

Genes GENES - GO Molecular Function Annotations

Used notations:

- **List Hits** - the number of genes annotated by the considered GO Molecular Function category or annotation cluster within the analyzed list of target genes
- **List Total** - the number of genes within the analyzed list of target genes having at least one GO Molecular Function annotation
- **Population Hits** - the number of genes, available on the entire microarray, annotated by the considered GO Molecular Function category or annotation cluster
- **Population Total** - the number of genes available on the entire microarray and having at least one GO Molecular Function annotation
- **P-value** - the significance p-value of the gene enrichment of the considered GO Molecular Function category or annotation cluster, calculated with a unilateral Fisher exact test

Terms

| Rank | ID | Term | List Hits | List Total | Population Hits | Population Total | P-value | Genes ID's | Genes Names |
|------|------------|---|-----------|------------|-----------------|------------------|----------|------------|---|
| 1 | GO:0005515 | protein binding | 267 | 470 | 5297 | 14962 | 6.14e-22 | | CD24 molecule |
| 2 | GO:0003723 | RNA binding | 38 | 470 | 608 | 14962 | 4.35e-05 | | synaptotagmin binding, cytoplasmic RNA interacting protein |
| 3 | GO:0003735 | structural constituent of ribosome | 26 | 470 | 158 | 14962 | 3.76e-12 | | mitochondrial ribosomal protein L21 |
| 4 | GO:0016491 | oxidoreductase activity | 23 | 470 | 441 | 14962 | 1.24e-02 | | peroxiredoxin 3 |
| 5 | GO:0042802 | identical protein binding | 20 | 470 | 360 | 14962 | 1.01e-02 | | nucleotide-binding oligomerization domain containing 1 |
| 6 | GO:0051082 | unfolded protein binding | 15 | 470 | 126 | 14962 | 9.63e-06 | | crystallin, alpha B |
| 7 | GO:0003713 | transcription coactivator activity | 14 | 470 | 203 | 14962 | 4.96e-03 | | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 |
| 8 | GO:0003924 | GTPase activity | 14 | 470 | 222 | 14962 | 1.06e-02 | | eukaryotic translation elongation factor 2 |
| 9 | GO:0016887 | ATPase activity | 12 | 470 | 142 | 14962 | 1.74e-03 | | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d |
| 10 | GO:0031625 | ubiquitin protein ligase binding | 10 | 470 | 90 | 14962 | 5.14e-04 | | deiodinase, iodothyronine, type II |
| 11 | GO:0003743 | translation initiation factor activity | 8 | 470 | 52 | 14962 | 1.99e-04 | | eukaryotic translation initiation factor 1 |
| 12 | GO:0032403 | protein complex binding | 8 | 470 | 107 | 14962 | 1.94e-02 | | laminin, beta 3 |
| 13 | GO:0046961 | proton-transporting ATPase activity, rotational mechanism | 8 | 470 | 19 | 14962 | 4.98e-08 | | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2 |
| 14 | GO:0022857 | transmembrane transporter activity | 7 | 470 | 36 | 14962 | 1.09e-04 | | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d |

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|----|------------|---|---|-----|----|-------|----------|---|
| 15 | GO:0004129 | cytochrome-c oxidase activity | 7 | 470 | 28 | 14962 | 1.93e-05 | cytochrome c oxidase subunit VIa polypeptide 1 |
| 16 | GO:0008430 | selenium binding | 7 | 470 | 13 | 14962 | 4.21e-08 | deiodinase, iodothyronine, type I |
| 17 | GO:0046933 | hydrogen ion transporting ATP synthase activity, rotational mechanism | 7 | 470 | 15 | 14962 | 1.49e-07 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2 |
| 18 | GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 7 | 470 | 44 | 14962 | 4.04e-04 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa |
| 19 | GO:0051087 | chaperone binding | 6 | 470 | 39 | 14962 | 1.26e-03 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) |
| 20 | GO:0030246 | carbohydrate binding | 6 | 470 | 30 | 14962 | 2.91e-04 | glucosidase, alpha; neutral AB |
| 21 | GO:0004601 | peroxidase activity | 5 | 470 | 20 | 14962 | 3.14e-04 | peroxiredoxin 3 |
| 22 | GO:0003729 | mRNA binding | 5 | 470 | 47 | 14962 | 1.55e-02 | nudix (nucleoside diphosphate linked moiety X)-type motif 21 |
| 23 | GO:0004579 | dolichyl-diphosphooligosaccharide-protein glycotransferase activity | 5 | 470 | 9 | 14962 | 3.4e-06 | defender against cell death 1 |
| 24 | GO:0031072 | heat shock protein binding | 5 | 470 | 62 | 14962 | 4.49e-02 | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) |
| 25 | GO:0015035 | protein disulfide oxidoreductase activity | 5 | 470 | 28 | 14962 | 1.62e-03 | protein disulfide isomerase family A, member 3 |
| 26 | GO:0008307 | structural constituent of muscle | 4 | 470 | 44 | 14962 | 4.86e-02 | myosin, light chain 9, regulatory |
| 27 | GO:0050681 | androgen receptor binding | 4 | 470 | 36 | 14962 | 2.56e-02 | peroxisome proliferator-activated receptor gamma, coactivator 1 alpha |
| 28 | GO:0008092 | cytoskeletal protein binding | 4 | 470 | 37 | 14962 | 2.8e-02 | dynein, light chain, LC8-type 2 |
| 29 | GO:0003756 | protein disulfide isomerase activity | 4 | 470 | 9 | 14962 | 1.07e-04 | endoplasmic reticulum protein 44 |
| 30 | GO:0043022 | ribosome binding | 4 | 470 | 21 | 14962 | 3.76e-03 | eukaryotic translation initiation factor 3, subunit K |
| 31 | GO:0004602 | glutathione peroxidase activity | 4 | 470 | 15 | 14962 | 9.96e-04 | glutathione peroxidase 3 (plasma) |
| 32 | GO:0031683 | G-protein beta/gamma-subunit complex binding | 3 | 470 | 20 | 14962 | 2.36e-02 | centrin, EF-hand protein, 2 |
| 33 | GO:0004180 | carboxypeptidase activity | 3 | 470 | 20 | 14962 | 2.36e-02 | NODAL modulator 1 |
| 34 | GO:0050839 | cell adhesion molecule binding | 3 | 470 | 20 | 14962 | 2.36e-02 | neuroplastin |
| 35 | GO:0019838 | growth factor binding | 3 | 470 | 23 | 14962 | 3.42e-02 | kinase insert domain receptor (a type III receptor tyrosine kinase) |
| 36 | GO:0046870 | cadmium ion binding | 3 | 470 | 7 | 14962 | 9.81e-04 | metallothionein 1A |
| | | hydrolase activity, acting | | | | | | |

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|----|------------|---|---|-----|----|-------|----------|--|
| 37 | GO:0016820 | on acid anhydrides, catalyzing transmembrane movement of substances | 3 | 470 | 23 | 14962 | 3.42e-02 | ATPase, Na+/K+ transporting, alpha 1 polypeptide |
| 38 | GO:0050699 | WW domain binding | 3 | 470 | 19 | 14962 | 2.05e-02 | WW domain binding protein 5 |
| 39 | GO:0004298 | threonine-type endopeptidase activity | 3 | 470 | 21 | 14962 | 2.69e-02 | proteasome (prosome, macropain) subunit, alpha type, 3 |
| 40 | GO:0030295 | protein kinase activator activity | 2 | 470 | 10 | 14962 | 3.75e-02 | target of myb1 (chicken)-like 1 |
| 41 | GO:0051920 | peroxiredoxin activity | 2 | 470 | 4 | 14962 | 5.66e-03 | peroxiredoxin 3 |
| 42 | GO:0050811 | GABA receptor binding | 2 | 470 | 8 | 14962 | 2.43e-02 | GABA(A) receptor-associated protein |
| 43 | GO:0004016 | adenylate cyclase activity | 2 | 470 | 11 | 14962 | 4.49e-02 | adenylate cyclase 9 |
| 44 | GO:0015116 | sulfate transmembrane transporter activity | 2 | 470 | 6 | 14962 | 1.36e-02 | solute carrier family 26, member 7 |
| 45 | GO:0004185 | serine-type carboxypeptidase activity | 2 | 470 | 5 | 14962 | 9.25e-03 | carboxypeptidase D |
| 46 | GO:0030276 | clathrin binding | 2 | 470 | 9 | 14962 | 3.06e-02 | adaptor-related protein complex 2, beta 1 subunit |
| 47 | GO:0003724 | RNA helicase activity | 2 | 470 | 10 | 14962 | 3.75e-02 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 |
| 48 | GO:0004800 | thyroxine 5'-deiodinase activity | 2 | 470 | 3 | 14962 | 2.89e-03 | deiodinase, iodothyronine, type I |
| 49 | GO:0042623 | ATPase activity, coupled | 2 | 470 | 10 | 14962 | 3.75e-02 | dynein, cytoplasmic 1, heavy chain 1 |
| 50 | GO:0043295 | glutathione binding | 2 | 470 | 7 | 14962 | 1.86e-02 | glutathione peroxidase 3 (plasma) |
| 51 | GO:0008121 | ubiquinol-cytochrome-c reductase activity | 2 | 470 | 8 | 14962 | 2.43e-02 | ubiquinol-cytochrome c reductase, complex III subunit X |
| 52 | GO:0003857 | 3-hydroxyacyl-CoA dehydrogenase activity | 2 | 470 | 8 | 14962 | 2.43e-02 | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit |
| 53 | GO:0004300 | enoyl-CoA hydratase activity | 2 | 470 | 6 | 14962 | 1.36e-02 | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit |
| 54 | GO:0016509 | long-chain-3-hydroxyacyl-CoA dehydrogenase activity | 2 | 470 | 3 | 14962 | 2.89e-03 | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit |
| 55 | GO:0044183 | protein binding involved in protein folding | 2 | 470 | 2 | 14962 | 9.85e-04 | heat shock 70kDa protein 1B |
| 56 | GO:0051787 | misfolded protein binding | 2 | 470 | 10 | 14962 | 3.75e-02 | heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) |
| 57 | GO:0030235 | nitric-oxide synthase regulator activity | 2 | 470 | 6 | 14962 | 1.36e-02 | heat shock protein 90kDa alpha (cytosolic), class A member 1 |
| 58 | GO:0030911 | TPR domain binding | 2 | 470 | 4 | 14962 | 5.66e-03 | heat shock protein 90kDa alpha (cytosolic), class A member 1 |
| 59 | GO:0004447 | iodide peroxidase activity | 2 | 470 | 2 | 14962 | 9.85e- | iodotyrosine deiodinase |

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| 60 | GO:0051019 | mitogen-activated protein kinase binding | 2 | 470 | 8 | 14962 | 2.43e-02 | | phosphatidylethanolamine binding protein 1 |
| 61 | GO:0008379 | thioredoxin peroxidase activity | 2 | 470 | 4 | 14962 | 5.66e-03 | | peroxiredoxin 1 |
| 62 | GO:0008553 | hydrogen-exporting ATPase activity, phosphorylative mechanism | 2 | 470 | 7 | 14962 | 1.86e-02 | | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide |
| 63 | GO:0052650 | NADP-retinol dehydrogenase activity | 2 | 470 | 4 | 14962 | 5.66e-03 | | retinol dehydrogenase 11 (all-trans/9-cis/11-cis) |
| 64 | GO:0004427 | inorganic diphosphatase activity | 2 | 470 | 4 | 14962 | 5.66e-03 | | pyrophosphatase (inorganic) 1 |
| 65 | GO:0008312 | 7S RNA binding | 2 | 470 | 6 | 14962 | 1.36e-02 | | signal recognition particle 14kDa (homologous Alu RNA binding protein) |
| 66 | GO:0005047 | signal recognition particle binding | 2 | 470 | 4 | 14962 | 5.66e-03 | | signal recognition particle 72kDa |
| 67 | GO:0001849 | complement component C1q binding | 2 | 470 | 3 | 14962 | 2.89e-03 | | complement component 1, q subcomponent binding protein |
| 68 | GO:0008785 | alkyl hydroperoxide reductase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | peroxiredoxin 3 |
| 69 | GO:0022803 | passive transmembrane transporter activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | solute carrier family 5 (iodide transporter), member 8 |
| 70 | GO:0003955 | NAD(P)H dehydrogenase (quinone) activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | NAD(P)H dehydrogenase, quinone 1 |
| 71 | GO:0004149 | dihydrolipoyllysine-residue succinyltransferase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) |
| 72 | GO:0018738 | S-formylglutathione hydrolase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | esterase D |
| 73 | GO:0033919 | glucan 1,3-alpha-glucosidase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | glucosidase, alpha; neutral AB |
| 74 | GO:0003957 | NAD(P) ⁺ transhydrogenase (B-specific) activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | nicotinamide nucleotide transhydrogenase |
| 75 | GO:0008750 | NAD(P) ⁺ transhydrogenase (AB-specific) activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | nicotinamide nucleotide transhydrogenase |
| 76 | GO:0015068 | glycine amidinotransferase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | glycine amidinotransferase (L-arginine:glycine amidinotransferase) |
| 77 | GO:0008449 | N-acetylglucosamine-6-sulfatase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | glucosamine (N-acetyl)-6-sulfatase |
| 78 | GO:0047066 | phospholipid-hydroperoxide glutathione peroxidase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | glutathione peroxidase 4 (phospholipid hydroperoxidase) |
| 79 | GO:0004411 | homogentisate 1,2-dioxygenase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | | homogentisate 1,2-dioxygenase |
| | | | | | | | 3.14e- | | hairy and enhancer of split 1, (Drosophila) |

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| 80 | GO:0071820 | N-box binding | 1 | 470 | 1 | 14962 | 02 | |
| 81 | GO:0005008 | hepatocyte growth factor receptor activity | 1 | 470 | 1 | 14962 | 3.14e-02 | met proto-oncogene (hepatocyte growth factor receptor) |
| 82 | GO:0015446 | arsenite-transporting ATPase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | arsA arsenite transporter, ATP-binding, homolog 1 (bacterial) |
| 83 | GO:0003869 | 4-nitrophenylphosphatase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | ATPase, Na+/K+ transporting, alpha 1 polypeptide |
| 84 | GO:0031775 | lutropin-choriogonadotropic hormone receptor binding | 1 | 470 | 1 | 14962 | 3.14e-02 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |
| 85 | GO:0034602 | oxoglutarate dehydrogenase (NAD+) activity | 1 | 470 | 1 | 14962 | 3.14e-02 | oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) |
| 86 | GO:0030228 | lipoprotein particle receptor activity | 1 | 470 | 1 | 14962 | 3.14e-02 | ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide |
| 87 | GO:0015320 | phosphate carrier activity | 1 | 470 | 1 | 14962 | 3.14e-02 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 |
| 88 | GO:0003968 | RNA-directed RNA polymerase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | polymerase (RNA) II (DNA directed) polypeptide A, 220kDa |
| 89 | GO:0008427 | calcium-dependent protein kinase inhibitor activity | 1 | 470 | 1 | 14962 | 3.14e-02 | calcium/calmodulin-dependent protein kinase II inhibitor 1 |
| 90 | GO:0016844 | strictosidine synthase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | chromosome 20 open reading frame 3 |
| 91 | GO:0019809 | spermidine binding | 1 | 470 | 1 | 14962 | 3.14e-02 | spermidine/spermine N1-acetyltransferase 1 |
| 92 | GO:0035497 | cAMP response element binding | 1 | 470 | 1 | 14962 | 3.14e-02 | cAMP responsive element binding protein 3-like 2 |
| 93 | GO:0015132 | prostaglandin transmembrane transporter activity | 1 | 470 | 1 | 14962 | 3.14e-02 | solute carrier organic anion transporter family, member 2A1 |
| 94 | GO:0004801 | sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glycerontransferase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | transaldolase 1 |
| 95 | GO:0015037 | peptide disulfide oxidoreductase activity | 1 | 470 | 1 | 14962 | 3.14e-02 | thioredoxin |
| 96 | GO:0016722 | oxidoreductase activity, oxidizing metal ions | 1 | 470 | 1 | 14962 | 3.14e-02 | cytochrome b reductase 1 |