 1.24E-03 | 2.33E-02 | | [embryonic morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048598) | [591](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048598&list=upload_1&organism=Homo%20sapiens) | 29.02 | 2.00 | + | 2.70E-06 | 1.13E-04 | | [embryo development](http://amigo.geneontology.org/amigo/term/GO:0009790) | [1059](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009790&list=upload_1&organism=Homo%20sapiens) | 52.00 | 1.87 | + | 2.48E-08 | 1.50E-06 | | [progesterone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0050847) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050847&reflist=1) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050847&list=upload_1&organism=Homo%20sapiens) | .44 | 9.05 | + | 2.43E-03 | 4.03E-02 | | [formation of cytoplasmic translation initiation complex](http://amigo.geneontology.org/amigo/term/GO:0001732) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001732&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001732&list=upload_1&organism=Homo%20sapiens) | .79 | 8.91 | + | 6.11E-05 | 1.78E-03 | | [cytoplasmic translational initiation](http://amigo.geneontology.org/amigo/term/GO:0002183) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002183&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002183&list=upload_1&organism=Homo%20sapiens) | 1.67 | 5.99 | + | 2.80E-05 | 9.07E-04 | | [cytoplasmic translation](http://amigo.geneontology.org/amigo/term/GO:0002181) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002181&list=upload_1&organism=Homo%20sapiens) | 6.09 | 12.48 | + | 6.64E-49 | 5.20E-45 | | [translation](http://amigo.geneontology.org/amigo/term/GO:0006412) | [379](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006412&reflist=1) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006412&list=upload_1&organism=Homo%20sapiens) | 18.61 | 6.02 | + | 3.41E-46 | 1.34E-42 | | [peptide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0043043) | [408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043043&reflist=1) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043043&list=upload_1&organism=Homo%20sapiens) | 20.03 | 5.64 | + | 2.72E-44 | 8.53E-41 | | [peptide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006518) | [537](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006518&reflist=1) | [121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006518&list=upload_1&organism=Homo%20sapiens) | 26.37 | 4.59 | + | 1.21E-39 | 2.36E-36 | | [cellular amide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0043603) | [802](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043603&reflist=1) | [127](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043603&list=upload_1&organism=Homo%20sapiens) | 39.38 | 3.22 | + | 2.81E-28 | 1.52E-25 | | [amide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0043604) | [527](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043604&reflist=1) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043604&list=upload_1&organism=Homo%20sapiens) | 25.88 | 4.52 | + | 8.55E-38 | 1.12E-34 | | [cellular nitrogen compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0044271) | [1588](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&reflist=1) | [213](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044271&list=upload_1&organism=Homo%20sapiens) | 77.98 | 2.73 | + | 2.63E-38 | 3.75E-35 | | [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) | 120.99 | 2.07 | + | 2.05E-27 | 1.00E-24 | | [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) | 127.82 | 2.02 | + | 6.33E-27 | 2.68E-24 | | [organonitrogen compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901566) | [1333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901566&reflist=1) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901566&list=upload_1&organism=Homo%20sapiens) | 65.46 | 2.38 | + | 7.15E-22 | 1.90E-19 | | [organic substance biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901576) | [2534](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&reflist=1) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901576&list=upload_1&organism=Homo%20sapiens) | 124.43 | 2.03 | + | 8.44E-27 | 3.48E-24 | | [cellular macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0034645) | [773](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034645&reflist=1) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034645&list=upload_1&organism=Homo%20sapiens) | 37.96 | 3.24 | + | 1.48E-27 | 7.48E-25 | | [cellular macromolecule metabolic process](http://amigo.geneontology.org/amigo/term/GO:0044260) | [2518](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&reflist=1) | [258](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044260&list=upload_1&organism=Homo%20sapiens) | 123.64 | 2.09 | + | 6.69E-29 | 4.04E-26 | | [macromolecule biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0009059) | [1487](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&reflist=1) | [198](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009059&list=upload_1&organism=Homo%20sapiens) | 73.02 | 2.71 | + | 7.40E-35 | 7.25E-32 | | [translational initiation](http://amigo.geneontology.org/amigo/term/GO:0006413) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006413&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006413&list=upload_1&organism=Homo%20sapiens) | 3.44 | 6.98 | + | 5.96E-12 | 5.99E-10 | | [pre-miRNA processing](http://amigo.geneontology.org/amigo/term/GO:0031054) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031054&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031054&list=upload_1&organism=Homo%20sapiens) | .69 | 8.73 | + | 2.28E-04 | 5.67E-03 | | [miRNA processing](http://amigo.geneontology.org/amigo/term/GO:0035196) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035196&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035196&list=upload_1&organism=Homo%20sapiens) | 1.67 | 5.39 | + | 1.39E-04 | 3.77E-03 | | [negative regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902894) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902894&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902894&list=upload_1&organism=Homo%20sapiens) | 1.03 | 8.73 | + | 6.11E-06 | 2.33E-04 | | [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) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045892&list=upload_1&organism=Homo%20sapiens) | 64.96 | 1.89 | + | 7.27E-11 | 5.97E-09 | | [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) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903507&list=upload_1&organism=Homo%20sapiens) | 65.06 | 1.91 | + | 4.56E-11 | 3.90E-09 | | [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) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902679&list=upload_1&organism=Homo%20sapiens) | 65.16 | 1.90 | + | 4.77E-11 | 4.07E-09 | | [negative regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000629) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000629&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000629&list=upload_1&organism=Homo%20sapiens) | 1.08 | 8.33 | + | 8.25E-06 | 3.04E-04 | | [regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000628) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000628&list=upload_1&organism=Homo%20sapiens) | 3.63 | 5.78 | + | 2.19E-09 | 1.52E-07 | | [regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902893) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902893&list=upload_1&organism=Homo%20sapiens) | 3.09 | 6.47 | + | 1.05E-09 | 7.56E-08 | | [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) | .59 | 8.49 | + | 8.59E-04 | 1.75E-02 | | [double-strand break repair via break-induced replication](http://amigo.geneontology.org/amigo/term/GO:0000727) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000727&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000727&list=upload_1&organism=Homo%20sapiens) | .59 | 8.49 | + | 8.59E-04 | 1.74E-02 | | [double-strand break repair via homologous recombination](http://amigo.geneontology.org/amigo/term/GO:0000724) | [113](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000724&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000724&list=upload_1&organism=Homo%20sapiens) | 5.55 | 2.52 | + | 2.51E-03 | 4.15E-02 | | [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) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006974&list=upload_1&organism=Homo%20sapiens) | 37.12 | 1.72 | + | 6.49E-05 | 1.88E-03 | | [cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0033554) | [1599](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033554&list=upload_1&organism=Homo%20sapiens) | 78.52 | 1.78 | + | 1.60E-10 | 1.27E-08 | | [response to stress](http://amigo.geneontology.org/amigo/term/GO:0006950) | [3466](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&reflist=1) | [291](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006950&list=upload_1&organism=Homo%20sapiens) | 170.19 | 1.71 | + | 5.82E-20 | 1.27E-17 | | [DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0006259) | [794](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006259&list=upload_1&organism=Homo%20sapiens) | 38.99 | 1.69 | + | 9.48E-05 | 2.65E-03 | | [positive regulation of miRNA maturation](http://amigo.geneontology.org/amigo/term/GO:1903800) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903800&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903800&list=upload_1&organism=Homo%20sapiens) | .59 | 8.49 | + | 8.59E-04 | 1.74E-02 | | [positive regulation of miRNA-mediated gene silencing](http://amigo.geneontology.org/amigo/term/GO:2000637) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000637&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000637&list=upload_1&organism=Homo%20sapiens) | 1.18 | 7.64 | + | 1.45E-05 | 5.08E-04 | | [positive regulation of post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:1900370) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900370&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900370&list=upload_1&organism=Homo%20sapiens) | 1.23 | 7.33 | + | 1.89E-05 | 6.32E-04 | | [positive regulation of post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060148) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060148&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060148&list=upload_1&organism=Homo%20sapiens) | 1.23 | 7.33 | + | 1.89E-05 | 6.34E-04 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060147&list=upload_1&organism=Homo%20sapiens) | 2.21 | 6.34 | + | 4.10E-07 | 2.05E-05 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900368&list=upload_1&organism=Homo%20sapiens) | 2.16 | 6.48 | + | 3.27E-07 | 1.66E-05 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060966&list=upload_1&organism=Homo%20sapiens) | 2.26 | 7.08 | + | 1.69E-08 | 1.06E-06 | | [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) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060964&list=upload_1&organism=Homo%20sapiens) | 2.06 | 6.79 | + | 2.04E-07 | 1.09E-05 | | [regulation of miRNA maturation](http://amigo.geneontology.org/amigo/term/GO:1903798) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903798&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903798&list=upload_1&organism=Homo%20sapiens) | 1.28 | 6.27 | + | 1.37E-04 | 3.73E-03 | | [regulation of production of small RNA involved in gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0070920) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070920&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070920&list=upload_1&organism=Homo%20sapiens) | 1.33 | 6.79 | + | 3.12E-05 | 1.00E-03 | | [positive regulation by host of viral transcription](http://amigo.geneontology.org/amigo/term/GO:0043923) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043923&list=upload_1&organism=Homo%20sapiens) | .83 | 8.39 | + | 8.27E-05 | 2.34E-03 | | [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) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030174&list=upload_1&organism=Homo%20sapiens) | .74 | 8.15 | + | 3.07E-04 | 7.28E-03 | | [regulation of DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006275) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006275&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.55 | + | 8.40E-04 | 1.72E-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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051052&list=upload_1&organism=Homo%20sapiens) | 26.57 | 2.71 | + | 7.16E-13 | 8.07E-11 | | [endodermal cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0001711) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001711&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001711&list=upload_1&organism=Homo%20sapiens) | .64 | 7.83 | + | 1.14E-03 | 2.21E-02 | | [cell fate commitment](http://amigo.geneontology.org/amigo/term/GO:0045165) | [250](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045165&list=upload_1&organism=Homo%20sapiens) | 12.28 | 2.12 | + | 7.65E-04 | 1.58E-02 | | [formation of primary germ layer](http://amigo.geneontology.org/amigo/term/GO:0001704) | [120](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001704&list=upload_1&organism=Homo%20sapiens) | 5.89 | 4.58 | + | 9.70E-10 | 7.05E-08 | | [gastrulation](http://amigo.geneontology.org/amigo/term/GO:0007369) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007369&list=upload_1&organism=Homo%20sapiens) | 8.30 | 3.62 | + | 1.48E-08 | 9.37E-07 | | [endodermal cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0035987) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035987&list=upload_1&organism=Homo%20sapiens) | 2.16 | 7.87 | + | 1.66E-09 | 1.18E-07 | | [endoderm formation](http://amigo.geneontology.org/amigo/term/GO:0001706) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001706&list=upload_1&organism=Homo%20sapiens) | 2.65 | 7.54 | + | 1.12E-10 | 9.04E-09 | | [endoderm development](http://amigo.geneontology.org/amigo/term/GO:0007492) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007492&list=upload_1&organism=Homo%20sapiens) | 3.98 | 6.29 | + | 1.45E-11 | 1.37E-09 | | [tissue development](http://amigo.geneontology.org/amigo/term/GO:0009888) | [1726](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&reflist=1) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009888&list=upload_1&organism=Homo%20sapiens) | 84.75 | 1.64 | + | 2.99E-08 | 1.78E-06 | | [negative regulation of release of sequestered calcium ion into cytosol](http://amigo.geneontology.org/amigo/term/GO:0051280) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051280&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051280&list=upload_1&organism=Homo%20sapiens) | .64 | 7.83 | + | 1.14E-03 | 2.21E-02 | | [positive regulation of sequestering of calcium ion](http://amigo.geneontology.org/amigo/term/GO:0051284) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051284&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051284&list=upload_1&organism=Homo%20sapiens) | .74 | 6.79 | + | 1.91E-03 | 3.35E-02 | | [positive regulation of T cell receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0050862) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050862&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050862&list=upload_1&organism=Homo%20sapiens) | .79 | 7.64 | + | 4.05E-04 | 9.28E-03 | | [regulation of immune response](http://amigo.geneontology.org/amigo/term/GO:0050776) | [935](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&reflist=1) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050776&list=upload_1&organism=Homo%20sapiens) | 45.91 | 1.92 | + | 3.25E-08 | 1.92E-06 | | [positive regulation of antigen receptor-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0050857) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050857&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050857&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.09 | + | 2.34E-03 | 3.94E-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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050778&list=upload_1&organism=Homo%20sapiens) | 28.97 | 1.90 | + | 1.72E-05 | 5.87E-04 | | [positive regulation of phosphoprotein phosphatase activity](http://amigo.geneontology.org/amigo/term/GO:0032516) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032516&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032516&list=upload_1&organism=Homo%20sapiens) | 1.08 | 7.41 | + | 5.22E-05 | 1.56E-03 | | [positive regulation of phosphatase activity](http://amigo.geneontology.org/amigo/term/GO:0010922) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010922&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010922&list=upload_1&organism=Homo%20sapiens) | 1.77 | 5.66 | + | 4.22E-05 | 1.29E-03 | | [positive regulation of dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035306) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035306&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035306&list=upload_1&organism=Homo%20sapiens) | 3.14 | 4.14 | + | 5.43E-05 | 1.62E-03 | | [positive regulation of phosphate metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045937) | [911](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045937&list=upload_1&organism=Homo%20sapiens) | 44.73 | 2.03 | + | 1.30E-09 | 9.26E-08 | | [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) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019220&list=upload_1&organism=Homo%20sapiens) | 68.94 | 1.87 | + | 6.19E-11 | 5.19E-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) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051174&list=upload_1&organism=Homo%20sapiens) | 68.99 | 1.87 | + | 6.28E-11 | 5.24E-09 | | [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) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010562&list=upload_1&organism=Homo%20sapiens) | 44.73 | 2.03 | + | 1.30E-09 | 9.30E-08 | | [regulation of dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035303) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035303&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035303&list=upload_1&organism=Homo%20sapiens) | 6.63 | 3.02 | + | 3.84E-05 | 1.19E-03 | | [positive regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051345) | [589](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051345&list=upload_1&organism=Homo%20sapiens) | 28.92 | 1.83 | + | 5.96E-05 | 1.75E-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) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043085&list=upload_1&organism=Homo%20sapiens) | 58.63 | 1.88 | + | 1.71E-09 | 1.20E-07 | | [regulation of hydrolase activity](http://amigo.geneontology.org/amigo/term/GO:0051336) | [1020](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051336&list=upload_1&organism=Homo%20sapiens) | 50.09 | 1.62 | + | 5.14E-05 | 1.55E-03 | | [regulation of phosphatase activity](http://amigo.geneontology.org/amigo/term/GO:0010921) | [86](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010921&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010921&list=upload_1&organism=Homo%20sapiens) | 4.22 | 3.55 | + | 6.99E-05 | 2.02E-03 | | [regulation of phosphoprotein phosphatase activity](http://amigo.geneontology.org/amigo/term/GO:0043666) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043666&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043666&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.49 | + | 2.60E-05 | 8.48E-04 | | [regulation of protein dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035304) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035304&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035304&list=upload_1&organism=Homo%20sapiens) | 4.62 | 3.68 | + | 1.56E-05 | 5.38E-04 | | [positive regulation of protein dephosphorylation](http://amigo.geneontology.org/amigo/term/GO:0035307) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035307&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035307&list=upload_1&organism=Homo%20sapiens) | 2.41 | 4.57 | + | 9.31E-05 | 2.61E-03 | | [positive regulation of protein modification process](http://amigo.geneontology.org/amigo/term/GO:0031401) | [1019](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&reflist=1) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031401&list=upload_1&organism=Homo%20sapiens) | 50.04 | 2.02 | + | 2.23E-10 | 1.74E-08 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006268&list=upload_1&organism=Homo%20sapiens) | 1.08 | 7.41 | + | 5.22E-05 | 1.56E-03 | | [DNA duplex unwinding](http://amigo.geneontology.org/amigo/term/GO:0032508) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032508&list=upload_1&organism=Homo%20sapiens) | 4.52 | 3.76 | + | 1.22E-05 | 4.35E-04 | | [DNA geometric change](http://amigo.geneontology.org/amigo/term/GO:0032392) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032392&list=upload_1&organism=Homo%20sapiens) | 4.81 | 3.74 | + | 7.33E-06 | 2.72E-04 | | [DNA conformation change](http://amigo.geneontology.org/amigo/term/GO:0071103) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071103&list=upload_1&organism=Homo%20sapiens) | 5.25 | 3.62 | + | 6.34E-06 | 2.38E-04 | | [chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0051276) | [444](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051276&list=upload_1&organism=Homo%20sapiens) | 21.80 | 2.29 | + | 3.82E-07 | 1.93E-05 | | [DNA replication](http://amigo.geneontology.org/amigo/term/GO:0006260) | [205](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006260&list=upload_1&organism=Homo%20sapiens) | 10.07 | 2.28 | + | 6.70E-04 | 1.43E-02 | | [cellular response to dexamethasone stimulus](http://amigo.geneontology.org/amigo/term/GO:0071549) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071549&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071549&list=upload_1&organism=Homo%20sapiens) | 1.37 | 7.27 | + | 6.89E-06 | 2.58E-04 | | [cellular response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901655) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901655&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901655&list=upload_1&organism=Homo%20sapiens) | 5.21 | 4.03 | + | 4.43E-07 | 2.21E-05 | | [response to ketone](http://amigo.geneontology.org/amigo/term/GO:1901654) | [206](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901654&list=upload_1&organism=Homo%20sapiens) | 10.12 | 2.97 | + | 6.85E-07 | 3.31E-05 | | [response to dexamethasone](http://amigo.geneontology.org/amigo/term/GO:0071548) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071548&list=upload_1&organism=Homo%20sapiens) | 2.16 | 6.02 | + | 1.72E-06 | 7.63E-05 | | [response to glucocorticoid](http://amigo.geneontology.org/amigo/term/GO:0051384) | [143](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051384&list=upload_1&organism=Homo%20sapiens) | 7.02 | 3.70 | + | 8.83E-08 | 4.96E-06 | | [response to corticosteroid](http://amigo.geneontology.org/amigo/term/GO:0031960) | [166](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031960&list=upload_1&organism=Homo%20sapiens) | 8.15 | 3.44 | + | 1.15E-07 | 6.35E-06 | | [cellular response to glucocorticoid stimulus](http://amigo.geneontology.org/amigo/term/GO:0071385) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071385&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071385&list=upload_1&organism=Homo%20sapiens) | 2.75 | 6.55 | + | 6.06E-09 | 3.99E-07 | | [cellular response to corticosteroid stimulus](http://amigo.geneontology.org/amigo/term/GO:0071384) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071384&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071384&list=upload_1&organism=Homo%20sapiens) | 3.19 | 5.64 | + | 4.18E-08 | 2.42E-06 | | [detection of mechanical stimulus involved in sensory perception of pain](http://amigo.geneontology.org/amigo/term/GO:0050966) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050966&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050966&list=upload_1&organism=Homo%20sapiens) | .69 | 7.27 | + | 1.49E-03 | 2.71E-02 | | [detection of stimulus involved in sensory perception of pain](http://amigo.geneontology.org/amigo/term/GO:0062149) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062149&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062149&list=upload_1&organism=Homo%20sapiens) | 1.33 | 6.03 | + | 1.70E-04 | 4.48E-03 | | [sensory perception of pain](http://amigo.geneontology.org/amigo/term/GO:0019233) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019233&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019233&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.48 | + | 2.48E-04 | 6.09E-03 | | [detection of mechanical stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050974) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050974&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050974&list=upload_1&organism=Homo%20sapiens) | 1.77 | 4.53 | + | 8.84E-04 | 1.79E-02 | | [detection of mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0050982) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050982&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050982&list=upload_1&organism=Homo%20sapiens) | 2.65 | 4.15 | + | 1.96E-04 | 5.03E-03 | | [response to mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0009612) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009612&list=upload_1&organism=Homo%20sapiens) | 10.70 | 3.55 | + | 2.87E-10 | 2.20E-08 | | [response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009605) | [2469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&reflist=1) | [219](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009605&list=upload_1&organism=Homo%20sapiens) | 121.24 | 1.81 | + | 4.72E-17 | 7.56E-15 | | [response to abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009628) | [1121](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&reflist=1) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009628&list=upload_1&organism=Homo%20sapiens) | 55.05 | 2.34 | + | 1.14E-17 | 2.00E-15 | | [detection of external stimulus](http://amigo.geneontology.org/amigo/term/GO:0009581) | [137](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009581&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009581&list=upload_1&organism=Homo%20sapiens) | 6.73 | 2.68 | + | 3.51E-04 | 8.23E-03 | | [detection of abiotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0009582) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009582&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009582&list=upload_1&organism=Homo%20sapiens) | 6.83 | 2.64 | + | 4.11E-04 | 9.33E-03 | | [negative regulation of miRNA-mediated gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060965) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060965&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060965&list=upload_1&organism=Homo%20sapiens) | .98 | 7.13 | + | 1.88E-04 | 4.84E-03 | | [negative regulation of post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:1900369) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900369&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900369&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.79 | + | 2.40E-04 | 5.95E-03 | | [negative regulation of post-transcriptional gene silencing](http://amigo.geneontology.org/amigo/term/GO:0060149) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060149&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060149&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.79 | + | 2.40E-04 | 5.97E-03 | | [negative regulation of gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0060967) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060967&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060967&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.79 | + | 2.40E-04 | 5.94E-03 | | [telomere maintenance via telomerase](http://amigo.geneontology.org/amigo/term/GO:0007004) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007004&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007004&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.79 | + | 2.40E-04 | 5.96E-03 | | [RNA-templated DNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0006278) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006278&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006278&list=upload_1&organism=Homo%20sapiens) | 1.67 | 4.19 | + | 2.69E-03 | 4.38E-02 | | [nucleobase-containing compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0034654) | [1007](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&reflist=1) | [95](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034654&list=upload_1&organism=Homo%20sapiens) | 49.45 | 1.92 | + | 7.50E-09 | 4.90E-07 | | [heterocycle biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0018130) | [1079](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018130&list=upload_1&organism=Homo%20sapiens) | 52.98 | 1.87 | + | 1.44E-08 | 9.15E-07 | | [organic cyclic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:1901362) | [1216](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901362&list=upload_1&organism=Homo%20sapiens) | 59.71 | 1.79 | + | 2.66E-08 | 1.60E-06 | | [aromatic compound biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0019438) | [1089](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&reflist=1) | [99](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019438&list=upload_1&organism=Homo%20sapiens) | 53.47 | 1.85 | + | 2.50E-08 | 1.51E-06 | | [telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:0010833) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010833&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010833&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.09 | + | 1.03E-03 | 2.02E-02 | | [telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0000723) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000723&list=upload_1&organism=Homo%20sapiens) | 4.62 | 3.47 | + | 5.25E-05 | 1.57E-03 | | [telomere organization](http://amigo.geneontology.org/amigo/term/GO:0032200) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032200&list=upload_1&organism=Homo%20sapiens) | 5.06 | 3.16 | + | 1.37E-04 | 3.73E-03 | | [hepatocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0070365) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070365&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070365&list=upload_1&organism=Homo%20sapiens) | .74 | 6.79 | + | 1.91E-03 | 3.35E-02 | | [epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030855) | [620](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030855&list=upload_1&organism=Homo%20sapiens) | 30.44 | 1.61 | + | 2.02E-03 | 3.49E-02 | | [epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060429) | [1072](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060429&list=upload_1&organism=Homo%20sapiens) | 52.64 | 1.54 | + | 2.44E-04 | 6.02E-03 | | [liver development](http://amigo.geneontology.org/amigo/term/GO:0001889) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001889&list=upload_1&organism=Homo%20sapiens) | 6.43 | 3.42 | + | 2.72E-06 | 1.14E-04 | | [gland development](http://amigo.geneontology.org/amigo/term/GO:0048732) | [422](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048732&list=upload_1&organism=Homo%20sapiens) | 20.72 | 2.41 | + | 1.01E-07 | 5.64E-06 | | [hepaticobiliary system development](http://amigo.geneontology.org/amigo/term/GO:0061008) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061008&list=upload_1&organism=Homo%20sapiens) | 6.58 | 3.34 | + | 3.77E-06 | 1.51E-04 | | [regulation of protein localization to chromosome, telomeric region](http://amigo.geneontology.org/amigo/term/GO:1904814) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904814&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904814&list=upload_1&organism=Homo%20sapiens) | .74 | 6.79 | + | 1.91E-03 | 3.35E-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) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032880&list=upload_1&organism=Homo%20sapiens) | 41.74 | 1.89 | + | 2.76E-07 | 1.42E-05 | | [regulation of cellular localization](http://amigo.geneontology.org/amigo/term/GO:0060341) | [962](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&reflist=1) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060341&list=upload_1&organism=Homo%20sapiens) | 47.24 | 1.86 | + | 1.14E-07 | 6.33E-06 | | [negative regulation of translational initiation](http://amigo.geneontology.org/amigo/term/GO:0045947) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045947&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045947&list=upload_1&organism=Homo%20sapiens) | 1.03 | 6.79 | + | 2.40E-04 | 5.93E-03 | | [negative regulation of translation](http://amigo.geneontology.org/amigo/term/GO:0017148) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017148&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0017148&list=upload_1&organism=Homo%20sapiens) | 8.35 | 3.71 | + | 4.90E-09 | 3.26E-07 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034249&list=upload_1&organism=Homo%20sapiens) | 9.43 | 3.39 | + | 1.86E-08 | 1.16E-06 | | [regulation of translational initiation](http://amigo.geneontology.org/amigo/term/GO:0006446) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006446&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006446&list=upload_1&organism=Homo%20sapiens) | 4.12 | 4.12 | + | 4.24E-06 | 1.67E-04 | | [negative regulation of mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0048025) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048025&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048025&list=upload_1&organism=Homo%20sapiens) | 1.18 | 6.79 | + | 8.63E-05 | 2.43E-03 | | [negative regulation of mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0050686) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050686&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050686&list=upload_1&organism=Homo%20sapiens) | 1.28 | 6.27 | + | 1.37E-04 | 3.73E-03 | | [regulation of mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0050684) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050684&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050684&list=upload_1&organism=Homo%20sapiens) | 6.87 | 3.78 | + | 6.10E-08 | 3.50E-06 | | [regulation of mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0048024) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048024&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048024&list=upload_1&organism=Homo%20sapiens) | 5.40 | 4.07 | + | 2.06E-07 | 1.09E-05 | | [regulation of RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0043484) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043484&list=upload_1&organism=Homo%20sapiens) | 8.89 | 3.49 | + | 1.78E-08 | 1.11E-06 | | [negative regulation of RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0033119) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033119&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033119&list=upload_1&organism=Homo%20sapiens) | 1.42 | 7.02 | + | 8.87E-06 | 3.22E-04 | | [positive regulation of interferon-alpha production](http://amigo.geneontology.org/amigo/term/GO:0032727) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032727&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032727&list=upload_1&organism=Homo%20sapiens) | 1.23 | 6.52 | + | 1.09E-04 | 3.03E-03 | | [positive regulation of type I interferon production](http://amigo.geneontology.org/amigo/term/GO:0032481) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032481&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032481&list=upload_1&organism=Homo%20sapiens) | 3.09 | 3.88 | + | 1.77E-04 | 4.62E-03 | | [regulation of type I interferon production](http://amigo.geneontology.org/amigo/term/GO:0032479) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032479&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032479&list=upload_1&organism=Homo%20sapiens) | 5.06 | 2.97 | + | 4.06E-04 | 9.30E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001819&list=upload_1&organism=Homo%20sapiens) | 23.62 | 2.20 | + | 6.33E-07 | 3.08E-05 | | [regulation of interferon-alpha production](http://amigo.geneontology.org/amigo/term/GO:0032647) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032647&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032647&list=upload_1&organism=Homo%20sapiens) | 1.52 | 5.91 | + | 7.66E-05 | 2.18E-03 | | [positive regulation of miRNA transcription](http://amigo.geneontology.org/amigo/term/GO:1902895) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902895&list=upload_1&organism=Homo%20sapiens) | 2.31 | 6.50 | + | 1.20E-07 | 6.65E-06 | | [positive regulation of miRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000630) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000630&list=upload_1&organism=Homo%20sapiens) | 2.60 | 6.15 | + | 8.70E-08 | 4.91E-06 | | [antiviral innate immune response](http://amigo.geneontology.org/amigo/term/GO:0140374) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140374&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140374&list=upload_1&organism=Homo%20sapiens) | 1.08 | 6.48 | + | 3.04E-04 | 7.27E-03 | | [innate immune response](http://amigo.geneontology.org/amigo/term/GO:0045087) | [832](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&reflist=1) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045087&list=upload_1&organism=Homo%20sapiens) | 40.85 | 1.86 | + | 1.11E-06 | 5.12E-05 | | [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) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098542&list=upload_1&organism=Homo%20sapiens) | 52.44 | 1.79 | + | 2.09E-07 | 1.11E-05 | | [response to other organism](http://amigo.geneontology.org/amigo/term/GO:0051707) | [1429](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&reflist=1) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051707&list=upload_1&organism=Homo%20sapiens) | 70.17 | 1.87 | + | 3.97E-11 | 3.42E-09 | | [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) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043207&list=upload_1&organism=Homo%20sapiens) | 70.32 | 1.88 | + | 2.60E-11 | 2.38E-09 | | [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) | 72.58 | 1.87 | + | 1.40E-11 | 1.33E-09 | | [defense response](http://amigo.geneontology.org/amigo/term/GO:0006952) | [1478](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&reflist=1) | [125](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006952&list=upload_1&organism=Homo%20sapiens) | 72.58 | 1.72 | + | 1.22E-08 | 7.90E-07 | | [immune response](http://amigo.geneontology.org/amigo/term/GO:0006955) | [1621](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&reflist=1) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006955&list=upload_1&organism=Homo%20sapiens) | 79.60 | 1.53 | + | 6.33E-06 | 2.39E-04 | | [defense response to virus](http://amigo.geneontology.org/amigo/term/GO:0051607) | [253](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051607&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051607&list=upload_1&organism=Homo%20sapiens) | 12.42 | 2.50 | + | 1.23E-05 | 4.38E-04 | | [response to virus](http://amigo.geneontology.org/amigo/term/GO:0009615) | [357](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009615&list=upload_1&organism=Homo%20sapiens) | 17.53 | 3.14 | + | 2.40E-12 | 2.47E-10 | | [defense response to symbiont](http://amigo.geneontology.org/amigo/term/GO:0140546) | [254](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140546&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0140546&list=upload_1&organism=Homo%20sapiens) | 12.47 | 2.49 | + | 1.31E-05 | 4.62E-04 | | [intrinsic apoptotic signaling pathway in response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0008631) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008631&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008631&list=upload_1&organism=Homo%20sapiens) | .93 | 6.43 | + | 8.52E-04 | 1.74E-02 | | [cell death in response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:0036473) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036473&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036473&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.49E-02 | | [cell death](http://amigo.geneontology.org/amigo/term/GO:0008219) | [1108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008219&list=upload_1&organism=Homo%20sapiens) | 54.41 | 2.02 | + | 2.65E-11 | 2.41E-09 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034599&list=upload_1&organism=Homo%20sapiens) | 10.90 | 2.48 | + | 5.15E-05 | 1.54E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0062197&list=upload_1&organism=Homo%20sapiens) | 13.41 | 2.46 | + | 8.02E-06 | 2.97E-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) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006979&list=upload_1&organism=Homo%20sapiens) | 18.02 | 2.33 | + | 2.25E-06 | 9.76E-05 | | [intrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097193) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097193&list=upload_1&organism=Homo%20sapiens) | 8.00 | 3.12 | + | 2.52E-06 | 1.07E-04 | | [apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0097190) | [316](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097190&list=upload_1&organism=Homo%20sapiens) | 15.52 | 2.45 | + | 2.48E-06 | 1.06E-04 | | [apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0006915) | [1033](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&reflist=1) | [102](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006915&list=upload_1&organism=Homo%20sapiens) | 50.72 | 2.01 | + | 1.89E-10 | 1.49E-08 | | [programmed cell death](http://amigo.geneontology.org/amigo/term/GO:0012501) | [1074](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0012501&list=upload_1&organism=Homo%20sapiens) | 52.74 | 2.03 | + | 3.81E-11 | 3.30E-09 | | [intracellular signal transduction](http://amigo.geneontology.org/amigo/term/GO:0035556) | [1511](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&reflist=1) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035556&list=upload_1&organism=Homo%20sapiens) | 74.20 | 1.91 | + | 1.07E-12 | 1.18E-10 | | [negative regulation of blood vessel endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0043537) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043537&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043537&list=upload_1&organism=Homo%20sapiens) | 1.72 | 6.40 | + | 6.60E-06 | 2.48E-04 | | [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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043535&list=upload_1&organism=Homo%20sapiens) | 4.47 | 3.58 | + | 3.72E-05 | 1.16E-03 | | [regulation of endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010594) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010594&list=upload_1&organism=Homo%20sapiens) | 8.30 | 2.41 | + | 6.89E-04 | 1.46E-02 | | [regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010632) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010632&list=upload_1&organism=Homo%20sapiens) | 11.24 | 2.49 | + | 3.45E-05 | 1.09E-03 | | [regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030334) | [929](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030334&list=upload_1&organism=Homo%20sapiens) | 45.62 | 1.58 | + | 2.94E-04 | 7.06E-03 | | [regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000145) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000145&list=upload_1&organism=Homo%20sapiens) | 48.56 | 1.48 | + | 1.66E-03 | 2.98E-02 | | [regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040012) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&reflist=1) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040012&list=upload_1&organism=Homo%20sapiens) | 50.77 | 1.46 | + | 2.09E-03 | 3.59E-02 | | [negative regulation of endothelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010596) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010596&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010596&list=upload_1&organism=Homo%20sapiens) | 2.60 | 4.23 | + | 1.70E-04 | 4.48E-03 | | [negative regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010633) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010633&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010633&list=upload_1&organism=Homo%20sapiens) | 3.34 | 3.29 | + | 1.09E-03 | 2.13E-02 | | [organ induction](http://amigo.geneontology.org/amigo/term/GO:0001759) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001759&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001759&list=upload_1&organism=Homo%20sapiens) | .79 | 6.36 | + | 2.42E-03 | 4.04E-02 | | [regulation of anatomical structure morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0022603) | [924](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022603&list=upload_1&organism=Homo%20sapiens) | 45.37 | 1.74 | + | 5.41E-06 | 2.08E-04 | | [regulation of developmental process](http://amigo.geneontology.org/amigo/term/GO:0050793) | [2489](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&reflist=1) | [199](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050793&list=upload_1&organism=Homo%20sapiens) | 122.22 | 1.63 | + | 2.30E-11 | 2.13E-09 | | [positive regulation of animal organ morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0110110) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110110&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0110110&list=upload_1&organism=Homo%20sapiens) | 1.57 | 4.45 | + | 1.99E-03 | 3.46E-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) | [124](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051094&list=upload_1&organism=Homo%20sapiens) | 65.75 | 1.89 | + | 8.70E-11 | 7.07E-09 | | [positive regulation of cardiocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:1905209) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905209&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905209&list=upload_1&organism=Homo%20sapiens) | .79 | 6.36 | + | 2.42E-03 | 4.03E-02 | | [regulation of cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045595) | [1581](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&reflist=1) | [140](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045595&list=upload_1&organism=Homo%20sapiens) | 77.63 | 1.80 | + | 8.48E-11 | 6.92E-09 | | [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) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045597&list=upload_1&organism=Homo%20sapiens) | 43.41 | 2.14 | + | 5.96E-11 | 5.02E-09 | | [branch elongation of an epithelium](http://amigo.geneontology.org/amigo/term/GO:0060602) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060602&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060602&list=upload_1&organism=Homo%20sapiens) | .79 | 6.36 | + | 2.42E-03 | 4.03E-02 | | [tissue morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0048729) | [568](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048729&list=upload_1&organism=Homo%20sapiens) | 27.89 | 1.79 | + | 2.07E-04 | 5.23E-03 | | [developmental growth involved in morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060560) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060560&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060560&list=upload_1&organism=Homo%20sapiens) | 6.43 | 2.49 | + | 2.32E-03 | 3.93E-02 | | [developmental growth](http://amigo.geneontology.org/amigo/term/GO:0048589) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048589&list=upload_1&organism=Homo%20sapiens) | 20.28 | 1.97 | + | 1.14E-04 | 3.14E-03 | | [growth](http://amigo.geneontology.org/amigo/term/GO:0040007) | [413](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040007&list=upload_1&organism=Homo%20sapiens) | 20.28 | 1.97 | + | 1.14E-04 | 3.15E-03 | | [positive regulation of leukocyte adhesion to vascular endothelial cell](http://amigo.geneontology.org/amigo/term/GO:1904996) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904996&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904996&list=upload_1&organism=Homo%20sapiens) | 1.13 | 6.20 | + | 3.81E-04 | 8.87E-03 | | [positive regulation of leukocyte cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:1903039) | [276](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903039&list=upload_1&organism=Homo%20sapiens) | 13.55 | 2.21 | + | 1.65E-04 | 4.38E-03 | | [regulation of cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0022407) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022407&list=upload_1&organism=Homo%20sapiens) | 23.77 | 1.73 | + | 1.54E-03 | 2.78E-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) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030155&list=upload_1&organism=Homo%20sapiens) | 38.74 | 1.76 | + | 2.18E-05 | 7.22E-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) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022409&list=upload_1&organism=Homo%20sapiens) | 15.91 | 2.07 | + | 2.00E-04 | 5.10E-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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045785&list=upload_1&organism=Homo%20sapiens) | 23.96 | 2.17 | + | 8.36E-07 | 4.00E-05 | | [regulation of leukocyte adhesion to vascular endothelial cell](http://amigo.geneontology.org/amigo/term/GO:1904994) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904994&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904994&list=upload_1&organism=Homo%20sapiens) | 1.47 | 4.75 | + | 1.45E-03 | 2.65E-02 | | [SRP-dependent cotranslational protein targeting to membrane](http://amigo.geneontology.org/amigo/term/GO:0006614) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006614&reflist=1) | [5](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006614&list=upload_1&organism=Homo%20sapiens) | .83 | 5.99 | + | 3.01E-03 | 4.79E-02 | | [intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0006886) | [682](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006886&list=upload_1&organism=Homo%20sapiens) | 33.49 | 1.58 | + | 1.79E-03 | 3.16E-02 | | [protein localization](http://amigo.geneontology.org/amigo/term/GO:0008104) | [1919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&reflist=1) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008104&list=upload_1&organism=Homo%20sapiens) | 94.23 | 1.44 | + | 2.88E-05 | 9.30E-04 | | [cellular macromolecule localization](http://amigo.geneontology.org/amigo/term/GO:0070727) | [1925](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&reflist=1) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070727&list=upload_1&organism=Homo%20sapiens) | 94.52 | 1.44 | + | 3.68E-05 | 1.15E-03 | | [protein localization to organelle](http://amigo.geneontology.org/amigo/term/GO:0033365) | [694](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033365&list=upload_1&organism=Homo%20sapiens) | 34.08 | 1.79 | + | 3.25E-05 | 1.03E-03 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072594&list=upload_1&organism=Homo%20sapiens) | 16.40 | 2.07 | + | 1.56E-04 | 4.16E-03 | | [cotranslational protein targeting to membrane](http://amigo.geneontology.org/amigo/term/GO:0006613) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006613&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006613&list=upload_1&organism=Homo%20sapiens) | 1.08 | 5.55 | + | 1.61E-03 | 2.90E-02 | | [positive regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051973) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051973&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051973&list=upload_1&organism=Homo%20sapiens) | 1.67 | 5.99 | + | 2.80E-05 | 9.05E-04 | | [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) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000573&list=upload_1&organism=Homo%20sapiens) | 3.68 | 4.89 | + | 2.62E-07 | 1.36E-05 | | [positive regulation of DNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0051054) | [305](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051054&list=upload_1&organism=Homo%20sapiens) | 14.98 | 3.20 | + | 3.17E-11 | 2.82E-09 | | [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) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000278&list=upload_1&organism=Homo%20sapiens) | 6.14 | 4.07 | + | 3.10E-08 | 1.83E-06 | | [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) | 28.97 | 2.24 | + | 1.48E-08 | 9.37E-07 | | [regulation of telomerase activity](http://amigo.geneontology.org/amigo/term/GO:0051972) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051972&list=upload_1&organism=Homo%20sapiens) | 2.46 | 6.11 | + | 2.35E-07 | 1.24E-05 | | [rRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0009303) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009303&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009303&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.94 | + | 4.72E-04 | 1.05E-02 | | [ncRNA transcription](http://amigo.geneontology.org/amigo/term/GO:0098781) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098781&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098781&list=upload_1&organism=Homo%20sapiens) | 2.06 | 3.88 | + | 2.09E-03 | 3.60E-02 | | [DNA-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0006351) | [613](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006351&list=upload_1&organism=Homo%20sapiens) | 30.10 | 2.19 | + | 1.81E-08 | 1.13E-06 | | [nucleic acid-templated transcription](http://amigo.geneontology.org/amigo/term/GO:0097659) | [614](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097659&list=upload_1&organism=Homo%20sapiens) | 30.15 | 2.19 | + | 2.82E-08 | 1.69E-06 | | [RNA biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0032774) | [624](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032774&list=upload_1&organism=Homo%20sapiens) | 30.64 | 2.15 | + | 3.74E-08 | 2.19E-06 | | [protein-DNA complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032986) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032986&list=upload_1&organism=Homo%20sapiens) | 1.03 | 5.82 | + | 1.32E-03 | 2.47E-02 | | [protein-DNA complex subunit organization](http://amigo.geneontology.org/amigo/term/GO:0071824) | [233](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071824&list=upload_1&organism=Homo%20sapiens) | 11.44 | 2.01 | + | 2.61E-03 | 4.29E-02 | | [protein-containing complex disassembly](http://amigo.geneontology.org/amigo/term/GO:0032984) | [134](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032984&list=upload_1&organism=Homo%20sapiens) | 6.58 | 2.74 | + | 2.76E-04 | 6.72E-03 | | [cellular component disassembly](http://amigo.geneontology.org/amigo/term/GO:0022411) | [318](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022411&list=upload_1&organism=Homo%20sapiens) | 15.62 | 1.99 | + | 7.34E-04 | 1.54E-02 | | [cytoplasmic pattern recognition receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002753) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002753&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002753&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.82 | + | 2.10E-04 | 5.28E-03 | | [immune response-regulating signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0002764) | [397](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002764&list=upload_1&organism=Homo%20sapiens) | 19.49 | 1.85 | + | 7.98E-04 | 1.65E-02 | | [maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)](http://amigo.geneontology.org/amigo/term/GO:0000462) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000462&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000462&list=upload_1&organism=Homo%20sapiens) | 1.92 | 5.74 | + | 1.56E-05 | 5.39E-04 | | [maturation of SSU-rRNA](http://amigo.geneontology.org/amigo/term/GO:0030490) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030490&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030490&list=upload_1&organism=Homo%20sapiens) | 2.70 | 5.18 | + | 3.08E-06 | 1.28E-04 | | [regulation of protein sumoylation](http://amigo.geneontology.org/amigo/term/GO:0033233) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033233&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033233&list=upload_1&organism=Homo%20sapiens) | 1.23 | 5.70 | + | 5.80E-04 | 1.26E-02 | | [heterotypic cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0034113) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034113&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034113&list=upload_1&organism=Homo%20sapiens) | 1.77 | 5.66 | + | 4.22E-05 | 1.29E-03 | | [cell-cell adhesion](http://amigo.geneontology.org/amigo/term/GO:0098609) | [543](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098609&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098609&list=upload_1&organism=Homo%20sapiens) | 26.66 | 1.95 | + | 1.78E-05 | 6.01E-04 | | [regulation of nuclease activity](http://amigo.geneontology.org/amigo/term/GO:0032069) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032069&list=upload_1&organism=Homo%20sapiens) | 1.08 | 5.55 | + | 1.61E-03 | 2.90E-02 | | [positive regulation of protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0042307) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042307&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042307&list=upload_1&organism=Homo%20sapiens) | 2.06 | 5.33 | + | 2.79E-05 | 9.07E-04 | | [positive regulation of nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0046824) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046824&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046824&list=upload_1&organism=Homo%20sapiens) | 3.14 | 5.41 | + | 1.64E-07 | 8.89E-06 | | [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) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032388&list=upload_1&organism=Homo%20sapiens) | 9.97 | 2.71 | + | 1.10E-05 | 3.94E-04 | | [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) | 16.79 | 2.14 | + | 6.09E-05 | 1.78E-03 | | [positive regulation of transport](http://amigo.geneontology.org/amigo/term/GO:0051050) | [919](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051050&list=upload_1&organism=Homo%20sapiens) | 45.13 | 1.62 | + | 1.47E-04 | 3.96E-03 | | [regulation of nucleocytoplasmic transport](http://amigo.geneontology.org/amigo/term/GO:0046822) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046822&list=upload_1&organism=Homo%20sapiens) | 5.50 | 4.55 | + | 4.63E-09 | 3.09E-07 | | [positive regulation of intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0090316) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090316&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090316&list=upload_1&organism=Homo%20sapiens) | 7.86 | 3.05 | + | 5.57E-06 | 2.14E-04 | | [positive regulation of protein transport](http://amigo.geneontology.org/amigo/term/GO:0051222) | [304](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051222&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051222&list=upload_1&organism=Homo%20sapiens) | 14.93 | 2.28 | + | 3.73E-05 | 1.16E-03 | | [regulation of protein transport](http://amigo.geneontology.org/amigo/term/GO:0051223) | [502](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051223&list=upload_1&organism=Homo%20sapiens) | 24.65 | 1.95 | + | 3.47E-05 | 1.09E-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) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070201&list=upload_1&organism=Homo%20sapiens) | 25.88 | 2.09 | + | 1.91E-06 | 8.43E-05 | | [positive regulation of establishment of protein localization](http://amigo.geneontology.org/amigo/term/GO:1904951) | [320](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904951&list=upload_1&organism=Homo%20sapiens) | 15.71 | 2.42 | + | 2.92E-06 | 1.22E-04 | | [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) | 22.69 | 2.12 | + | 5.64E-06 | 2.16E-04 | | [regulation of intracellular protein transport](http://amigo.geneontology.org/amigo/term/GO:0033157) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033157&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033157&list=upload_1&organism=Homo%20sapiens) | 11.34 | 2.56 | + | 1.77E-05 | 6.01E-04 | | [regulation of protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0042306) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042306&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042306&list=upload_1&organism=Homo%20sapiens) | 3.04 | 4.60 | + | 1.01E-05 | 3.65E-04 | | [regulation of protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:1900180) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900180&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900180&list=upload_1&organism=Homo%20sapiens) | 6.92 | 3.61 | + | 2.37E-07 | 1.24E-05 | | [positive regulation of protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:1900182) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900182&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900182&list=upload_1&organism=Homo%20sapiens) | 4.37 | 3.43 | + | 9.84E-05 | 2.75E-03 | | [response to interferon-alpha](http://amigo.geneontology.org/amigo/term/GO:0035455) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035455&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035455&list=upload_1&organism=Homo%20sapiens) | 1.13 | 5.31 | + | 1.95E-03 | 3.39E-02 | | [response to cytokine](http://amigo.geneontology.org/amigo/term/GO:0034097) | [808](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&reflist=1) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034097&list=upload_1&organism=Homo%20sapiens) | 39.68 | 2.32 | + | 1.39E-12 | 1.51E-10 | | [positive regulation of DNA binding](http://amigo.geneontology.org/amigo/term/GO:0043388) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043388&list=upload_1&organism=Homo%20sapiens) | 2.85 | 5.27 | + | 1.16E-06 | 5.32E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051101&list=upload_1&organism=Homo%20sapiens) | 6.09 | 3.45 | + | 4.05E-06 | 1.61E-04 | | [regulation of glial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0060251) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060251&list=upload_1&organism=Homo%20sapiens) | 1.72 | 5.24 | + | 1.68E-04 | 4.42E-03 | | [regulation of cell population proliferation](http://amigo.geneontology.org/amigo/term/GO:0042127) | [1674](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&reflist=1) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042127&list=upload_1&organism=Homo%20sapiens) | 82.20 | 1.81 | + | 1.12E-11 | 1.08E-09 | | [translational elongation](http://amigo.geneontology.org/amigo/term/GO:0006414) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006414&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006414&list=upload_1&organism=Homo%20sapiens) | 2.16 | 5.09 | + | 4.03E-05 | 1.24E-03 | | [regulation of osteoblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0033688) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033688&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033688&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.09 | + | 1.03E-03 | 2.03E-02 | | [positive regulation of stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:2000738) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000738&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000738&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.09 | + | 2.34E-03 | 3.95E-02 | | [regulation of stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:2000736) | [82](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000736&list=upload_1&organism=Homo%20sapiens) | 4.03 | 4.22 | + | 3.20E-06 | 1.33E-04 | | [negative regulation of stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:2000737) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000737&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000737&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.09 | + | 1.03E-03 | 2.03E-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) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045596&list=upload_1&organism=Homo%20sapiens) | 33.19 | 1.78 | + | 5.52E-05 | 1.63E-03 | | [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) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051093&list=upload_1&organism=Homo%20sapiens) | 45.32 | 1.59 | + | 2.79E-04 | 6.80E-03 | | [T cell lineage commitment](http://amigo.geneontology.org/amigo/term/GO:0002360) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002360&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002360&list=upload_1&organism=Homo%20sapiens) | 1.18 | 5.09 | + | 2.34E-03 | 3.94E-02 | | [T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0030217) | [169](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030217&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030217&list=upload_1&organism=Homo%20sapiens) | 8.30 | 2.65 | + | 9.23E-05 | 2.59E-03 | | [T cell activation](http://amigo.geneontology.org/amigo/term/GO:0042110) | [300](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042110&list=upload_1&organism=Homo%20sapiens) | 14.73 | 2.17 | + | 1.12E-04 | 3.08E-03 | | [lymphocyte activation](http://amigo.geneontology.org/amigo/term/GO:0046649) | [465](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046649&list=upload_1&organism=Homo%20sapiens) | 22.83 | 2.19 | + | 1.24E-06 | 5.64E-05 | | [lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0030098) | [280](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030098&list=upload_1&organism=Homo%20sapiens) | 13.75 | 2.40 | + | 1.68E-05 | 5.77E-04 | | [transcription by RNA polymerase I](http://amigo.geneontology.org/amigo/term/GO:0006360) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006360&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006360&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.09 | + | 1.03E-03 | 2.03E-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) | 1.57 | 5.09 | + | 4.53E-04 | 1.01E-02 | | [positive regulation of viral process](http://amigo.geneontology.org/amigo/term/GO:0048524) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048524&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048524&list=upload_1&organism=Homo%20sapiens) | 3.19 | 4.07 | + | 6.24E-05 | 1.82E-03 | | [regulation of viral process](http://amigo.geneontology.org/amigo/term/GO:0050792) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050792&list=upload_1&organism=Homo%20sapiens) | 8.05 | 2.86 | + | 2.28E-05 | 7.50E-04 | | [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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045069&list=upload_1&organism=Homo%20sapiens) | 4.27 | 3.51 | + | 7.85E-05 | 2.23E-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) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903900&list=upload_1&organism=Homo%20sapiens) | 6.97 | 2.72 | + | 1.97E-04 | 5.04E-03 | | [positive regulation of epithelial to mesenchymal transition](http://amigo.geneontology.org/amigo/term/GO:0010718) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010718&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010718&list=upload_1&organism=Homo%20sapiens) | 2.55 | 5.09 | + | 8.16E-06 | 3.01E-04 | | [regulation of epithelial to mesenchymal transition](http://amigo.geneontology.org/amigo/term/GO:0010717) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010717&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010717&list=upload_1&organism=Homo%20sapiens) | 4.76 | 3.36 | + | 7.32E-05 | 2.09E-03 | | [exploration behavior](http://amigo.geneontology.org/amigo/term/GO:0035640) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035640&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035640&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.92 | + | 1.22E-03 | 2.32E-02 | | [positive regulation of peptidyl-threonine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0010800) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010800&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010800&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.92 | + | 1.22E-03 | 2.31E-02 | | [regulation of protein phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0001932) | [1105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&reflist=1) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001932&list=upload_1&organism=Homo%20sapiens) | 54.26 | 1.81 | + | 7.18E-08 | 4.08E-06 | | [regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042325) | [1248](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&reflist=1) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042325&list=upload_1&organism=Homo%20sapiens) | 61.28 | 1.86 | + | 1.10E-09 | 7.88E-08 | | [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) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001934&list=upload_1&organism=Homo%20sapiens) | 36.73 | 1.99 | + | 1.28E-07 | 7.06E-06 | | [positive regulation of phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0042327) | [826](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&reflist=1) | [81](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042327&list=upload_1&organism=Homo%20sapiens) | 40.56 | 2.00 | + | 2.06E-08 | 1.27E-06 | | [positive regulation of alpha-beta T cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0046641) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046641&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046641&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.92 | + | 1.22E-03 | 2.31E-02 | | [regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002694) | [684](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002694&list=upload_1&organism=Homo%20sapiens) | 33.59 | 1.58 | + | 1.84E-03 | 3.23E-02 | | [regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050865) | [741](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&reflist=1) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050865&list=upload_1&organism=Homo%20sapiens) | 36.39 | 1.62 | + | 5.95E-04 | 1.29E-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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050870&list=upload_1&organism=Homo%20sapiens) | 12.42 | 2.09 | + | 8.47E-04 | 1.73E-02 | | [positive regulation of leukocyte activation](http://amigo.geneontology.org/amigo/term/GO:0002696) | [469](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&reflist=1) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002696&list=upload_1&organism=Homo%20sapiens) | 23.03 | 1.78 | + | 8.87E-04 | 1.79E-02 | | [positive regulation of cell activation](http://amigo.geneontology.org/amigo/term/GO:0050867) | [486](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050867&list=upload_1&organism=Homo%20sapiens) | 23.86 | 1.76 | + | 7.82E-04 | 1.62E-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) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008284&list=upload_1&organism=Homo%20sapiens) | 46.60 | 1.82 | + | 4.83E-07 | 2.39E-05 | | [positive regulation of vascular endothelial growth factor production](http://amigo.geneontology.org/amigo/term/GO:0010575) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010575&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010575&list=upload_1&organism=Homo%20sapiens) | 1.42 | 4.92 | + | 1.22E-03 | 2.31E-02 | | [regulation of vascular endothelial growth factor production](http://amigo.geneontology.org/amigo/term/GO:0010574) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010574&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010574&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.32 | + | 2.32E-03 | 3.92E-02 | | [lung epithelial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060487) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060487&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.50E-02 | | [lung cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0060479) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060479&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.49E-02 | | [lung development](http://amigo.geneontology.org/amigo/term/GO:0030324) | [182](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030324&list=upload_1&organism=Homo%20sapiens) | 8.94 | 2.57 | + | 1.48E-04 | 3.99E-03 | | [respiratory tube development](http://amigo.geneontology.org/amigo/term/GO:0030323) | [186](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030323&list=upload_1&organism=Homo%20sapiens) | 9.13 | 2.52 | + | 1.72E-04 | 4.50E-03 | | [lung epithelium development](http://amigo.geneontology.org/amigo/term/GO:0060428) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060428&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060428&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.03E-02 | | [maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)](http://amigo.geneontology.org/amigo/term/GO:0000466) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000466&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000466&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.48E-02 | | [maturation of 5.8S rRNA](http://amigo.geneontology.org/amigo/term/GO:0000460) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000460&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000460&list=upload_1&organism=Homo%20sapiens) | 1.77 | 4.53 | + | 8.84E-04 | 1.78E-02 | | [programmed necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0097300) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097300&reflist=1) | [6](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0097300&list=upload_1&organism=Homo%20sapiens) | 1.23 | 4.89 | + | 2.79E-03 | 4.48E-02 | | [necrotic cell death](http://amigo.geneontology.org/amigo/term/GO:0070265) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070265&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070265&list=upload_1&organism=Homo%20sapiens) | 1.37 | 5.09 | + | 1.03E-03 | 2.03E-02 | | [spliceosomal snRNP assembly](http://amigo.geneontology.org/amigo/term/GO:0000387) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000387&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000387&list=upload_1&organism=Homo%20sapiens) | 1.87 | 4.82 | + | 2.84E-04 | 6.89E-03 | | [mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0000398) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000398&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000398&list=upload_1&organism=Homo%20sapiens) | 11.93 | 4.02 | + | 2.28E-14 | 3.05E-12 | | [mRNA processing](http://amigo.geneontology.org/amigo/term/GO:0006397) | [451](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006397&list=upload_1&organism=Homo%20sapiens) | 22.15 | 2.80 | + | 7.63E-12 | 7.52E-10 | | [mRNA metabolic process](http://amigo.geneontology.org/amigo/term/GO:0016071) | [607](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016071&list=upload_1&organism=Homo%20sapiens) | 29.81 | 2.65 | + | 1.26E-13 | 1.55E-11 | | [RNA splicing, via transesterification reactions with bulged adenosine as nucleophile](http://amigo.geneontology.org/amigo/term/GO:0000377) | [243](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000377&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000377&list=upload_1&organism=Homo%20sapiens) | 11.93 | 4.02 | + | 2.28E-14 | 3.03E-12 | | [RNA splicing, via transesterification reactions](http://amigo.geneontology.org/amigo/term/GO:0000375) | [247](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000375&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000375&list=upload_1&organism=Homo%20sapiens) | 12.13 | 3.96 | + | 3.89E-14 | 5.08E-12 | | [RNA splicing](http://amigo.geneontology.org/amigo/term/GO:0008380) | [368](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&reflist=1) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008380&list=upload_1&organism=Homo%20sapiens) | 18.07 | 3.21 | + | 2.56E-13 | 3.02E-11 | | [substantia nigra development](http://amigo.geneontology.org/amigo/term/GO:0021762) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021762&list=upload_1&organism=Homo%20sapiens) | 2.31 | 4.77 | + | 6.74E-05 | 1.95E-03 | | [midbrain development](http://amigo.geneontology.org/amigo/term/GO:0030901) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030901&list=upload_1&organism=Homo%20sapiens) | 4.37 | 2.75 | + | 2.67E-03 | 4.36E-02 | | [brain development](http://amigo.geneontology.org/amigo/term/GO:0007420) | [775](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007420&list=upload_1&organism=Homo%20sapiens) | 38.06 | 1.58 | + | 1.05E-03 | 2.05E-02 | | [central nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007417) | [1034](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&reflist=1) | [80](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007417&list=upload_1&organism=Homo%20sapiens) | 50.77 | 1.58 | + | 1.40E-04 | 3.78E-03 | | [nervous system development](http://amigo.geneontology.org/amigo/term/GO:0007399) | [2191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&reflist=1) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007399&list=upload_1&organism=Homo%20sapiens) | 107.59 | 1.49 | + | 1.04E-06 | 4.85E-05 | | [head development](http://amigo.geneontology.org/amigo/term/GO:0060322) | [823](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&reflist=1) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060322&list=upload_1&organism=Homo%20sapiens) | 40.41 | 1.58 | + | 6.08E-04 | 1.32E-02 | | [neural nucleus development](http://amigo.geneontology.org/amigo/term/GO:0048857) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048857&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048857&list=upload_1&organism=Homo%20sapiens) | 3.34 | 4.49 | + | 6.27E-06 | 2.38E-04 | | [cellular response to interleukin-6](http://amigo.geneontology.org/amigo/term/GO:0071354) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071354&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071354&list=upload_1&organism=Homo%20sapiens) | 1.47 | 4.75 | + | 1.45E-03 | 2.65E-02 | | [cellular response to cytokine stimulus](http://amigo.geneontology.org/amigo/term/GO:0071345) | [714](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&reflist=1) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071345&list=upload_1&organism=Homo%20sapiens) | 35.06 | 2.42 | + | 1.27E-12 | 1.39E-10 | | [response to interleukin-6](http://amigo.geneontology.org/amigo/term/GO:0070741) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070741&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070741&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.32 | + | 2.32E-03 | 3.93E-02 | | [positive regulation of lamellipodium assembly](http://amigo.geneontology.org/amigo/term/GO:0010592) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010592&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010592&list=upload_1&organism=Homo%20sapiens) | 1.47 | 4.75 | + | 1.45E-03 | 2.65E-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) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044087&list=upload_1&organism=Homo%20sapiens) | 46.70 | 1.56 | + | 3.44E-04 | 8.08E-03 | | [regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031344) | [656](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031344&list=upload_1&organism=Homo%20sapiens) | 32.21 | 1.68 | + | 5.38E-04 | 1.18E-02 | | [regulation of cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0051128) | [2364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&reflist=1) | [181](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051128&list=upload_1&organism=Homo%20sapiens) | 116.08 | 1.56 | + | 5.60E-09 | 3.70E-07 | | [regulation of plasma membrane bounded cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0120035) | [640](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&reflist=1) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0120035&list=upload_1&organism=Homo%20sapiens) | 31.43 | 1.69 | + | 4.67E-04 | 1.04E-02 | | [positive regulation of cell projection organization](http://amigo.geneontology.org/amigo/term/GO:0031346) | [351](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031346&list=upload_1&organism=Homo%20sapiens) | 17.24 | 1.80 | + | 3.04E-03 | 4.82E-02 | | [positive regulation of cellular component organization](http://amigo.geneontology.org/amigo/term/GO:0051130) | [1054](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&reflist=1) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051130&list=upload_1&organism=Homo%20sapiens) | 51.76 | 1.72 | + | 2.40E-06 | 1.03E-04 | | [positive regulation of cellular component biogenesis](http://amigo.geneontology.org/amigo/term/GO:0044089) | [501](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044089&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044089&list=upload_1&organism=Homo%20sapiens) | 24.60 | 1.71 | + | 1.36E-03 | 2.51E-02 | | [integrin-mediated signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007229) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007229&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007229&list=upload_1&organism=Homo%20sapiens) | 4.96 | 4.64 | + | 1.38E-08 | 8.83E-07 | | [cellular response to estradiol stimulus](http://amigo.geneontology.org/amigo/term/GO:0071392) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071392&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071392&list=upload_1&organism=Homo%20sapiens) | 1.96 | 4.58 | + | 3.94E-04 | 9.09E-03 | | [response to estradiol](http://amigo.geneontology.org/amigo/term/GO:0032355) | [123](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032355&list=upload_1&organism=Homo%20sapiens) | 6.04 | 2.65 | + | 8.05E-04 | 1.66E-02 | | [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) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048146&list=upload_1&organism=Homo%20sapiens) | 2.65 | 4.53 | + | 4.92E-05 | 1.49E-03 | | [regulation of fibroblast proliferation](http://amigo.geneontology.org/amigo/term/GO:0048145) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048145&list=upload_1&organism=Homo%20sapiens) | 4.37 | 4.35 | + | 5.83E-07 | 2.87E-05 | | [positive regulation of interferon-beta production](http://amigo.geneontology.org/amigo/term/GO:0032728) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032728&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032728&list=upload_1&organism=Homo%20sapiens) | 2.01 | 4.47 | + | 4.61E-04 | 1.03E-02 | | [regulation of interferon-beta production](http://amigo.geneontology.org/amigo/term/GO:0032648) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032648&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032648&list=upload_1&organism=Homo%20sapiens) | 2.85 | 3.51 | + | 1.19E-03 | 2.29E-02 | | [regulation of protein export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0046825) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046825&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046825&list=upload_1&organism=Homo%20sapiens) | 1.57 | 4.45 | + | 1.99E-03 | 3.46E-02 | | [response to arsenic-containing substance](http://amigo.geneontology.org/amigo/term/GO:0046685) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046685&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046685&list=upload_1&organism=Homo%20sapiens) | 1.57 | 4.45 | + | 1.99E-03 | 3.45E-02 | | [negative regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033144) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033144&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.03E-02 | | [negative regulation of signal transduction](http://amigo.geneontology.org/amigo/term/GO:0009968) | [1257](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009968&list=upload_1&organism=Homo%20sapiens) | 61.72 | 1.57 | + | 2.59E-05 | 8.47E-04 | | [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) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010648&list=upload_1&organism=Homo%20sapiens) | 66.63 | 1.58 | + | 1.16E-05 | 4.15E-04 | | [negative regulation of signaling](http://amigo.geneontology.org/amigo/term/GO:0023057) | [1363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&reflist=1) | [105](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0023057&list=upload_1&organism=Homo%20sapiens) | 66.93 | 1.57 | + | 1.23E-05 | 4.37E-04 | | [regulation of intracellular steroid hormone receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0033143) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033143&list=upload_1&organism=Homo%20sapiens) | 3.58 | 3.35 | + | 5.82E-04 | 1.27E-02 | | [positive regulation of lipid kinase activity](http://amigo.geneontology.org/amigo/term/GO:0090218) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090218&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090218&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.03E-02 | | [positive regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0033674) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033674&list=upload_1&organism=Homo%20sapiens) | 24.50 | 2.00 | + | 1.38E-05 | 4.86E-04 | | [regulation of kinase activity](http://amigo.geneontology.org/amigo/term/GO:0043549) | [783](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&reflist=1) | [68](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043549&list=upload_1&organism=Homo%20sapiens) | 38.45 | 1.77 | + | 2.01E-05 | 6.72E-04 | | [positive regulation of lipid metabolic process](http://amigo.geneontology.org/amigo/term/GO:0045834) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045834&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045834&list=upload_1&organism=Homo%20sapiens) | 7.56 | 2.38 | + | 1.46E-03 | 2.67E-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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035066&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.02E-02 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000758&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.79 | + | 2.38E-03 | 3.99E-02 | | [positive regulation of histone modification](http://amigo.geneontology.org/amigo/term/GO:0031058) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031058&list=upload_1&organism=Homo%20sapiens) | 5.25 | 2.85 | + | 5.81E-04 | 1.27E-02 | | [positive regulation of smooth muscle cell migration](http://amigo.geneontology.org/amigo/term/GO:0014911) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014911&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014911&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.02E-02 | | [regulation of smooth muscle cell migration](http://amigo.geneontology.org/amigo/term/GO:0014910) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014910&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014910&list=upload_1&organism=Homo%20sapiens) | 3.24 | 3.09 | + | 2.79E-03 | 4.47E-02 | | [positive regulation of cell migration](http://amigo.geneontology.org/amigo/term/GO:0030335) | [532](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030335&list=upload_1&organism=Homo%20sapiens) | 26.12 | 2.11 | + | 1.29E-06 | 5.78E-05 | | [positive regulation of cell motility](http://amigo.geneontology.org/amigo/term/GO:2000147) | [558](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000147&list=upload_1&organism=Homo%20sapiens) | 27.40 | 2.01 | + | 3.87E-06 | 1.55E-04 | | [positive regulation of locomotion](http://amigo.geneontology.org/amigo/term/GO:0040017) | [574](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&reflist=1) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0040017&list=upload_1&organism=Homo%20sapiens) | 28.19 | 1.95 | + | 8.35E-06 | 3.06E-04 | | [cell-matrix adhesion](http://amigo.geneontology.org/amigo/term/GO:0007160) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007160&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007160&list=upload_1&organism=Homo%20sapiens) | 6.63 | 4.37 | + | 5.96E-10 | 4.43E-08 | | [cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0031589) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031589&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031589&list=upload_1&organism=Homo%20sapiens) | 9.53 | 3.15 | + | 2.20E-07 | 1.16E-05 | | [granulocyte activation](http://amigo.geneontology.org/amigo/term/GO:0036230) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036230&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036230&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.32 | + | 2.32E-03 | 3.92E-02 | | [post-transcriptional gene silencing by RNA](http://amigo.geneontology.org/amigo/term/GO:0035194) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035194&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035194&list=upload_1&organism=Homo%20sapiens) | 1.62 | 4.32 | + | 2.32E-03 | 3.92E-02 | | [positive regulation of nitric oxide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0045429) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045429&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045429&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.26 | + | 6.23E-04 | 1.34E-02 | | [positive regulation of nitric oxide metabolic process](http://amigo.geneontology.org/amigo/term/GO:1904407) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904407&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904407&list=upload_1&organism=Homo%20sapiens) | 2.21 | 4.07 | + | 8.28E-04 | 1.70E-02 | | [regulation of nitric oxide metabolic process](http://amigo.geneontology.org/amigo/term/GO:0080164) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080164&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080164&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.82 | + | 2.02E-04 | 5.13E-03 | | [regulation of nitric oxide biosynthetic process](http://amigo.geneontology.org/amigo/term/GO:0045428) | [59](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045428&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045428&list=upload_1&organism=Homo%20sapiens) | 2.90 | 4.14 | + | 1.03E-04 | 2.87E-03 | | [cellular response to epidermal growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0071364) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071364&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071364&list=upload_1&organism=Homo%20sapiens) | 2.11 | 4.26 | + | 6.23E-04 | 1.34E-02 | | [response to epidermal growth factor](http://amigo.geneontology.org/amigo/term/GO:0070849) | [47](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070849&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070849&list=upload_1&organism=Homo%20sapiens) | 2.31 | 4.33 | + | 2.81E-04 | 6.82E-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) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070848&list=upload_1&organism=Homo%20sapiens) | 24.90 | 2.17 | + | 7.11E-07 | 3.42E-05 | | [cellular response to growth factor stimulus](http://amigo.geneontology.org/amigo/term/GO:0071363) | [477](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071363&list=upload_1&organism=Homo%20sapiens) | 23.42 | 2.05 | + | 1.30E-05 | 4.60E-04 | | [mismatch repair](http://amigo.geneontology.org/amigo/term/GO:0006298) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006298&list=upload_1&organism=Homo%20sapiens) | 1.67 | 4.19 | + | 2.69E-03 | 4.38E-02 | | [positive regulation of telomere maintenance via telomerase](http://amigo.geneontology.org/amigo/term/GO:0032212) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032212&reflist=1) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032212&list=upload_1&organism=Homo%20sapiens) | 1.67 | 4.19 | + | 2.69E-03 | 4.37E-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) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032210&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.77 | + | 7.33E-04 | 1.54E-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) | 3.04 | 3.94 | + | 1.55E-04 | 4.16E-03 | | [regulation of telomere maintenance](http://amigo.geneontology.org/amigo/term/GO:0032204) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032204&list=upload_1&organism=Homo%20sapiens) | 4.96 | 3.63 | + | 1.06E-05 | 3.80E-04 | | [regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:0033044) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&reflist=1) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033044&list=upload_1&organism=Homo%20sapiens) | 12.37 | 2.59 | + | 5.30E-06 | 2.04E-04 | | [regulation of organelle organization](http://amigo.geneontology.org/amigo/term/GO:0033043) | [1189](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&reflist=1) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0033043&list=upload_1&organism=Homo%20sapiens) | 58.38 | 1.83 | + | 8.55E-09 | 5.57E-07 | | [positive regulation of telomere maintenance via telomere lengthening](http://amigo.geneontology.org/amigo/term/GO:1904358) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904358&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904358&list=upload_1&organism=Homo%20sapiens) | 1.82 | 4.40 | + | 1.03E-03 | 2.03E-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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032206&list=upload_1&organism=Homo%20sapiens) | 3.24 | 4.01 | + | 7.16E-05 | 2.05E-03 | | [positive regulation of chromosome organization](http://amigo.geneontology.org/amigo/term/GO:2001252) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001252&list=upload_1&organism=Homo%20sapiens) | 5.21 | 3.46 | + | 1.88E-05 | 6.32E-04 | | [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) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010638&list=upload_1&organism=Homo%20sapiens) | 24.94 | 1.96 | + | 2.41E-05 | 7.91E-04 | | [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) | [7](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048147&list=upload_1&organism=Homo%20sapiens) | 1.67 | 4.19 | + | 2.69E-03 | 4.37E-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) | [71](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008285&list=upload_1&organism=Homo%20sapiens) | 35.01 | 2.03 | + | 9.96E-08 | 5.58E-06 | | [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) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045740&list=upload_1&organism=Homo%20sapiens) | 1.96 | 4.07 | + | 1.60E-03 | 2.88E-02 | | [ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070371) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070371&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070371&list=upload_1&organism=Homo%20sapiens) | 2.70 | 4.07 | + | 2.26E-04 | 5.65E-03 | | [MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0000165) | [220](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000165&list=upload_1&organism=Homo%20sapiens) | 10.80 | 2.78 | + | 2.31E-06 | 9.95E-05 | | [positive regulation of neuron apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043525) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043525&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043525&list=upload_1&organism=Homo%20sapiens) | 2.70 | 4.07 | + | 2.26E-04 | 5.64E-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) | 10.70 | 2.80 | + | 1.95E-06 | 8.56E-05 | | [regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901214) | [325](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901214&list=upload_1&organism=Homo%20sapiens) | 15.96 | 2.76 | + | 1.31E-08 | 8.40E-07 | | [positive regulation of neuron death](http://amigo.geneontology.org/amigo/term/GO:1901216) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901216&list=upload_1&organism=Homo%20sapiens) | 4.57 | 4.16 | + | 1.04E-06 | 4.85E-05 | | [regulation of alternative mRNA splicing, via spliceosome](http://amigo.geneontology.org/amigo/term/GO:0000381) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000381&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000381&list=upload_1&organism=Homo%20sapiens) | 3.04 | 3.94 | + | 1.55E-04 | 4.17E-03 | | [osteoblast differentiation](http://amigo.geneontology.org/amigo/term/GO:0001649) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001649&list=upload_1&organism=Homo%20sapiens) | 6.97 | 3.87 | + | 2.22E-08 | 1.36E-06 | | [ossification](http://amigo.geneontology.org/amigo/term/GO:0001503) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001503&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001503&list=upload_1&organism=Homo%20sapiens) | 14.24 | 2.67 | + | 3.99E-07 | 2.01E-05 | | [negative regulation of fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045599) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045599&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.84 | + | 6.45E-04 | 1.38E-02 | | [regulation of fat cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045598) | [135](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045598&list=upload_1&organism=Homo%20sapiens) | 6.63 | 2.41 | + | 2.64E-03 | 4.33E-02 | | [positive regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048661) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048661&list=upload_1&organism=Homo%20sapiens) | 4.17 | 3.83 | + | 1.78E-05 | 6.03E-04 | | [regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048660) | [142](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048660&list=upload_1&organism=Homo%20sapiens) | 6.97 | 3.87 | + | 2.22E-08 | 1.35E-06 | | [positive regulation of glial cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045687) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045687&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045687&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.79 | + | 2.38E-03 | 4.00E-02 | | [positive regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014015) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014015&list=upload_1&organism=Homo%20sapiens) | 3.24 | 4.32 | + | 1.86E-05 | 6.26E-04 | | [regulation of gliogenesis](http://amigo.geneontology.org/amigo/term/GO:0014013) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014013&list=upload_1&organism=Homo%20sapiens) | 4.96 | 3.43 | + | 3.51E-05 | 1.10E-03 | | [regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050767) | [373](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050767&list=upload_1&organism=Homo%20sapiens) | 18.32 | 2.02 | + | 1.33E-04 | 3.63E-03 | | [regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051960) | [452](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051960&list=upload_1&organism=Homo%20sapiens) | 22.19 | 1.80 | + | 7.26E-04 | 1.52E-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) | [112](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000026&list=upload_1&organism=Homo%20sapiens) | 67.91 | 1.65 | + | 6.33E-07 | 3.09E-05 | | [regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0060284) | [513](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060284&list=upload_1&organism=Homo%20sapiens) | 25.19 | 1.98 | + | 1.64E-05 | 5.65E-04 | | [positive regulation of neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0050769) | [231](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050769&list=upload_1&organism=Homo%20sapiens) | 11.34 | 2.20 | + | 4.96E-04 | 1.10E-02 | | [positive regulation of nervous system development](http://amigo.geneontology.org/amigo/term/GO:0051962) | [279](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051962&list=upload_1&organism=Homo%20sapiens) | 13.70 | 1.97 | + | 1.52E-03 | 2.76E-02 | | [positive regulation of cell development](http://amigo.geneontology.org/amigo/term/GO:0010720) | [308](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&reflist=1) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010720&list=upload_1&organism=Homo%20sapiens) | 15.12 | 2.25 | + | 4.20E-05 | 1.29E-03 | | [positive regulation of interleukin-12 production](http://amigo.geneontology.org/amigo/term/GO:0032735) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032735&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032735&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.79 | + | 2.38E-03 | 3.99E-02 | | [regulation of interleukin-12 production](http://amigo.geneontology.org/amigo/term/GO:0032655) | [63](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032655&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032655&list=upload_1&organism=Homo%20sapiens) | 3.09 | 4.20 | + | 4.71E-05 | 1.43E-03 | | [T cell selection](http://amigo.geneontology.org/amigo/term/GO:0045058) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045058&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045058&list=upload_1&organism=Homo%20sapiens) | 2.11 | 3.79 | + | 2.38E-03 | 3.98E-02 | | [protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0043491) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043491&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043491&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.77 | + | 7.33E-04 | 1.53E-02 | | [cellular response to mechanical stimulus](http://amigo.geneontology.org/amigo/term/GO:0071260) | [76](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071260&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071260&list=upload_1&organism=Homo%20sapiens) | 3.73 | 3.75 | + | 7.22E-05 | 2.07E-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) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071496&list=upload_1&organism=Homo%20sapiens) | 15.96 | 2.51 | + | 5.88E-07 | 2.89E-05 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071214&list=upload_1&organism=Homo%20sapiens) | 16.01 | 3.00 | + | 2.40E-10 | 1.86E-08 | | [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) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0104004&list=upload_1&organism=Homo%20sapiens) | 16.01 | 3.00 | + | 2.40E-10 | 1.85E-08 | | [cell fate determination](http://amigo.geneontology.org/amigo/term/GO:0001709) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001709&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001709&list=upload_1&organism=Homo%20sapiens) | 2.16 | 3.70 | + | 2.70E-03 | 4.39E-02 | | [regulation of chromatin organization](http://amigo.geneontology.org/amigo/term/GO:1902275) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902275&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902275&list=upload_1&organism=Homo%20sapiens) | 2.16 | 3.70 | + | 2.70E-03 | 4.38E-02 | | [neuron projection organization](http://amigo.geneontology.org/amigo/term/GO:0106027) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0106027&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0106027&list=upload_1&organism=Homo%20sapiens) | 2.16 | 3.70 | + | 2.70E-03 | 4.38E-02 | | [regulation of vascular associated smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:1904705) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904705&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904705&list=upload_1&organism=Homo%20sapiens) | 3.00 | 3.67 | + | 4.93E-04 | 1.09E-02 | | [I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0007249) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007249&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007249&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.65 | + | 2.93E-04 | 7.05E-03 | | [positive regulation of NIK/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:1901224) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901224&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901224&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.65 | + | 2.93E-04 | 7.04E-03 | | [regulation of NIK/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:1901222) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901222&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901222&list=upload_1&organism=Homo%20sapiens) | 4.91 | 3.67 | + | 9.36E-06 | 3.39E-04 | | [lung morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0060425) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060425&reflist=1) | [8](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060425&list=upload_1&organism=Homo%20sapiens) | 2.21 | 3.62 | + | 3.05E-03 | 4.84E-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) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034644&list=upload_1&organism=Homo%20sapiens) | 4.42 | 3.62 | + | 3.31E-05 | 1.05E-03 | | [cellular response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0071482) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071482&list=upload_1&organism=Homo%20sapiens) | 5.70 | 3.34 | + | 1.75E-05 | 5.94E-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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071478&list=upload_1&organism=Homo%20sapiens) | 8.94 | 3.24 | + | 2.00E-07 | 1.07E-05 | | [response to radiation](http://amigo.geneontology.org/amigo/term/GO:0009314) | [449](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&reflist=1) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009314&list=upload_1&organism=Homo%20sapiens) | 22.05 | 2.54 | + | 2.66E-09 | 1.83E-07 | | [response to light stimulus](http://amigo.geneontology.org/amigo/term/GO:0009416) | [317](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009416&list=upload_1&organism=Homo%20sapiens) | 15.57 | 2.44 | + | 2.58E-06 | 1.09E-04 | | [response to UV](http://amigo.geneontology.org/amigo/term/GO:0009411) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009411&list=upload_1&organism=Homo%20sapiens) | 7.41 | 3.24 | + | 2.29E-06 | 9.91E-05 | | [negative regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000059) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000059&list=upload_1&organism=Homo%20sapiens) | 2.50 | 3.59 | + | 1.79E-03 | 3.17E-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) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903050&list=upload_1&organism=Homo%20sapiens) | 11.20 | 2.05 | + | 2.21E-03 | 3.78E-02 | | [regulation of proteolysis](http://amigo.geneontology.org/amigo/term/GO:0030162) | [743](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&reflist=1) | [62](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030162&list=upload_1&organism=Homo%20sapiens) | 36.48 | 1.70 | + | 1.17E-04 | 3.22E-03 | | [regulation of ubiquitin-dependent protein catabolic process](http://amigo.geneontology.org/amigo/term/GO:2000058) | [172](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000058&list=upload_1&organism=Homo%20sapiens) | 8.45 | 2.49 | + | 3.84E-04 | 8.88E-03 | | [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) | 3.09 | 3.56 | + | 6.26E-04 | 1.34E-02 | | [negative regulation of wound healing](http://amigo.geneontology.org/amigo/term/GO:0061045) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061045&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061045&list=upload_1&organism=Homo%20sapiens) | 3.39 | 3.54 | + | 3.71E-04 | 8.68E-03 | | [negative regulation of response to wounding](http://amigo.geneontology.org/amigo/term/GO:1903035) | [85](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903035&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903035&list=upload_1&organism=Homo%20sapiens) | 4.17 | 3.35 | + | 2.06E-04 | 5.21E-03 | | [regulation of response to wounding](http://amigo.geneontology.org/amigo/term/GO:1903034) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903034&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903034&list=upload_1&organism=Homo%20sapiens) | 7.95 | 2.39 | + | 1.03E-03 | 2.03E-02 | | [negative regulation of response to external stimulus](http://amigo.geneontology.org/amigo/term/GO:0032102) | [391](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032102&list=upload_1&organism=Homo%20sapiens) | 19.20 | 1.82 | + | 1.55E-03 | 2.80E-02 | | [positive regulation of myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002763) | [58](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002763&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002763&list=upload_1&organism=Homo%20sapiens) | 2.85 | 3.51 | + | 1.19E-03 | 2.28E-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) | 8.99 | 2.78 | + | 1.53E-05 | 5.32E-04 | | [positive regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903708) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903708&list=upload_1&organism=Homo%20sapiens) | 8.99 | 2.78 | + | 1.53E-05 | 5.31E-04 | | [regulation of hemopoiesis](http://amigo.geneontology.org/amigo/term/GO:1903706) | [398](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903706&list=upload_1&organism=Homo%20sapiens) | 19.54 | 2.15 | + | 1.69E-05 | 5.79E-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) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902105&list=upload_1&organism=Homo%20sapiens) | 15.52 | 2.45 | + | 2.48E-06 | 1.06E-04 | | [regulation of myeloid leukocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0002761) | [122](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002761&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002761&list=upload_1&organism=Homo%20sapiens) | 5.99 | 2.67 | + | 7.44E-04 | 1.55E-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) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045637&list=upload_1&organism=Homo%20sapiens) | 9.82 | 2.14 | + | 1.98E-03 | 3.45E-02 | | [positive regulation of myeloid cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045639) | [100](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045639&list=upload_1&organism=Homo%20sapiens) | 4.91 | 2.85 | + | 8.85E-04 | 1.78E-02 | | [response to cAMP](http://amigo.geneontology.org/amigo/term/GO:0051591) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051591&list=upload_1&organism=Homo%20sapiens) | 4.57 | 3.50 | + | 4.69E-05 | 1.43E-03 | | [response to purine-containing compound](http://amigo.geneontology.org/amigo/term/GO:0014074) | [147](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014074&list=upload_1&organism=Homo%20sapiens) | 7.22 | 2.91 | + | 4.01E-05 | 1.24E-03 | | [response to organophosphorus](http://amigo.geneontology.org/amigo/term/GO:0046683) | [132](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046683&list=upload_1&organism=Homo%20sapiens) | 6.48 | 2.93 | + | 8.40E-05 | 2.37E-03 | | [cardiac cell development](http://amigo.geneontology.org/amigo/term/GO:0055006) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055006&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0055006&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.50 | + | 7.03E-04 | 1.49E-02 | | [cardiocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0035051) | [114](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035051&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035051&list=upload_1&organism=Homo%20sapiens) | 5.60 | 2.86 | + | 3.82E-04 | 8.87E-03 | | [heart development](http://amigo.geneontology.org/amigo/term/GO:0007507) | [555](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&reflist=1) | [49](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007507&list=upload_1&organism=Homo%20sapiens) | 27.25 | 1.80 | + | 1.82E-04 | 4.71E-03 | | [circulatory system development](http://amigo.geneontology.org/amigo/term/GO:0072359) | [909](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&reflist=1) | [72](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072359&list=upload_1&organism=Homo%20sapiens) | 44.64 | 1.61 | + | 1.86E-04 | 4.80E-03 | | [cell development](http://amigo.geneontology.org/amigo/term/GO:0048468) | [1725](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&reflist=1) | [133](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048468&list=upload_1&organism=Homo%20sapiens) | 84.70 | 1.57 | + | 6.77E-07 | 3.27E-05 | | [positive regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000379) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000379&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000379&list=upload_1&organism=Homo%20sapiens) | 3.44 | 3.49 | + | 4.17E-04 | 9.44E-03 | | [regulation of reactive oxygen species metabolic process](http://amigo.geneontology.org/amigo/term/GO:2000377) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000377&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2000377&list=upload_1&organism=Homo%20sapiens) | 7.07 | 3.25 | + | 3.44E-06 | 1.42E-04 | | [cellular response to virus](http://amigo.geneontology.org/amigo/term/GO:0098586) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098586&list=upload_1&organism=Homo%20sapiens) | 4.32 | 3.47 | + | 8.80E-05 | 2.48E-03 | | [negative regulation of smooth muscle cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0048662) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048662&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048662&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.26E-03 | 3.86E-02 | | [negative regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010823) | [53](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010823&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010823&list=upload_1&organism=Homo%20sapiens) | 2.60 | 3.46 | + | 2.26E-03 | 3.86E-02 | | [regulation of mitochondrion organization](http://amigo.geneontology.org/amigo/term/GO:0010821) | [152](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010821&list=upload_1&organism=Homo%20sapiens) | 7.46 | 2.55 | + | 6.94E-04 | 1.47E-02 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010639&list=upload_1&organism=Homo%20sapiens) | 16.94 | 2.01 | + | 3.04E-04 | 7.25E-03 | | [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) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051129&list=upload_1&organism=Homo%20sapiens) | 33.88 | 1.92 | + | 2.49E-06 | 1.06E-04 | | [cellular response to interferon-gamma](http://amigo.geneontology.org/amigo/term/GO:0071346) | [107](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071346&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071346&list=upload_1&organism=Homo%20sapiens) | 5.25 | 3.43 | + | 2.10E-05 | 7.00E-04 | | [response to interferon-gamma](http://amigo.geneontology.org/amigo/term/GO:0034341) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034341&list=upload_1&organism=Homo%20sapiens) | 6.38 | 2.98 | + | 7.00E-05 | 2.02E-03 | | [mesenchyme morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0072132) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072132&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0072132&list=upload_1&organism=Homo%20sapiens) | 2.65 | 3.39 | + | 2.53E-03 | 4.18E-02 | | [mesenchyme development](http://amigo.geneontology.org/amigo/term/GO:0060485) | [239](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060485&list=upload_1&organism=Homo%20sapiens) | 11.74 | 2.56 | + | 1.25E-05 | 4.42E-04 | | [histone deacetylation](http://amigo.geneontology.org/amigo/term/GO:0016575) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016575&list=upload_1&organism=Homo%20sapiens) | 2.95 | 3.39 | + | 1.49E-03 | 2.71E-02 | | [protein deacetylation](http://amigo.geneontology.org/amigo/term/GO:0006476) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006476&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.18 | + | 2.28E-03 | 3.89E-02 | | [protein deacylation](http://amigo.geneontology.org/amigo/term/GO:0035601) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035601&list=upload_1&organism=Homo%20sapiens) | 3.68 | 2.99 | + | 2.20E-03 | 3.78E-02 | | [macromolecule deacylation](http://amigo.geneontology.org/amigo/term/GO:0098732) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098732&list=upload_1&organism=Homo%20sapiens) | 3.88 | 2.84 | + | 3.16E-03 | 4.95E-02 | | [response to cadmium ion](http://amigo.geneontology.org/amigo/term/GO:0046686) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046686&list=upload_1&organism=Homo%20sapiens) | 3.00 | 3.34 | + | 1.66E-03 | 2.98E-02 | | [response to metal ion](http://amigo.geneontology.org/amigo/term/GO:0010038) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010038&list=upload_1&organism=Homo%20sapiens) | 17.82 | 2.02 | + | 1.71E-04 | 4.47E-03 | | [response to inorganic substance](http://amigo.geneontology.org/amigo/term/GO:0010035) | [533](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&reflist=1) | [60](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010035&list=upload_1&organism=Homo%20sapiens) | 26.17 | 2.29 | + | 2.88E-08 | 1.72E-06 | | [nucleotide-excision repair](http://amigo.geneontology.org/amigo/term/GO:0006289) | [56](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&reflist=1) | [9](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006289&list=upload_1&organism=Homo%20sapiens) | 2.75 | 3.27 | + | 3.15E-03 | 4.94E-02 | | [cellular response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0071479) | [75](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071479&list=upload_1&organism=Homo%20sapiens) | 3.68 | 3.26 | + | 7.20E-04 | 1.52E-02 | | [response to ionizing radiation](http://amigo.geneontology.org/amigo/term/GO:0010212) | [144](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010212&list=upload_1&organism=Homo%20sapiens) | 7.07 | 2.40 | + | 1.91E-03 | 3.35E-02 | | [response to activity](http://amigo.geneontology.org/amigo/term/GO:0014823) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014823&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0014823&list=upload_1&organism=Homo%20sapiens) | 3.44 | 3.20 | + | 1.35E-03 | 2.51E-02 | | [regulation of potassium ion transmembrane transporter activity](http://amigo.geneontology.org/amigo/term/GO:1901016) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901016&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901016&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.18 | + | 2.28E-03 | 3.88E-02 | | [regulation of potassium ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:1901379) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901379&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901379&list=upload_1&organism=Homo%20sapiens) | 4.47 | 3.13 | + | 3.83E-04 | 8.87E-03 | | [regulation of potassium ion transport](http://amigo.geneontology.org/amigo/term/GO:0043266) | [106](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043266&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043266&list=upload_1&organism=Homo%20sapiens) | 5.21 | 3.07 | + | 1.84E-04 | 4.75E-03 | | [regulation of ion transmembrane transporter activity](http://amigo.geneontology.org/amigo/term/GO:0032412) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032412&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032412&list=upload_1&organism=Homo%20sapiens) | 13.36 | 2.02 | + | 1.25E-03 | 2.34E-02 | | [regulation of transmembrane transporter activity](http://amigo.geneontology.org/amigo/term/GO:0022898) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022898&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022898&list=upload_1&organism=Homo%20sapiens) | 13.85 | 2.02 | + | 9.50E-04 | 1.89E-02 | | [regulation of transporter activity](http://amigo.geneontology.org/amigo/term/GO:0032409) | [299](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032409&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032409&list=upload_1&organism=Homo%20sapiens) | 14.68 | 2.04 | + | 5.12E-04 | 1.12E-02 | | [positive regulation of response to cytokine stimulus](http://amigo.geneontology.org/amigo/term/GO:0060760) | [64](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060760&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060760&list=upload_1&organism=Homo%20sapiens) | 3.14 | 3.18 | + | 2.28E-03 | 3.88E-02 | | [positive regulation of cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0010811) | [129](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010811&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010811&list=upload_1&organism=Homo%20sapiens) | 6.33 | 3.16 | + | 2.15E-05 | 7.14E-04 | | [regulation of cell-substrate adhesion](http://amigo.geneontology.org/amigo/term/GO:0010810) | [219](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010810&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010810&list=upload_1&organism=Homo%20sapiens) | 10.75 | 2.60 | + | 2.14E-05 | 7.10E-04 | | [regulation of morphogenesis of an epithelium](http://amigo.geneontology.org/amigo/term/GO:1905330) | [65](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905330&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1905330&list=upload_1&organism=Homo%20sapiens) | 3.19 | 3.13 | + | 2.53E-03 | 4.17E-02 | | [mRNA transport](http://amigo.geneontology.org/amigo/term/GO:0051028) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051028&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051028&list=upload_1&organism=Homo%20sapiens) | 6.78 | 3.10 | + | 1.74E-05 | 5.93E-04 | | [cellular response to hydrogen peroxide](http://amigo.geneontology.org/amigo/term/GO:0070301) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070301&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070301&list=upload_1&organism=Homo%20sapiens) | 3.24 | 3.09 | + | 2.79E-03 | 4.47E-02 | | [cellular response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0034614) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034614&list=upload_1&organism=Homo%20sapiens) | 5.75 | 2.78 | + | 4.95E-04 | 1.10E-02 | | [response to reactive oxygen species](http://amigo.geneontology.org/amigo/term/GO:0000302) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000302&list=upload_1&organism=Homo%20sapiens) | 8.20 | 2.56 | + | 3.20E-04 | 7.57E-03 | | [response to hydrogen peroxide](http://amigo.geneontology.org/amigo/term/GO:0042542) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042542&list=upload_1&organism=Homo%20sapiens) | 5.06 | 2.77 | + | 1.14E-03 | 2.21E-02 | | [regulation of oxidative stress-induced cell death](http://amigo.geneontology.org/amigo/term/GO:1903201) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903201&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1903201&list=upload_1&organism=Homo%20sapiens) | 3.58 | 3.07 | + | 1.82E-03 | 3.21E-02 | | [regulation of cellular response to oxidative stress](http://amigo.geneontology.org/amigo/term/GO:1900407) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900407&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1900407&list=upload_1&organism=Homo%20sapiens) | 4.12 | 2.91 | + | 1.73E-03 | 3.08E-02 | | [regulation of cellular response to stress](http://amigo.geneontology.org/amigo/term/GO:0080135) | [709](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0080135&list=upload_1&organism=Homo%20sapiens) | 34.81 | 1.98 | + | 3.68E-07 | 1.86E-05 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032869&list=upload_1&organism=Homo%20sapiens) | 7.22 | 3.05 | + | 1.39E-05 | 4.89E-04 | | [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) | 10.46 | 2.77 | + | 3.48E-06 | 1.42E-04 | | [response to peptide hormone](http://amigo.geneontology.org/amigo/term/GO:0043434) | [363](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043434&list=upload_1&organism=Homo%20sapiens) | 17.82 | 2.36 | + | 1.98E-06 | 8.67E-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) | 11.83 | 2.87 | + | 2.46E-07 | 1.29E-05 | | [positive regulation of lipase activity](http://amigo.geneontology.org/amigo/term/GO:0060193) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060193&reflist=1) | [10](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060193&list=upload_1&organism=Homo%20sapiens) | 3.29 | 3.04 | + | 3.07E-03 | 4.87E-02 | | [intrinsic apoptotic signaling pathway in response to DNA damage](http://amigo.geneontology.org/amigo/term/GO:0008630) | [74](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008630&list=upload_1&organism=Homo%20sapiens) | 3.63 | 3.03 | + | 2.00E-03 | 3.47E-02 | | [response to nutrient](http://amigo.geneontology.org/amigo/term/GO:0007584) | [149](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007584&list=upload_1&organism=Homo%20sapiens) | 7.32 | 3.01 | + | 1.68E-05 | 5.77E-04 | | [response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031667) | [470](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&reflist=1) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031667&list=upload_1&organism=Homo%20sapiens) | 23.08 | 2.25 | + | 2.90E-07 | 1.49E-05 | | [response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0009991) | [500](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009991&list=upload_1&organism=Homo%20sapiens) | 24.55 | 2.20 | + | 3.63E-07 | 1.84E-05 | | [positive regulation of protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0051897) | [116](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051897&list=upload_1&organism=Homo%20sapiens) | 5.70 | 2.98 | + | 1.61E-04 | 4.27E-03 | | [regulation of protein kinase B signaling](http://amigo.geneontology.org/amigo/term/GO:0051896) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051896&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051896&list=upload_1&organism=Homo%20sapiens) | 8.35 | 2.52 | + | 3.54E-04 | 8.29E-03 | | [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) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071356&list=upload_1&organism=Homo%20sapiens) | 8.74 | 2.97 | + | 3.55E-06 | 1.44E-04 | | [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) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034612&list=upload_1&organism=Homo%20sapiens) | 9.92 | 2.82 | + | 3.76E-06 | 1.51E-04 | | [positive regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0032092) | [89](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032092&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032092&list=upload_1&organism=Homo%20sapiens) | 4.37 | 2.97 | + | 9.42E-04 | 1.88E-02 | | [regulation of protein binding](http://amigo.geneontology.org/amigo/term/GO:0043393) | [201](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043393&list=upload_1&organism=Homo%20sapiens) | 9.87 | 2.43 | + | 1.71E-04 | 4.48E-03 | | [transforming growth factor beta receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007179) | [96](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007179&list=upload_1&organism=Homo%20sapiens) | 4.71 | 2.97 | + | 6.18E-04 | 1.34E-02 | | [cellular response to transforming growth factor beta stimulus](http://amigo.geneontology.org/amigo/term/GO:0071560) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071560&list=upload_1&organism=Homo%20sapiens) | 7.56 | 2.64 | + | 1.94E-04 | 5.00E-03 | | [response to transforming growth factor beta](http://amigo.geneontology.org/amigo/term/GO:0071559) | [161](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071559&list=upload_1&organism=Homo%20sapiens) | 7.91 | 2.53 | + | 4.93E-04 | 1.09E-02 | | [response to heat](http://amigo.geneontology.org/amigo/term/GO:0009408) | [103](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009408&list=upload_1&organism=Homo%20sapiens) | 5.06 | 2.97 | + | 4.06E-04 | 9.29E-03 | | [response to temperature stimulus](http://amigo.geneontology.org/amigo/term/GO:0009266) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009266&list=upload_1&organism=Homo%20sapiens) | 8.74 | 2.52 | + | 2.47E-04 | 6.07E-03 | | [circadian rhythm](http://amigo.geneontology.org/amigo/term/GO:0007623) | [138](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007623&list=upload_1&organism=Homo%20sapiens) | 6.78 | 2.95 | + | 5.07E-05 | 1.53E-03 | | [rhythmic process](http://amigo.geneontology.org/amigo/term/GO:0048511) | [272](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048511&list=upload_1&organism=Homo%20sapiens) | 13.36 | 2.70 | + | 4.43E-07 | 2.21E-05 | | [positive regulation of cell morphogenesis involved in differentiation](http://amigo.geneontology.org/amigo/term/GO:0010770) | [83](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010770&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010770&list=upload_1&organism=Homo%20sapiens) | 4.08 | 2.94 | + | 1.58E-03 | 2.85E-02 | | [regulation of cell morphogenesis](http://amigo.geneontology.org/amigo/term/GO:0022604) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022604&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022604&list=upload_1&organism=Homo%20sapiens) | 15.42 | 1.88 | + | 2.65E-03 | 4.34E-02 | | [diencephalon development](http://amigo.geneontology.org/amigo/term/GO:0021536) | [77](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021536&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0021536&list=upload_1&organism=Homo%20sapiens) | 3.78 | 2.91 | + | 2.65E-03 | 4.34E-02 | | [RNA export from nucleus](http://amigo.geneontology.org/amigo/term/GO:0006405) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006405&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006405&list=upload_1&organism=Homo%20sapiens) | 4.12 | 2.91 | + | 1.73E-03 | 3.08E-02 | | [regulation of calcium-mediated signaling](http://amigo.geneontology.org/amigo/term/GO:0050848) | [84](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050848&reflist=1) | [12](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050848&list=upload_1&organism=Homo%20sapiens) | 4.12 | 2.91 | + | 1.73E-03 | 3.08E-02 | | [negative regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001237) | [98](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001237&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.91 | + | 7.42E-04 | 1.55E-02 | | [negative regulation of apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001234) | [229](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001234&list=upload_1&organism=Homo%20sapiens) | 11.24 | 2.49 | + | 3.45E-05 | 1.09E-03 | | [negative regulation of apoptotic process](http://amigo.geneontology.org/amigo/term/GO:0043066) | [898](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&reflist=1) | [91](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043066&list=upload_1&organism=Homo%20sapiens) | 44.10 | 2.06 | + | 6.20E-10 | 4.59E-08 | | [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) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043069&list=upload_1&organism=Homo%20sapiens) | 45.08 | 2.06 | + | 3.68E-10 | 2.80E-08 | | [negative regulation of cell death](http://amigo.geneontology.org/amigo/term/GO:0060548) | [1022](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&reflist=1) | [104](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060548&list=upload_1&organism=Homo%20sapiens) | 50.18 | 2.07 | + | 3.32E-11 | 2.94E-09 | | [regulation of extrinsic apoptotic signaling pathway](http://amigo.geneontology.org/amigo/term/GO:2001236) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001236&list=upload_1&organism=Homo%20sapiens) | 7.56 | 2.25 | + | 3.08E-03 | 4.87E-02 | | [positive regulation of protein polymerization](http://amigo.geneontology.org/amigo/term/GO:0032273) | [92](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032273&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032273&list=upload_1&organism=Homo%20sapiens) | 4.52 | 2.88 | + | 1.24E-03 | 2.33E-02 | | [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) | [41](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043254&list=upload_1&organism=Homo%20sapiens) | 20.23 | 2.03 | + | 6.36E-05 | 1.85E-03 | | [positive regulation of protein-containing complex assembly](http://amigo.geneontology.org/amigo/term/GO:0031334) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031334&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031334&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.41 | + | 2.55E-04 | 6.25E-03 | | [response to hypoxia](http://amigo.geneontology.org/amigo/term/GO:0001666) | [277](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001666&list=upload_1&organism=Homo%20sapiens) | 13.60 | 2.87 | + | 3.43E-08 | 2.02E-06 | | [response to decreased oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0036293) | [290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036293&list=upload_1&organism=Homo%20sapiens) | 14.24 | 2.81 | + | 3.79E-08 | 2.21E-06 | | [response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0070482) | [319](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&reflist=1) | [43](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070482&list=upload_1&organism=Homo%20sapiens) | 15.66 | 2.75 | + | 2.14E-08 | 1.31E-06 | | [cellular response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990830) | [93](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990830&list=upload_1&organism=Homo%20sapiens) | 4.57 | 2.85 | + | 1.35E-03 | 2.50E-02 | | [response to leukemia inhibitory factor](http://amigo.geneontology.org/amigo/term/GO:1990823) | [94](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1990823&list=upload_1&organism=Homo%20sapiens) | 4.62 | 2.82 | + | 1.47E-03 | 2.69E-02 | | [negative regulation of ion transmembrane transporter activity](http://amigo.geneontology.org/amigo/term/GO:0032413) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032413&reflist=1) | [11](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032413&list=upload_1&organism=Homo%20sapiens) | 3.88 | 2.84 | + | 3.16E-03 | 4.96E-02 | | [protein import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0006606) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006606&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006606&list=upload_1&organism=Homo%20sapiens) | 5.65 | 2.83 | + | 4.17E-04 | 9.44E-03 | | [protein localization to nucleus](http://amigo.geneontology.org/amigo/term/GO:0034504) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034504&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.83 | + | 5.21E-06 | 2.02E-04 | | [import into nucleus](http://amigo.geneontology.org/amigo/term/GO:0051170) | [119](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051170&list=upload_1&organism=Homo%20sapiens) | 5.84 | 2.91 | + | 2.11E-04 | 5.30E-03 | | [positive regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070374) | [217](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070374&list=upload_1&organism=Homo%20sapiens) | 10.66 | 2.72 | + | 4.82E-06 | 1.88E-04 | | [regulation of ERK1 and ERK2 cascade](http://amigo.geneontology.org/amigo/term/GO:0070372) | [303](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0070372&list=upload_1&organism=Homo%20sapiens) | 14.88 | 2.49 | + | 1.84E-06 | 8.11E-05 | | [regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043408) | [672](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&reflist=1) | [69](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043408&list=upload_1&organism=Homo%20sapiens) | 33.00 | 2.09 | + | 6.56E-08 | 3.74E-06 | | [positive regulation of MAPK cascade](http://amigo.geneontology.org/amigo/term/GO:0043410) | [484](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043410&reflist=1) | [50](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043410&list=upload_1&organism=Homo%20sapiens) | 23.77 | 2.10 | + | 3.43E-06 | 1.42E-04 | | [protein stabilization](http://amigo.geneontology.org/amigo/term/GO:0050821) | [218](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&reflist=1) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050821&list=upload_1&organism=Homo%20sapiens) | 10.70 | 2.71 | + | 5.23E-06 | 2.02E-04 | | [regulation of protein stability](http://amigo.geneontology.org/amigo/term/GO:0031647) | [333](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&reflist=1) | [40](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031647&list=upload_1&organism=Homo%20sapiens) | 16.35 | 2.45 | + | 1.28E-06 | 5.77E-05 | | [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) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904035&list=upload_1&organism=Homo%20sapiens) | 4.81 | 2.70 | + | 2.06E-03 | 3.55E-02 | | [stem cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0048863) | [183](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048863&list=upload_1&organism=Homo%20sapiens) | 8.99 | 2.67 | + | 4.06E-05 | 1.25E-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) | [55](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009410&list=upload_1&organism=Homo%20sapiens) | 20.77 | 2.65 | + | 8.36E-10 | 6.13E-08 | | [RNA catabolic process](http://amigo.geneontology.org/amigo/term/GO:0006401) | [162](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006401&list=upload_1&organism=Homo%20sapiens) | 7.95 | 2.64 | + | 1.39E-04 | 3.78E-03 | | [cellular macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0044265) | [785](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&reflist=1) | [67](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044265&list=upload_1&organism=Homo%20sapiens) | 38.55 | 1.74 | + | 3.10E-05 | 9.99E-04 | | [macromolecule catabolic process](http://amigo.geneontology.org/amigo/term/GO:0009057) | [989](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009057&list=upload_1&organism=Homo%20sapiens) | 48.56 | 1.63 | + | 5.45E-05 | 1.62E-03 | | [organic substance catabolic process](http://amigo.geneontology.org/amigo/term/GO:1901575) | [1679](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&reflist=1) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901575&list=upload_1&organism=Homo%20sapiens) | 82.45 | 1.33 | + | 2.85E-03 | 4.57E-02 | | [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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901361&list=upload_1&organism=Homo%20sapiens) | 18.36 | 1.85 | + | 1.23E-03 | 2.31E-02 | | [viral entry into host cell](http://amigo.geneontology.org/amigo/term/GO:0046718) | [108](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046718&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0046718&list=upload_1&organism=Homo%20sapiens) | 5.30 | 2.64 | + | 1.72E-03 | 3.07E-02 | | [viral life cycle](http://amigo.geneontology.org/amigo/term/GO:0019058) | [178](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019058&reflist=1) | [26](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0019058&list=upload_1&organism=Homo%20sapiens) | 8.74 | 2.97 | + | 3.55E-06 | 1.44E-04 | | [viral process](http://amigo.geneontology.org/amigo/term/GO:0016032) | [251](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016032&list=upload_1&organism=Homo%20sapiens) | 12.33 | 2.92 | + | 7.61E-08 | 4.31E-06 | | [entry into host](http://amigo.geneontology.org/amigo/term/GO:0044409) | [110](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044409&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044409&list=upload_1&organism=Homo%20sapiens) | 5.40 | 2.59 | + | 2.00E-03 | 3.46E-02 | | [movement in host](http://amigo.geneontology.org/amigo/term/GO:0044000) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044000&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044000&list=upload_1&organism=Homo%20sapiens) | 6.83 | 2.64 | + | 4.11E-04 | 9.34E-03 | | [biological process involved in interaction with host](http://amigo.geneontology.org/amigo/term/GO:0051701) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051701&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051701&list=upload_1&organism=Homo%20sapiens) | 7.66 | 2.87 | + | 3.16E-05 | 1.01E-03 | | [regulation of endothelial cell proliferation](http://amigo.geneontology.org/amigo/term/GO:0001936) | [139](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001936&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001936&list=upload_1&organism=Homo%20sapiens) | 6.83 | 2.64 | + | 4.11E-04 | 9.36E-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) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050678&list=upload_1&organism=Homo%20sapiens) | 18.12 | 1.99 | + | 2.95E-04 | 7.08E-03 | | [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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043524&list=upload_1&organism=Homo%20sapiens) | 7.61 | 2.63 | + | 2.10E-04 | 5.29E-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) | [29](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901215&list=upload_1&organism=Homo%20sapiens) | 10.80 | 2.68 | + | 6.13E-06 | 2.33E-04 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043467&list=upload_1&organism=Homo%20sapiens) | 6.48 | 2.62 | + | 6.21E-04 | 1.34E-02 | | [regulation of oxidoreductase activity](http://amigo.geneontology.org/amigo/term/GO:0051341) | [101](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&reflist=1) | [13](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051341&list=upload_1&organism=Homo%20sapiens) | 4.96 | 2.62 | + | 2.61E-03 | 4.30E-02 | | [positive regulation of T cell differentiation](http://amigo.geneontology.org/amigo/term/GO:0045582) | [117](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&reflist=1) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045582&list=upload_1&organism=Homo%20sapiens) | 5.75 | 2.61 | + | 1.32E-03 | 2.47E-02 | | [positive regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045621) | [131](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045621&list=upload_1&organism=Homo%20sapiens) | 6.43 | 2.64 | + | 5.75E-04 | 1.26E-02 | | [regulation of lymphocyte differentiation](http://amigo.geneontology.org/amigo/term/GO:0045619) | [210](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045619&list=upload_1&organism=Homo%20sapiens) | 10.31 | 2.33 | + | 4.34E-04 | 9.78E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0090100&list=upload_1&organism=Homo%20sapiens) | 5.79 | 2.59 | + | 1.43E-03 | 2.62E-02 | | [aging](http://amigo.geneontology.org/amigo/term/GO:0007568) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007568&list=upload_1&organism=Homo%20sapiens) | 8.54 | 2.57 | + | 2.15E-04 | 5.37E-03 | | [positive regulation of I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0043123) | [190](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043123&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043123&list=upload_1&organism=Homo%20sapiens) | 9.33 | 2.57 | + | 1.03E-04 | 2.86E-03 | | [regulation of I-kappaB kinase/NF-kappaB signaling](http://amigo.geneontology.org/amigo/term/GO:0043122) | [252](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043122&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0043122&list=upload_1&organism=Homo%20sapiens) | 12.37 | 2.26 | + | 1.57E-04 | 4.18E-03 | | [positive regulation of epithelial cell migration](http://amigo.geneontology.org/amigo/term/GO:0010634) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010634&list=upload_1&organism=Homo%20sapiens) | 7.41 | 2.56 | + | 3.97E-04 | 9.15E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042752&list=upload_1&organism=Homo%20sapiens) | 5.89 | 2.55 | + | 1.66E-03 | 2.97E-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) | [15](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045931&list=upload_1&organism=Homo%20sapiens) | 5.94 | 2.52 | + | 1.78E-03 | 3.16E-02 | | [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) | [52](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007346&list=upload_1&organism=Homo%20sapiens) | 24.21 | 2.15 | + | 1.46E-06 | 6.50E-05 | | [positive regulation of cell cycle](http://amigo.geneontology.org/amigo/term/GO:0045787) | [353](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045787&list=upload_1&organism=Homo%20sapiens) | 17.33 | 1.79 | + | 3.16E-03 | 4.96E-02 | | [positive regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0045739) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045739&list=upload_1&organism=Homo%20sapiens) | 6.38 | 2.51 | + | 1.36E-03 | 2.52E-02 | | [positive regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001022) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001022&list=upload_1&organism=Homo%20sapiens) | 8.25 | 2.79 | + | 3.20E-05 | 1.02E-03 | | [regulation of response to DNA damage stimulus](http://amigo.geneontology.org/amigo/term/GO:2001020) | [314](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&reflist=1) | [35](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001020&list=upload_1&organism=Homo%20sapiens) | 15.42 | 2.27 | + | 2.79E-05 | 9.09E-04 | | [regulation of DNA repair](http://amigo.geneontology.org/amigo/term/GO:0006282) | [212](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006282&list=upload_1&organism=Homo%20sapiens) | 10.41 | 2.21 | + | 8.56E-04 | 1.74E-02 | | [endocrine system development](http://amigo.geneontology.org/amigo/term/GO:0035270) | [130](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0035270&list=upload_1&organism=Homo%20sapiens) | 6.38 | 2.51 | + | 1.36E-03 | 2.51E-02 | | [metencephalon development](http://amigo.geneontology.org/amigo/term/GO:0022037) | [115](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022037&reflist=1) | [14](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022037&list=upload_1&organism=Homo%20sapiens) | 5.65 | 2.48 | + | 2.90E-03 | 4.64E-02 | | [hindbrain development](http://amigo.geneontology.org/amigo/term/GO:0030902) | [156](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030902&list=upload_1&organism=Homo%20sapiens) | 7.66 | 2.48 | + | 7.91E-04 | 1.63E-02 | | [response to glucose](http://amigo.geneontology.org/amigo/term/GO:0009749) | [141](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009749&list=upload_1&organism=Homo%20sapiens) | 6.92 | 2.46 | + | 1.70E-03 | 3.04E-02 | | [response to hexose](http://amigo.geneontology.org/amigo/term/GO:0009746) | [146](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009746&list=upload_1&organism=Homo%20sapiens) | 7.17 | 2.51 | + | 1.07E-03 | 2.08E-02 | | [response to monosaccharide](http://amigo.geneontology.org/amigo/term/GO:0034284) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0034284&list=upload_1&organism=Homo%20sapiens) | 7.56 | 2.64 | + | 1.94E-04 | 4.99E-03 | | [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) | 8.89 | 2.70 | + | 3.46E-05 | 1.09E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032434&list=upload_1&organism=Homo%20sapiens) | 6.97 | 2.44 | + | 1.77E-03 | 3.13E-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) | [34](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042176&list=upload_1&organism=Homo%20sapiens) | 18.02 | 1.89 | + | 1.10E-03 | 2.13E-02 | | [peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0018108) | [168](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018108&list=upload_1&organism=Homo%20sapiens) | 8.25 | 2.42 | + | 6.56E-04 | 1.40E-02 | | [peptidyl-tyrosine modification](http://amigo.geneontology.org/amigo/term/GO:0018212) | [170](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018212&list=upload_1&organism=Homo%20sapiens) | 8.35 | 2.40 | + | 7.23E-04 | 1.52E-02 | | [peptidyl-amino acid modification](http://amigo.geneontology.org/amigo/term/GO:0018193) | [882](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&reflist=1) | [70](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0018193&list=upload_1&organism=Homo%20sapiens) | 43.31 | 1.62 | + | 2.05E-04 | 5.20E-03 | | [regulation of macroautophagy](http://amigo.geneontology.org/amigo/term/GO:0016241) | [160](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016241&list=upload_1&organism=Homo%20sapiens) | 7.86 | 2.42 | + | 9.35E-04 | 1.87E-02 | | [regulation of autophagy](http://amigo.geneontology.org/amigo/term/GO:0010506) | [345](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0010506&list=upload_1&organism=Homo%20sapiens) | 16.94 | 1.83 | + | 2.76E-03 | 4.46E-02 | | [cellular response to decreased oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0036294) | [136](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&reflist=1) | [16](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0036294&list=upload_1&organism=Homo%20sapiens) | 6.68 | 2.40 | + | 2.74E-03 | 4.44E-02 | | [cellular response to oxygen levels](http://amigo.geneontology.org/amigo/term/GO:0071453) | [153](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071453&list=upload_1&organism=Homo%20sapiens) | 7.51 | 2.40 | + | 1.40E-03 | 2.57E-02 | | [receptor-mediated endocytosis](http://amigo.geneontology.org/amigo/term/GO:0006898) | [171](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006898&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006898&list=upload_1&organism=Homo%20sapiens) | 8.40 | 2.38 | + | 7.61E-04 | 1.58E-02 | | [endocytosis](http://amigo.geneontology.org/amigo/term/GO:0006897) | [528](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006897&reflist=1) | [45](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006897&list=upload_1&organism=Homo%20sapiens) | 25.93 | 1.74 | + | 8.39E-04 | 1.72E-02 | | [regeneration](http://amigo.geneontology.org/amigo/term/GO:0031099) | [154](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&reflist=1) | [18](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031099&list=upload_1&organism=Homo%20sapiens) | 7.56 | 2.38 | + | 1.46E-03 | 2.67E-02 | | [negative regulation of binding](http://amigo.geneontology.org/amigo/term/GO:0051100) | [163](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051100&list=upload_1&organism=Homo%20sapiens) | 8.00 | 2.37 | + | 1.08E-03 | 2.10E-02 | | [potassium ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0071805) | [164](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071805&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071805&list=upload_1&organism=Homo%20sapiens) | 8.05 | 2.36 | + | 1.13E-03 | 2.20E-02 | | [potassium ion transport](http://amigo.geneontology.org/amigo/term/GO:0006813) | [175](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006813&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006813&list=upload_1&organism=Homo%20sapiens) | 8.59 | 2.44 | + | 4.40E-04 | 9.89E-03 | | [inorganic cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0098662) | [606](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098662&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098662&list=upload_1&organism=Homo%20sapiens) | 29.76 | 1.71 | + | 4.63E-04 | 1.03E-02 | | [cation transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0098655) | [675](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098655&reflist=1) | [54](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098655&list=upload_1&organism=Homo%20sapiens) | 33.15 | 1.63 | + | 8.97E-04 | 1.80E-02 | | [inorganic ion transmembrane transport](http://amigo.geneontology.org/amigo/term/GO:0098660) | [701](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098660&reflist=1) | [57](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0098660&list=upload_1&organism=Homo%20sapiens) | 34.42 | 1.66 | + | 4.27E-04 | 9.62E-03 | | [positive regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051091) | [268](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051091&list=upload_1&organism=Homo%20sapiens) | 13.16 | 2.36 | + | 3.94E-05 | 1.22E-03 | | [regulation of DNA-binding transcription factor activity](http://amigo.geneontology.org/amigo/term/GO:0051090) | [438](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&reflist=1) | [42](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0051090&list=upload_1&organism=Homo%20sapiens) | 21.51 | 1.95 | + | 1.06E-04 | 2.95E-03 | | [female pregnancy](http://amigo.geneontology.org/amigo/term/GO:0007565) | [174](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007565&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007565&list=upload_1&organism=Homo%20sapiens) | 8.54 | 2.34 | + | 8.91E-04 | 1.79E-02 | | [multi-organism reproductive process](http://amigo.geneontology.org/amigo/term/GO:0044703) | [195](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044703&reflist=1) | [21](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0044703&list=upload_1&organism=Homo%20sapiens) | 9.58 | 2.19 | + | 1.63E-03 | 2.94E-02 | | [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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001056&list=upload_1&organism=Homo%20sapiens) | 7.27 | 2.34 | + | 2.29E-03 | 3.88E-02 | | [chromatin remodeling](http://amigo.geneontology.org/amigo/term/GO:0006338) | [323](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006338&list=upload_1&organism=Homo%20sapiens) | 15.86 | 2.33 | + | 7.22E-06 | 2.69E-04 | | [chromatin organization](http://amigo.geneontology.org/amigo/term/GO:0006325) | [585](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&reflist=1) | [51](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006325&list=upload_1&organism=Homo%20sapiens) | 28.73 | 1.78 | + | 1.80E-04 | 4.69E-03 | | [positive regulation of peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0050731) | [193](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050731&reflist=1) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050731&list=upload_1&organism=Homo%20sapiens) | 9.48 | 2.32 | + | 5.32E-04 | 1.17E-02 | | [regulation of peptidyl-tyrosine phosphorylation](http://amigo.geneontology.org/amigo/term/GO:0050730) | [261](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050730&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050730&list=upload_1&organism=Homo%20sapiens) | 12.82 | 2.18 | + | 3.36E-04 | 7.91E-03 | | [regulation of heart contraction](http://amigo.geneontology.org/amigo/term/GO:0008016) | [202](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008016&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008016&list=upload_1&organism=Homo%20sapiens) | 9.92 | 2.32 | + | 6.20E-04 | 1.34E-02 | | [positive regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045766) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045766&list=upload_1&organism=Homo%20sapiens) | 8.20 | 2.32 | + | 1.33E-03 | 2.47E-02 | | [regulation of angiogenesis](http://amigo.geneontology.org/amigo/term/GO:0045765) | [288](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045765&list=upload_1&organism=Homo%20sapiens) | 14.14 | 1.98 | + | 1.15E-03 | 2.21E-02 | | [regulation of vasculature development](http://amigo.geneontology.org/amigo/term/GO:1901342) | [292](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901342&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1901342&list=upload_1&organism=Homo%20sapiens) | 14.34 | 1.95 | + | 1.83E-03 | 3.23E-02 | | [positive regulation of vasculature development](http://amigo.geneontology.org/amigo/term/GO:1904018) | [167](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904018&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1904018&list=upload_1&organism=Homo%20sapiens) | 8.20 | 2.32 | + | 1.33E-03 | 2.47E-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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071222&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.31 | + | 5.63E-04 | 1.23E-02 | | [response to lipopolysaccharide](http://amigo.geneontology.org/amigo/term/GO:0032496) | [313](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0032496&list=upload_1&organism=Homo%20sapiens) | 15.37 | 2.02 | + | 6.71E-04 | 1.43E-02 | | [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) | [32](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002237&list=upload_1&organism=Homo%20sapiens) | 16.25 | 1.97 | + | 6.07E-04 | 1.32E-02 | | [response to bacterium](http://amigo.geneontology.org/amigo/term/GO:0009617) | [754](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&reflist=1) | [61](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009617&list=upload_1&organism=Homo%20sapiens) | 37.02 | 1.65 | + | 3.48E-04 | 8.17E-03 | | [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) | [22](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071219&list=upload_1&organism=Homo%20sapiens) | 10.02 | 2.20 | + | 1.20E-03 | 2.31E-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) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0071216&list=upload_1&organism=Homo%20sapiens) | 11.34 | 2.12 | + | 1.37E-03 | 2.53E-02 | | [placenta development](http://amigo.geneontology.org/amigo/term/GO:0001890) | [151](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&reflist=1) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0001890&list=upload_1&organism=Homo%20sapiens) | 7.41 | 2.29 | + | 2.65E-03 | 4.34E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009267&list=upload_1&organism=Homo%20sapiens) | 8.74 | 2.29 | + | 1.11E-03 | 2.15E-02 | | [cellular response to nutrient levels](http://amigo.geneontology.org/amigo/term/GO:0031669) | [226](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&reflist=1) | [27](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031669&list=upload_1&organism=Homo%20sapiens) | 11.10 | 2.43 | + | 6.49E-05 | 1.88E-03 | | [cellular response to extracellular stimulus](http://amigo.geneontology.org/amigo/term/GO:0031668) | [256](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0031668&list=upload_1&organism=Homo%20sapiens) | 12.57 | 2.23 | + | 1.91E-04 | 4.91E-03 | | [response to starvation](http://amigo.geneontology.org/amigo/term/GO:0042594) | [215](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042594&list=upload_1&organism=Homo%20sapiens) | 10.56 | 2.27 | + | 5.03E-04 | 1.11E-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) | [17](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030856&list=upload_1&organism=Homo%20sapiens) | 7.46 | 2.28 | + | 2.78E-03 | 4.49E-02 | | [regulation of canonical Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0060828) | [255](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060828&reflist=1) | [28](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0060828&list=upload_1&organism=Homo%20sapiens) | 12.52 | 2.24 | + | 1.81E-04 | 4.71E-03 | | [regulation of Wnt signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0030111) | [332](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030111&reflist=1) | [31](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0030111&list=upload_1&organism=Homo%20sapiens) | 16.30 | 1.90 | + | 1.48E-03 | 2.70E-02 | | [regulation of cation channel activity](http://amigo.geneontology.org/amigo/term/GO:2001257) | [185](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001257&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:2001257&list=upload_1&organism=Homo%20sapiens) | 9.08 | 2.20 | + | 2.16E-03 | 3.70E-02 | | [positive regulation of supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:1902905) | [176](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902905&reflist=1) | [19](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902905&list=upload_1&organism=Homo%20sapiens) | 8.64 | 2.20 | + | 2.96E-03 | 4.73E-02 | | [regulation of supramolecular fiber organization](http://amigo.geneontology.org/amigo/term/GO:1902903) | [383](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902903&reflist=1) | [33](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902903&list=upload_1&organism=Homo%20sapiens) | 18.81 | 1.75 | + | 3.14E-03 | 4.93E-02 | | [response to wounding](http://amigo.geneontology.org/amigo/term/GO:0009611) | [447](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&reflist=1) | [48](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009611&list=upload_1&organism=Homo%20sapiens) | 21.95 | 2.19 | + | 2.29E-06 | 9.92E-05 | | [B cell activation](http://amigo.geneontology.org/amigo/term/GO:0042113) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0042113&list=upload_1&organism=Homo%20sapiens) | 9.38 | 2.13 | + | 2.67E-03 | 4.36E-02 | | [muscle contraction](http://amigo.geneontology.org/amigo/term/GO:0006936) | [230](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006936&reflist=1) | [24](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006936&list=upload_1&organism=Homo%20sapiens) | 11.29 | 2.13 | + | 1.34E-03 | 2.50E-02 | | [muscle system process](http://amigo.geneontology.org/amigo/term/GO:0003012) | [282](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003012&reflist=1) | [30](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003012&list=upload_1&organism=Homo%20sapiens) | 13.85 | 2.17 | + | 2.01E-04 | 5.11E-03 | | [regulation of innate immune response](http://amigo.geneontology.org/amigo/term/GO:0045088) | [240](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045088&reflist=1) | [25](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0045088&list=upload_1&organism=Homo%20sapiens) | 11.78 | 2.12 | + | 1.01E-03 | 2.00E-02 | | [regulation of response to biotic stimulus](http://amigo.geneontology.org/amigo/term/GO:0002831) | [364](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002831&reflist=1) | [38](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0002831&list=upload_1&organism=Homo%20sapiens) | 17.87 | 2.13 | + | 3.91E-05 | 1.21E-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) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:1902806&list=upload_1&organism=Homo%20sapiens) | 9.43 | 2.12 | + | 2.78E-03 | 4.49E-02 | | [Ras protein signal transduction](http://amigo.geneontology.org/amigo/term/GO:0007265) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007265&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.10 | + | 3.01E-03 | 4.79E-02 | | [regulation of synaptic plasticity](http://amigo.geneontology.org/amigo/term/GO:0048167) | [194](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048167&reflist=1) | [20](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048167&list=upload_1&organism=Homo%20sapiens) | 9.53 | 2.10 | + | 3.01E-03 | 4.79E-02 | | [modulation of chemical synaptic transmission](http://amigo.geneontology.org/amigo/term/GO:0050804) | [438](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050804&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050804&list=upload_1&organism=Homo%20sapiens) | 21.51 | 1.81 | + | 8.79E-04 | 1.78E-02 | | [regulation of trans-synaptic signaling](http://amigo.geneontology.org/amigo/term/GO:0099177) | [439](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099177&reflist=1) | [39](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0099177&list=upload_1&organism=Homo%20sapiens) | 21.56 | 1.81 | + | 8.91E-04 | 1.79E-02 | | [adaptive immune response based on somatic recombination of immune 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polymerase II](http://amigo.geneontology.org/amigo/term/GO:0000122) | [974](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&reflist=1) | [97](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0000122&list=upload_1&organism=Homo%20sapiens) | 47.83 | 2.03 | + | 3.99E-10 | 2.99E-08 | | [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) | [191](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0006357&list=upload_1&organism=Homo%20sapiens) | 127.96 | 1.49 | + | 4.02E-08 | 2.34E-06 | | [response to toxic substance](http://amigo.geneontology.org/amigo/term/GO:0009636) | [232](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009636&reflist=1) | [23](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0009636&list=upload_1&organism=Homo%20sapiens) | 11.39 | 2.02 | + | 2.52E-03 | 4.16E-02 | | [positive regulation of protein kinase 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[408](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008015&reflist=1) | [36](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0008015&list=upload_1&organism=Homo%20sapiens) | 20.03 | 1.80 | + | 1.35E-03 | 2.51E-02 | | [circulatory system process](http://amigo.geneontology.org/amigo/term/GO:0003013) | [498](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003013&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0003013&list=upload_1&organism=Homo%20sapiens) | 24.45 | 1.80 | + | 4.07E-04 | 9.29E-03 | | [muscle structure development](http://amigo.geneontology.org/amigo/term/GO:0061061) | [499](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&reflist=1) | [44](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0061061&list=upload_1&organism=Homo%20sapiens) | 24.50 | 1.80 | + | 4.15E-04 | 9.42E-03 | | [embryonic organ development](http://amigo.geneontology.org/amigo/term/GO:0048568) | [454](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048568&reflist=1) | 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| 7.29E-06 | 2.71E-04 | | [cell cycle process](http://amigo.geneontology.org/amigo/term/GO:0022402) | [841](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&reflist=1) | [66](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022402&list=upload_1&organism=Homo%20sapiens) | 41.30 | 1.60 | + | 3.81E-04 | 8.86E-03 | | [cell migration](http://amigo.geneontology.org/amigo/term/GO:0016477) | [903](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&reflist=1) | [73](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0016477&list=upload_1&organism=Homo%20sapiens) | 44.34 | 1.65 | + | 7.08E-05 | 2.04E-03 | | [cell motility](http://amigo.geneontology.org/amigo/term/GO:0048870) | [1061](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&reflist=1) | [79](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0048870&list=upload_1&organism=Homo%20sapiens) | 52.10 | 1.52 | + | 5.11E-04 | 1.12E-02 | | [neurogenesis](http://amigo.geneontology.org/amigo/term/GO:0022008) | [1290](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&reflist=1) | [88](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0022008&list=upload_1&organism=Homo%20sapiens) | 63.34 | 1.39 | + | 2.94E-03 | 4.70E-02 | | [G protein-coupled receptor signaling pathway](http://amigo.geneontology.org/amigo/term/GO:0007186) | [1223](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007186&reflist=1) | [37](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0007186&list=upload_1&organism=Homo%20sapiens) | 60.05 | .62 | - | 1.91E-03 | 3.36E-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) | [4](http://pantherdb.org/tools/gxIdsList.do?acc=GO:0050911&list=upload_1&organism=Homo%20sapiens) | 21.75 | .18 | - | 1.17E-05 | 4.18E-04 | | [detection of chemical stimulus involved in sensory perception](http://amigo.geneontology.org/amigo/term/GO:0050907) 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