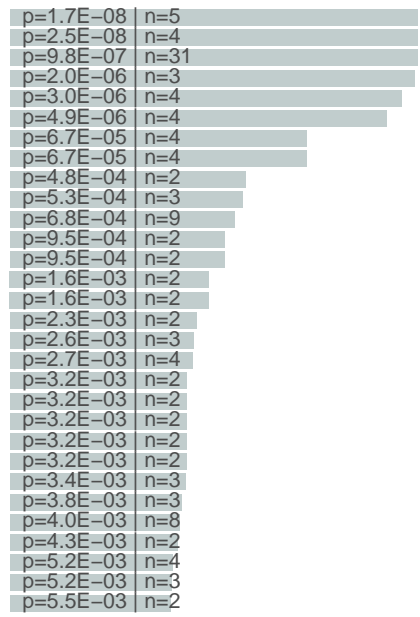


GO:BP
gc022

fraction genes in fg and expected value

collagen catabolic process	GO:0030574
neutrophil extravasation	GO:0072672
proteolysis	GO:0006508
peptidoglycan catabolic process	GO:0009253
mature conventional dendritic cell differentiation	GO:0097029
cell–cell junction maintenance	GO:0045217
membrane protein ectodomain proteolysis	GO:0006509
negative regulation of phagocytosis	GO:0050765
chorio–allantoic fusion	GO:0060710
defense response to Gram–positive bacterium	GO:0050830
epithelial cell differentiation	GO:0030855
artery smooth muscle contraction	GO:0014824
glycolytic process from galactose	GO:0061623
galactose catabolic process via UDP–galactose 4-epimerase	GO:0033499
regulation of vascular associated smooth muscle cell contraction	GO:1905063
chondrocyte proliferation	GO:0035988
B cell proliferation	GO:0042100
epithelial to mesenchymal transition	GO:0001837
negative regulation of bile acid biosynthesis	GO:0070858
folic acid catabolic process	GO:0046657
clathrin coat assembly	GO:0048268
negative regulation of bone resorption	GO:0045779
positive regulation of viral entry into host cell	GO:0046598
pancreas development	GO:0031016
peptide catabolic process	GO:0043171
blood vessel morphogenesis	GO:0048514
response to hydroperoxide	GO:0033194
regulation of B cell activation	GO:0050864
behavioral fear response	GO:0001662
positive regulation of extracellular matrix organization	GO:1903055



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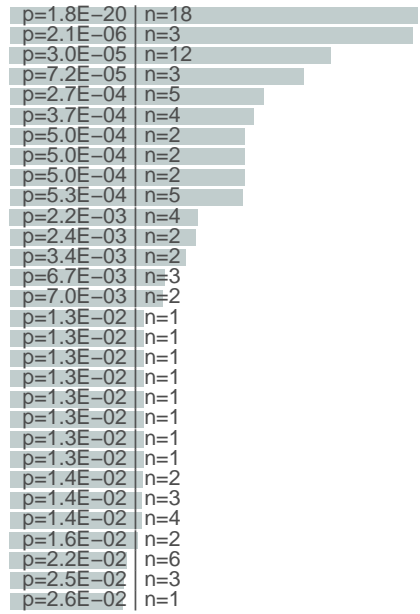
–log(p)
n=97/240 input genes with annotations

fraction

GO:MF
gc022

fraction genes in fg and expected value

serine–type endopeptidase activity	GO:0004252
lysozyme activity	GO:0003796
calcium ion binding	GO:0005509
scavenger receptor activity	GO:0005044
collagen binding	GO:0005518
heparin binding	GO:0008201
DNA binding, bending	GO:0008301
NAD(P)+ nucleosidase activity	GO:0050135
NAD+ nucleotidase, cyclic ADP–ribose generated	GO:0061809
DNA–binding transcription repressor activity	GO:0001227
extracellular matrix structural constituent	GO:0005201
para–aminobenzoyl–glutamate hydrolase activity	GO:0071713
sodium channel regulator activity	GO:0017080
carboxypeptidase activity	GO:0004180
clathrin adaptor activity	GO:0035615
amylase activity	GO:0016160
beta–galactosidase activity	GO:0004565
methanethiol oxidase activity	GO:0018549
alpha–amylase activity	GO:0004556
leukotriene–C(4) hydrolase	GO:0002951
peptidyltransferase activity	GO:0000048
isopeptidase activity	GO:0070122
UDP–glucose:hexose–1–phosphate uridylyltransferase activity	GO:0008108
dipeptidase activity	GO:0016805
aminopeptidase activity	GO:0004177
intramolecular oxidoreductase activity	GO:0016860
prostaglandin–D synthase activity	GO:0004667
exopeptidase activity	GO:0008238
metalloexopeptidase activity	GO:0008235
polysaccharide binding	GO:0030247



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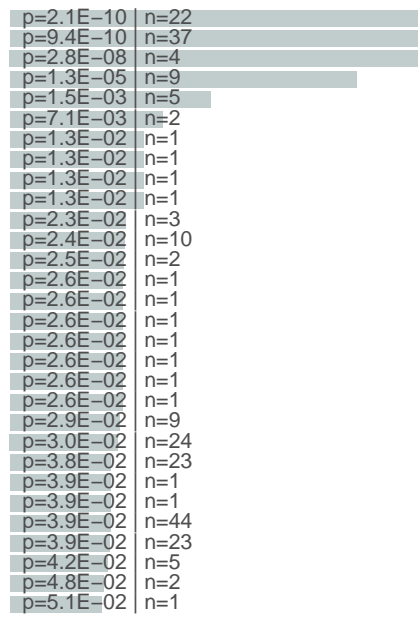
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n=98/240 input genes with annotations

fraction

GO:CC
gc022

fraction genes in fg and expected value

extracellular space	GO:0005615
extracellular region	GO:0005576
azurophil granule lumen	GO:0035578
collagen–containing extracellular matrix	GO:0062023
plasma membrane raft	GO:0044853
clathrin coat of coated pit	GO:0030132
dense body	GO:0097433
postsynaptic Golgi apparatus	GO:0150051
pinosome	GO:0044352
macropinosome	GO:0044354
coated vesicle membrane	GO:0030662
secretory granule	GO:0030141
clathrin–coated vesicle membrane	GO:0030665
cyclin D2–CDK4 complex	GO:0097129
catalase complex	GO:0062151
peptidase inhibitor complex	GO:1904090
cAMP–dependent protein kinase complex	GO:0005952
UTP–C complex	GO:0034456
MPP7–DLG1–LIN7 complex	GO:0097025
CURI complex	GO:0032545
cell surface	GO:0009986
vesicle	GO:0031982
cytoplasmic vesicle	GO:0031410
elastic fiber	GO:0071953
microtubule bundle	GO:0097427
cell periphery	GO:0071944
intracellular vesicle	GO:0097708
apical plasma membrane	GO:0016324
excitatory synapse	GO:0060076
apical plasma membrane urothelial plaque	GO:0120001



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–log(p)
n=100/240 input genes with annotations

fraction