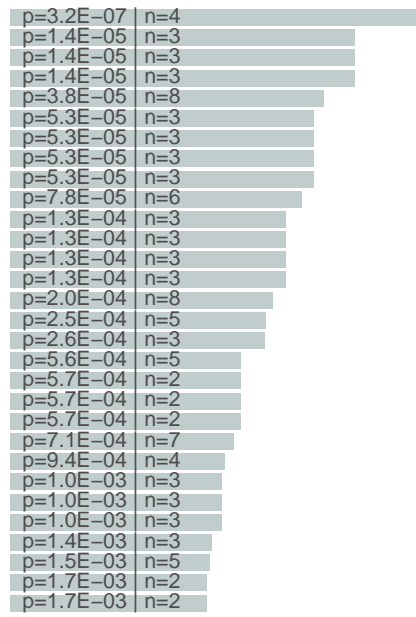


GO:BP
gc024

fraction genes in fg and expected value

chondroitin sulfate catabolic process	GO:0030207
male courtship behavior	GO:0008049
ganglioside catabolic process	GO:0006689
dermatan sulfate catabolic process	GO:0030209
regulation of cell shape	GO:0008360
penetration of zona pellucida	GO:0007341
positive regulation of integrin activation	GO:0033625
negative regulation of lymphocyte migration	GO:2000402
monounsaturated fatty acid biosynthetic process	GO:1903966
integrin-mediated signaling pathway	GO:0007229
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063
hyaluronan catabolic process	GO:0030214
astrocyte cell migration	GO:0043615
glutathione catabolic process	GO:0006751
positive regulation of NF-kappaB transcription	GO:0051092
basement membrane organization	GO:0071711
thyroid hormone generation	GO:0006590
tumor necrosis factor-mediated signaling pathway	GO:0033209
glycine biosynthetic process, by transamination	GO:0019265
L-alanine catabolic process	GO:0042853
leukotriene D4 catabolic process	GO:1901749
substrate adhesion-dependent cell spreading	GO:0034446
positive regulation of cell-matrix adhesion	GO:0001954
positive regulation of cell adhesion mediated by cell surface receptor	GO:0033630
N-acetylglucosamine metabolic process	GO:0006044
positive regulation of protein tyrosine phosphorylation	GO:0061098
positive regulation of filopodium assembly	GO:0051491
activation of cysteine-type endopeptidase activity	GO:0097202
glyoxylate catabolic process	GO:0009436
retinal blood vessel morphogenesis	GO:0061304



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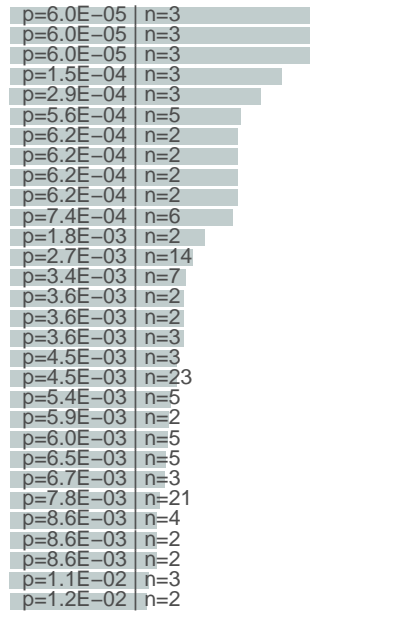
-log(p)
n=189/458 input genes with annotations

fraction

GO:MF
gc024

fraction genes in fg and expected value

stearoyl-CoA 9-desaturase activity	GO:0004768
palmitoyl-CoA 9-desaturase activity	GO:0032896
N-acetyl-beta-D-galactosaminidase activity	GO:0102148
beta-N-acetylglucosaminidase activity	GO:0016231
metalloidpeptidase activity	GO:0070573
integrin binding	GO:0005178
alanine-glyoxylate transaminase activity	GO:0008453
extracellular matrix structural constituent	GO:0030020
Ac-Asp-Glu binding	GO:1904492
tetrahydrofolyl-poly(glutamate) polymerization	GO:1904493
dipeptidase activity	GO:0016805
alkaline phosphatase activity	GO:0004035
actin binding	GO:0003779
actin filament binding	GO:0051015
platelet-derived growth factor binding	GO:0048407
beta-lactamase activity	GO:0008800
transmembrane receptor protein tyrosine kinase activity	GO:0004714
carbonyl reductase (NADPH) activity	GO:0004090
signaling receptor binding	GO:0005102
collagen binding	GO:0005518
ephrin receptor binding	GO:0046875
acetylglucosaminyltransferase activity	GO:0008375
cysteine-type endopeptidase activator activity	GO:0008656
non-membrane spanning protein tyrosine kinase activity	GO:0004715
transition metal ion binding	GO:0046914
carboxypeptidase activity	GO:0004180
proteoglycan binding	GO:0043394
cysteine-type endopeptidase inhibitor activity	GO:0043027
thyroid hormone transmembrane transporter activity	GO:0015349
oxidoreductase activity, acting on paired electron donors	GO:0016715



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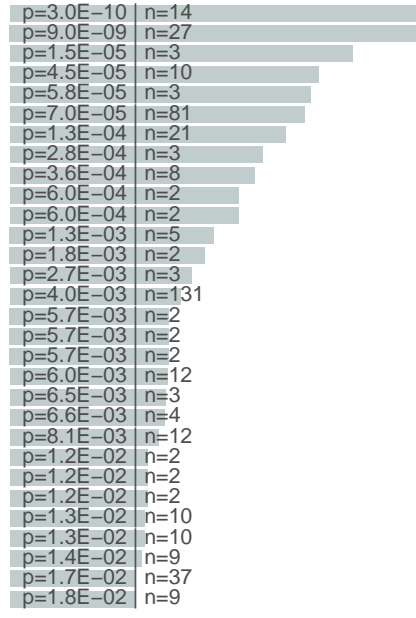
-log(p)
n=195/458 input genes with annotations

fraction

GO:CC
gc024

fraction genes in fg and expected value

focal adhesion	GO:0005925
extracellular space	GO:0005615
beta-N-acetylhexosaminidase complex	GO:1905379
external side of plasma membrane	GO:0009897
cortical granule	GO:0060473
plasma membrane	GO:0005886
lysosome	GO:0005764
azurophilic granule	GO:0042582
lamellipodium	GO:0030027
muscle cell projection membrane	GO:0036195
collagen type IV trimer	GO:0005587
peroxisomal membrane	GO:0005778
actin cap	GO:0030478
lysosomal lumen	GO:0043202
membrane	GO:0016020
alveolar lamellar body	GO:0097208
T cell receptor complex	GO:0042101
integrin complex	GO:0008305
apical part of cell	GO:0045177
melanosome	GO:0042470
apoptosome	GO:0043293
actin cytoskeleton	GO:0015629
phagocytic vesicle membrane	GO:0030670
apical dendrite	GO:0097440
Arp2/3 protein complex	GO:0005885
extracellular matrix	GO:0031012
external encapsulating structure	GO:0030312
cell-cell junction	GO:0005911
extracellular region	GO:0005576
collagen-containing extracellular matrix	GO:0062023



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-log(p)
n=195/458 input genes with annotations

fraction