

While parsing your click empty space and and drag to zoom

interpretation of the coordinate axes?

Could not parse GO ID from line: 'Term'. Line will be skipped.

Go term 102337 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Go term 102338 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Go term 102336 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 102391 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Go term 1904831 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Tip: your resulting list of GO terms seems to be quite long. If you want to reduce it further, press the Back button in your browser and choose a different setting for the "allowed similarity" parameter.

Hide/show dispensable GO terms

Export results to text table (CSV)



| term ID | description | frequency | pin? | uniqueness | dispensability |
|-------------------|--|-----------|--------|------------|----------------|
| GO:0008152 | metabolic process | 82.183 % | | 1.00 | 0.00 |
| GO:0016192 | vesicle-mediated transport | 0.381 % | | 0.94 | 0.00 |
| GO:0019835 | cytolysis | 0.185 % | | 0.96 | 0.00 |
| <u>GO:0030212</u> | hyaluronan metabolic process | 0.003 % | | 0.93 | 0.00 |
| <u>GO:0034616</u> | response to laminar fluid shear stress | 0.001 % | | 0.91 | 0.00 |
| GO:0040008 | regulation of growth | 0.042 % | | 0.87 | 0.00 |
| <u>GO:0090245</u> | axis elongation involved in somitogenesis | 0.000 % | -[iii] | 0.86 | 0.70 |
| <u>GO:0030308</u> | negative regulation of cell growth | 0.008 % | -[= | 0.75 | 0.83 |
| GO:0070988 | demethylation | 0.007 % | | 0.92 | 0.00 |
| GO:0060155 | platelet dense granule organization | 0.000 % | | 0.93 | 0.01 |
| GO:0035338 | long-chain fatty-acyl-CoA biosynthetic process | 0.000 % | | 0.91 | 0.02 |
| | | | | | |

| Section Sect | 30.00/1200 | 'de novo' L-methionine biosynthetic process | 0.059 % | -[= | 0.77 | 0.58 | |
|--|---|--|---|---------------------------------------|--|--|--|
| Co. 2007.51 | <u>GO:0006084</u> | acetyl-CoA metabolic process | 0.146 % | | 0.89 | 0.57 | |
| | GO:0045445 | myoblast differentiation | 0.004 % | | 0.89 | 0.03 | |
| Controlled Con | GO:0036155 | acylglycerol acyl-chain remodeling | 0.000 % | | 0.84 | 0.04 | |
| Commons Comm | <u>GO:0006641</u> | triglyceride metabolic process | 0.005 % | -[= | 0.80 | 0.75 | |
| Controlled Control C | GO:0001771 | immunological synapse formation | 0.000 % | | 0.88 | 0.04 | |
| Control Cont | | | | | | | |
| Controlled Con | | | | -[= | | | |
| Commonweight Comm | | | | | | | |
| 10.00000000000000000000000000000000000 | | · | | | | | |
| Decomposition Control Control | | | | | | | |
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| CO.0005255 Security in company of the property in process CO.000 S CO.00 S C | | | | | | | |
| Co.0010666 Double-requisition of cardioc musics cell apoptotic process O.000 % O.22 | | | | | | | |
| | GO:0046166 | glyceraldehyde-3-phosphate biosynthetic process | 0.000 % | | 0.87 | 0.16 | |
| | GO:0010666 | positive regulation of cardiac muscle cell apoptotic process | 0.000 % | | 0.82 | 0.16 | |
| COUNTIEST Upprocess metabolic process 0.000 % 0.01 | <u>GO:2001234</u> | negative regulation of apoptotic signaling pathway | 0.011 % | -[=] | 0.72 | 0.61 | |
| COUNTY- | <u>GO:0010664</u> | negative regulation of striated muscle cell apoptotic process | | -[=] | 0.81 | | |
| | | • • | | | | | |
| Co.0.19922 regulation of cell tycle City phose transition 0.004 % 0.18 0.18 0.005 | | • | | | | | |
| Description of the process of the | | · | | | | | |
| Co-0703098 Inich Innocentation | | · · | | _1=1 | | | |
| | | | | [| | | |
| Conditional Control of Process Control of Control of Process Control of Control of Control of Control of Con | : | • | | -[= | | | |
| December December | | | | | | | |
| December December | | | | | | | |
| Co.0008252 Co.0008262 | <u>GO:0070328</u> | triglyceride homeostasis | 0.002 % | -[=] | 0.85 | 0.84 | |
| CR to Codig viscite mediated transport | GO:0050746 | regulation of lipoprotein metabolic process | 0.001 % | | 0.86 | 0.19 | |
| CO.005746 publisher explication of phosposytaxis 0.001 % | GO:0030521 | androgen receptor signaling pathway | 0.003 % | | 0.81 | 0.20 | |
| Co.0006211 co.000621 co.000621 co.00062 co.00062 co.000621 co.000622 co.00 | GO:0006888 | ER to Golgi vesicle-mediated transport | 0.019 % | | 0.88 | 0.20 | |
| 0.00031142 0.00031142 0.000314 0.000 | <u>GO:0050766</u> | positive regulation of phagocytosis | 0.002 % | -[=] | 0.75 | 0.82 | |
| Co.0018272 protein protein binnetic transport 0.00 % 0.92 0.24 | <u>GO:0006911</u> | phagocytosis, engulfment | 0.001 % | -[=] | | | |
| December December | | • | | | | | |
| Co.0015917 amiophospholipit transport | | | | | | | |
| C0.0023202 Department De | | · | | | | | |
| Description | : | | | -[=] | | | |
| Co.0031314 choiesterol efflux | | | | | | | |
| Co:00173167 Intracellular cholesteral transport | 00.0013332 | phosphotipia transtocation | | | 0.72 | 0.72 | |
| G0:0015908 fatty acid transport 0.003 % | GO:0033344 | cholesterol efflux | | | 0.86 | 0.50 | |
| GO:0016062 adaptation of rhodopsin mediated signaling 0.000 % 0.80 0.26 | | | 0.002 % | -[= | | | |
| G0:0006953 acute-phase response 0.002 % 0.89 0.27 | <u>GO:0032367</u> | intracellular cholesterol transport | 0.002 % 0.001 % | -[ii | 0.86 | 0.88 | |
| GO:0019346 transulfuration | <u>G0:0032367</u> <u>G0:0015908</u> | intracellular cholesterol transport fatty acid transport | 0.002 % 0.001 % 0.003 % | | 0.86 | 0.88 0.67 | |
| G0:0006514 slycine metabolic process 0.250 % | <u>G0:0032367</u> <u>G0:0015908</u> <u>G0:0043314</u> | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation | 0.002 % 0.001 % 0.003 % 0.000 % | | 0.86 0.86 0.70 | 0.88 0.67 0.66 | |
| GO:0008202 Serine family amino acid biosynthetic process 0.413 % | <u>G0:0032367</u> <u>G0:0015908</u> <u>G0:0043314</u> <u>G0:0016062</u> | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % | | 0.86 0.86 0.70 0.80 | 0.88 0.67 0.66 0.26 | |
| G0:0008202 steroid metabolic process 0.040 % 0.80 0.28 -G0:0008299 isoprenoid biosynthetic process 0.463 % -□ 0.74 0.73 -G0:0006631 fatty acid metabolic process 0.669 % -□ 0.71 0.79 -G0:0006631 fatty acid biosynthetic process 0.669 % -□ 0.74 0.58 -G0:0008610 lipid biosynthetic process 0.000 % 0.90 0.32 -G0:0008623 typophan transport 0.000 % 0.90 0.32 -G0:0008631 cetrahydrofelate interconversion 0.140 % 0.84 0.33 -G0:0035999 tetrahydrofelate interconversion 0.010 % 0.88 0.33 -G0:0002790 peptide secretion 0.010 % 0.88 0.33 -G0:0002791 cetrahydrofelate interconversion 0.000 % 0.78 0.34 -G0:00042761 very long-chain fatty acid biosynthetic process 0.001 % 0.78 0.34 -G0:00042761 very long-chain fatty acid biosynthetic process 0.000 % 0.81 0.34 -G0:00042761 very long-chain fatty acid biosynthetic process 0.000 % 0.81 0.34 -G0:00045908 negative regulation of blood vessel remodeling 0.000 % 0.81 0.34 -G0:0045908 negative regulation of vasodilation 0.000 % 0.89 0.36 -G0:0005808 0.0005804 0.000580 0 | <u>G0:0032367</u> <u>G0:0015908</u> <u>G0:0043314</u> G0:0016062 G0:0006953 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % | | 0.86 0.86 0.70 0.80 0.89 | 0.88 0.67 0.66 0.26 0.27 | |
| GO:0008299 Isoprenoid biosynthetic process 0.463 % | <u>GO:0032367</u> <u>GO:0015908</u> <u>GO:0043314</u> GO:0016062 GO:0006953 GO:0019346 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % | 古古古 | 0.86 0.86 0.70 0.80 0.89 0.84 | 0.88 0.67 0.66 0.26 0.27 0.28 | |
| GO:0006631 fatty acid metabolic process 0.867 % | <u>GO:0032367</u> <u>GO:0015908</u> <u>GO:0043314</u> GO:0016062 GO:0006953 GO:0019346 <u>GO:0009070</u> | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % | 古古古 | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 | |
| GQ:0006631 fatty acid biosynthetic process Q.629 % | GO:0032367 GO:0015908 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0009070 GO:0008202 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % | | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 | |
| CG:0008610 Itiple biosynthetic process 2.706 % | GO:0032367 GO:0015908 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0008202 GO:0008299 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % | 1 1 1 1 1 | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 | |
| Co:0015827 Co:0006743 Ubiquinone metabolic process Co:0006743 Ubiquinone metabolic process Co:0006743 Ubiquinone metabolic process Co:0006743 Ubiquinone metabolic process Co:0002790 Co:0002790 Deptide secretion Co:0002790 Deptide secretion Co:0002790 Deptide secretion Co:0002790 | GO:0032367 GO:0015908 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0008202 GO:0008299 GO:0006631 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process fatty acid metabolic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % 0.867 % | 1 | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 0.74 0.71 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 0.73 0.79 | |
| GO:0006743 Ubiquinone metabolic process O.140 % O.84 O.33 | GO:0032367 GO:0015908 GO:0043314 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0008202 GO:0008299 GO:0006631 GO:0006633 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process fatty acid metabolic process fatty acid biosynthetic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % 0.867 % 0.629 % | | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 0.74 0.71 0.69 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 0.73 0.79 0.76 | |
| G0:0035999 tetrahydrofolate interconversion 0.102 | GO:0032367 GO:0015908 GO:0015908 GO:0043314 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0008202 GO:0008202 GO:0006631 GO:0008610 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process fatty acid metabolic process fatty acid biosynthetic process lipid biosynthetic process | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % 0.867 % 0.629 % 2.206 % | | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 0.74 0.71 0.69 0.74 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 0.73 0.79 0.76 0.58 | |
| GO:0002790 peptide secretion 0.010 % 0.88 0.33 GO:0042761 very long-chain fatty acid biosynthetic process 0.001 % 0.78 0.34 GO:0000717 nucleotide-excision repair, DNA duplex unwinding 0.000 % 0.81 0.34 GO:0060313 negative regulation of blood vessel remodeling 0.000 % 0.81 0.34 L GO:0045908 negative regulation of vasodilation 0.000 % □ 0.89 0.36 GO:000558 proteolysis 3.705 % 0.89 0.36 GO:0007584 response to nutrient 0.004 % 0.89 0.37 L GO:00042493 response to drug 0.207 % □ 0.88 0.50 GO:0009083 branched-chain amino acid catabolic process 0.010 % 0.83 0.38 L GO:0006104 negative regulation of wound healing 0.000 % 0.81 0.59 GO:0061045 negative regulation of wound healing 0.000 % 0.79 0.38 GO:0061045 negative regulation of wound healing nembryonic process involved in female pregnancy 0.000 % 0.88 0.38 GO:0060136 nembryonic neurocranium morphosenesis 0.000 % □ 0.88 0.3 | GO:0032367 GO:0015908 GO:0015908 GO:0043314 GO:0016062 GO:0006953 GO:0019346 GO:0006544 GO:0008202 GO:0008202 GO:0006631 GO:0008610 GO:0015827 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process fatty acid metabolic process fatty acid biosynthetic process lipid biosynthetic process tryptophan transport | 0.002 % 0.001 % 0.003 % 0.000 % 0.000 % 0.002 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % 0.867 % 0.629 % 2.206 % 0.000 % | | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 0.74 0.71 0.69 0.74 0.90 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 0.73 0.79 0.76 0.58 0.32 | |
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| GO:0042493 response to drug 0.207 % | GO:0032367 GO:0015908 GO:0015908 GO:0043314 GO:0016062 GO:0006953 GO:0006544 GO:0009070 GO:0008202 GO:0006631 GO:0006631 GO:0006631 GO:0006743 GO:0006743 GO:0002790 GO:0002790 GO:00042761 GO:0006717 GO:00060313 GO:0045908 | intracellular cholesterol transport fatty acid transport negative regulation of neutrophil degranulation adaptation of rhodopsin mediated signaling acute-phase response transsulfuration glycine metabolic process serine family amino acid biosynthetic process steroid metabolic process isoprenoid biosynthetic process fatty acid metabolic process fatty acid biosynthetic process lipid biosynthetic process tryptophan transport ubiquinone metabolic process tetrahydrofolate interconversion peptide secretion very long-chain fatty acid biosynthetic process nucleotide-excision repair, DNA duplex unwinding negative regulation of blood vessel remodeling negative regulation of vasodilation | 0.002 % 0.001 % 0.000 % 0.000 % 0.000 % 0.000 % 0.250 % 0.413 % 0.040 % 0.463 % 0.867 % 0.629 % 2.206 % 0.000 % 0.140 % 0.102 % 0.010 % 0.001 % 0.000 % 0.000 % | | 0.86 0.86 0.70 0.80 0.89 0.84 0.80 0.76 0.80 0.74 0.71 0.69 0.74 0.90 0.84 0.79 0.88 0.78 0.81 0.81 0.79 | 0.88 0.67 0.66 0.26 0.27 0.28 0.50 0.87 0.28 0.73 0.79 0.76 0.58 0.32 0.33 0.52 0.33 0.34 0.34 0.34 0.34 0.58 | |
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| <u>GO:0034626</u> | fatty acid elongation, polyunsaturated fatty acid | 0.000 % | -[=] | 0.77 | 0.95 |
|-------------------|--|---------|-------|------|------|
| <u>GO:0019367</u> | fatty acid elongation, saturated fatty acid | 0.000 % | -[=] | 0.77 | 0.86 |
| GO:0042574 | retinal metabolic process | 0.001 % | | 0.81 | 0.42 |
| <u>GO:0042572</u> | retinol metabolic process | 0.001 % | -[ii] | 0.70 | 0.91 |
| GO:0002357 | defense response to tumor cell | 0.000 % | | 0.89 | 0.42 |
| <u>GO:0002418</u> | immune response to tumor cell | 0.001 % | -[ii | 0.86 | 0.92 |
| GO:0006694 | steroid biosynthetic process | 0.030 % | | 0.76 | 0.42 |
| <u>GO:0008203</u> | cholesterol metabolic process | 0.007 % | -[=] | 0.75 | 0.88 |
| <u>GO:0016126</u> | sterol biosynthetic process | 0.006 % | -[ii | 0.74 | 0.93 |
| <u>GO:0006695</u> | cholesterol biosynthetic process | 0.002 % | -[ii] | 0.75 | 0.89 |
| <u>GO:0033488</u> | cholesterol biosynthetic process via 24,25-dihydrolanosterol | 0.000 % | -[ii | 0.80 | 0.64 |
| GO:0032489 | regulation of Cdc42 protein signal transduction | 0.001 % | | 0.79 | 0.45 |
| GO:0006936 | muscle contraction | 0.018 % | | 0.88 | 0.46 |
| <u>GO:0007275</u> | multicellular organismal development | 0.460 % | -[ii | 0.86 | 0.69 |
| GO:0006636 | unsaturated fatty acid biosynthetic process | 0.007 % | | 0.76 | 0.47 |
| GO:0030819 | positive regulation of cAMP biosynthetic process | 0.003 % | | 0.75 | 0.47 |
| <u>GO:0001970</u> | positive regulation of activation of membrane attack complex | 0.000 % | -[=] | 0.72 | 0.68 |
| <u>GO:0006957</u> | complement activation, alternative pathway | 0.000 % | -[=] | 0.74 | 0.70 |
| <u>GO:0006958</u> | complement activation, classical pathway | 0.001 % | -[ii | 0.73 | 0.76 |
| <u>GO:0006956</u> | complement activation | 0.069 % | -[ii] | 0.68 | 0.56 |
| GO:0055098 | response to low-density lipoprotein particle | 0.001 % | | 0.90 | 0.48 |
| : | response to ethanol | 0.003 % | -[=] | 0.89 | 0.52 |

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Could not parse GO ID from line: 'Term'. Line will be skipped.
Go term 102337 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Go term 102338 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 102336 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 102391 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 1904831 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

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Export results to text table (CSV)



Make R script for plotting

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|-------------------|--|--|-------|------------|----------------|
| term ID | description | frequency | pin? | uniqueness | dispensability |
| GO:0005576 | extracellular region | 4.572 % | | 0.93 | 0.00 |
| <u>GO:0005615</u> | extracellular space | 0.249 % | | 0.86 | 0.00 |
| <u>GO:0016020</u> | membrane | 51.720 % | | 0.97 | 0.00 |
| GO:0045121 | membrane raft | 0.025 % | | 0.83 | 0.00 |
| <u>GO:0016324</u> | apical plasma membrane | 0.024 % | -[=] | 0.79 | 0.75 |
| GO:0097447 | dendritic tree | 0.006 % | | 0.85 | 0.00 |
| <u>GO:0043025</u> | neuronal cell body | 0.028 % | -[ii] | 0.85 | 0.78 |
| GO:0005811 | lipid particle | 0.010 % | | 0.70 | 0.02 |
| <u>GO:0005579</u> | membrane attack complex | 0.002 % | | 0.80 | 0.07 |
| <u>GO:0030118</u> | clathrin coat | 0.051 % | -[ii | 0.66 | 0.62 |
| GO:0016021 | integral component of membrane | 35.230 % | | 0.89 | 0.14 |
| <u>GO:0044194</u> | cytolytic granule | 0.000 % | | 0.66 | 0.15 |
| <u>GO:0005764</u> | lysosome | 0.049 % | -[=] | 0.59 | 0.76 |
| <u>GO:0031904</u> | endosome lumen | 0.000 % | | 0.61 | 0.17 |
| <u>GO:0030176</u> | integral component of endoplasmic reticulum membrane | 0.034 % | -[ii] | 0.50 | 0.90 |
| <u>GO:0005783</u> | endoplasmic reticulum | 0.299 % | -[=] | 0.52 | 0.50 |
| <u>GO:0005789</u> | endoplasmic reticulum membrane | 0.136 % | -[= | 0.47 | 0.80 |
| GO:0031410 | cytoplasmic vesicle | 0.167 % | | 0.61 | 0.20 |
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| GO:0070062 | extracellular exosome | 0.300 % | -[=] | 0.53 | 0.88 |
|-------------------|--|---------|-------|------|------|
| GO:0008274 | gamma-tubulin ring complex | 0.001 % | | 0.66 | 0.22 |
| GO:0005833 | hemoglobin complex | 0.014 % | | 0.71 | 0.23 |
| GO:0031430 | M band | 0.002 % | | 0.66 | 0.24 |
| GO:0005856 | cytoskeleton | 0.714 % | | 0.64 | 0.34 |
| GO:0005778 | peroxisomal membrane | 0.027 % | | 0.52 | 0.37 |
| GO:0005739 | mitochondrion | 3.808 % | | 0.51 | 0.39 |
| <u>GO:0043231</u> | intracellular membrane-bounded organelle | 8.847 % | -[ii] | 0.52 | 0.77 |
| GO:0072562 | blood microparticle | 0.012 % | | 0.87 | 0.46 |
| GO:0005759 | mitochondrial matrix | 0.055 % | | 0.56 | 0.49 |
| <u>GO:0005654</u> | nucleoplasm | 0.221 % | -[=] | 0.55 | 0.77 |

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While parsing your data, warning(s) were encountered:
Could not parse GO ID from line: 'Term'. Line will be skipped.
Go term 102337 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Go term 102338 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 102336 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 102391 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped. Go term 1904831 was not found in the current version of the GeneOntology, dated 26:06:2015 07:17. GO term will be skipped.

Hide/show dispensable GO terms



Export results to text table (CSV)



Make R script for plotting

| <u>Indersitor</u> | r dispensable do ternis | <u>Export resut</u> | to to text | table (est) | make it script for ptotting |
|-------------------|---|---------------------|------------|-------------|-----------------------------|
| term ID | description | frequency | pin? | uniqueness | dispensability |
| GO:0003713 | transcription coactivator activity | 0.025 % | | 0.94 | 0.00 |
| <u>GO:0001105</u> | RNA polymerase II transcription coactivator activity | 0.002 % | -[ii | 0.94 | 0.77 |
| GO:0003824 | catalytic activity | 69.295 % | | 0.99 | 0.00 |
| GO:0005044 | scavenger receptor activity | 0.013 % | | 0.95 | 0.00 |
| GO:0016874 | ligase activity | 3.868 % | | 0.95 | 0.00 |
| GO:0022829 | wide pore channel activity | 0.137 % | | 0.93 | 0.00 |
| GO:0030247 | polysaccharide binding | 0.035 % | | 0.94 | 0.00 |
| GO:0030294 | receptor signaling protein tyrosine kinase inhibitor activity | 0.000 % | | 0.91 | 0.00 |
| <u>GO:0004866</u> | endopeptidase inhibitor activity | 0.084 % | -[ii | 0.89 | 0.61 |
| <u>GO:0004867</u> | serine-type endopeptidase inhibitor activity | 0.030 % | -[ii] | 0.89 | 0.93 |
| <u>GO:0004869</u> | cysteine-type endopeptidase inhibitor activity | 0.025 % | -[ii] | 0.89 | 0.92 |
| GO:0009922 | fatty acid elongase activity | 0.000 % | | 0.94 | 0.01 |
| GO:0008398 | sterol 14-demethylase activity | 0.001 % | | 0.92 | 0.01 |
| <u>GO:0004506</u> | squalene monooxygenase activity | 0.002 % | -[ii] | 0.92 | 0.62 |
| GO:0080146 | L-cysteine desulfhydrase activity | 0.002 % | | 0.92 | 0.02 |
| <u>GO:0004123</u> | cystathionine gamma-lyase activity | 0.002 % | -[ii | 0.92 | 0.61 |
| <u>GO:0044540</u> | L-cystine L-cysteine-lyase (deaminating) | 0.002 % | -[=] | 0.92 | 0.60 |
| GO:0004075 | biotin carboxylase activity | 0.108 % | | 0.88 | 0.02 |
| | | | | | |

| GO:0008234 | cysteine-type peptidase activity | 0.221 % | | 0.90 | 0.02 |
|-------------------|---|----------|-------|------|------|
| <u>GO:0004252</u> | serine-type endopeptidase activity | 0.675 % | -[ii] | 0.89 | 0.94 |
| <u>GO:0008236</u> | serine-type peptidase activity | 1.044 % | -[=] | 0.89 | 0.64 |
| GO:0034186 | apolipoprotein A-I binding | 0.000 % | | 0.90 | 0.02 |
| GO:0019825 | oxygen binding | 0.074 % | | 0.94 | 0.03 |
| GO:0005543 | phospholipid binding | 0.064 % | | 0.92 | 0.04 |
| GO:0044822 | poly(A) RNA binding | 0.135 % | | 0.94 | 0.04 |
| GO:0016491 | oxidoreductase activity | 14.657 % | | 0.95 | 0.04 |
| GO:0005515 | protein binding | 2.482 % | | 0.93 | 0.05 |
| GO:0048037 | cofactor binding | 6.702 % | | 0.93 | 0.08 |
| GO:0000234 | phosphoethanolamine N-methyltransferase activity | 0.000 % | | 0.94 | 0.09 |
| GO:0015020 | glucuronosyltransferase activity | 0.003 % | | 0.94 | 0.10 |
| GO:0005509 | calcium ion binding | 0.365 % | | 0.92 | 0.11 |
| GO:0003962 | cystathionine gamma-synthase activity | 0.010 % | | 0.94 | 0.12 |
| GO:0052650 | NADP-retinol dehydrogenase activity | 0.000 % | | 0.92 | 0.13 |
| GO:0008201 | heparin binding | 0.013 % | | 0.91 | 0.15 |
| GO:0070402 | NADPH binding | 0.068 % | | 0.90 | 0.17 |
| GO:0005344 | oxygen transporter activity | 0.039 % | | 0.93 | 0.26 |
| GO:0050733 | RS domain binding | 0.000 % | | 0.90 | 0.28 |
| GO:0000166 | nucleotide binding | 20.353 % | | 0.91 | 0.29 |
| GO:0005548 | phospholipid transporter activity | 0.019 % | | 0.90 | 0.30 |
| <u>GO:0090556</u> | phosphatidylserine-translocating ATPase activity | 0.012 % | -[=] | 0.87 | 0.80 |
| <u>GO:0090554</u> | phosphatidylcholine-translocating ATPase activity | 0.012 % | -[= | 0.85 | 1.00 |
| <u>GO:0047676</u> | arachidonate-CoA ligase activity | 0.000 % | | 0.88 | 0.30 |
| GO:0004745 | retinol dehydrogenase activity | 0.001 % | | 0.91 | 0.31 |
| GO:0051117 | ATPase binding | 0.002 % | | 0.89 | 0.31 |
| GO:0004372 | glycine hydroxymethyltransferase activity | 0.056 % | | 0.93 | 0.33 |
| GO:0005506 | iron ion binding | 2.467 % | | 0.91 | 0.34 |
| GO:0042282 | hydroxymethylglutaryl-CoA reductase activity | 0.002 % | | 0.91 | 0.35 |
| GO:0034188 | apolipoprotein A-I receptor activity | 0.000 % | | 0.95 | 0.35 |
| GO:0004658 | propionyl-CoA carboxylase activity | 0.003 % | | 0.88 | 0.36 |
| <u>GO:0003989</u> | acetyl-CoA carboxylase activity | 0.129 % | -[= | 0.87 | 0.78 |
| GO:0001848 | complement binding | 0.018 % | | 0.88 | 0.37 |
| GO:0016901 | oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor | 0.136 % | | 0.90 | 0.42 |
| GO:0030170 | pyridoxal phosphate binding | 1.703 % | | 0.89 | 0.44 |
| <u>GO:0009374</u> | biotin binding | 0.000 % | | 0.90 | 0.45 |
| <u>GO:0031177</u> | phosphopantetheine binding | 0.062 % | -[ii] | 0.90 | 0.52 |
| GO:0031957 | very long-chain fatty acid-CoA ligase activity | 0.001 % | | 0.87 | 0.48 |
| <u>GO:0030729</u> | acetoacetate-CoA ligase activity | 0.005 % | -[=] | 0.87 | 0.57 |
| <u>GO:0004467</u> | long-chain fatty acid-CoA ligase activity | 0.016 % | -[ii] | 0.86 | 0.80 |
| GO:0042802 | identical protein binding | 0.154 % | | 0.87 | 0.48 |
| <u>GO:0005102</u> | receptor binding | 0.416 % | -[ii] | 0.87 | 0.60 |
| | | | | | |

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Frequent keywords within your set of GO terms:

metabolism multicellular morphology activitory heterocycle single-organism subcellular coo- trigger transform aged compound oils dismantle microbody culminates non-living similarly lipids very-long-chain individual reactions metabolic deteriorating cease organic attack inherited renovation non-encoded flippase proteinase saturated fatty-acid immunological skeleton peptidolysis organonitrogen glyceride vacuoles acids proteolytic Caspases chemical gradually leucocyte tcc encapsulating biochemical net organismal mac simply actions abiotic non-membrane-bounded organism-specific halting substances peptidase immune subcomponent monocarboxylic immunogenic organelle pathways process bounded cellular macromolecules

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