

G protein–coupled receptor activity GO:0004930
DNA–binding transcription repressor acti... GO:0001227
growth hormone–releasing hormone recepto... GO:0016520
growth hormone secretagogue receptor act... GO:0001616
peptide hormone binding GO:0017046
G protein–coupled photoreceptor activity GO:0008020
substance K receptor activity GO:0016497
ganglioside GM1 binding GO:1905573
bradykinin receptor activity GO:0004947
beta–2 adrenergic receptor binding GO:0031698
MAP kinase tyrosine/serine/threonine pho... GO:0017017
type 1 angiotensin receptor binding GO:0031702
MAP kinase phosphatase activity GO:0033549
selenocysteine insertion sequence bindin... GO:0035368
L–arginine transmembrane transporter act... GO:0061459
peptide receptor activity GO:0001653
arginine transmembrane transporter activ... GO:0015171
protein–disulfide reductase (NAD(P)) act... GO:0015174
protein–disulfide reductase (NAD(P)) act... GO:0016684
adrenergic receptor binding GO:0031690
phosphatidylinositol–5–phosphate binding GO:0031690
phosphatidylinositol–5–phosphate binding GO:0031690
angiotensin receptor activity GO:0016500
angiotensin receptor binding GO:0031701
GTPase activating protein binding GO:0032794
guanylate cyclase activity GO:0004383
phosphatidic acid binding GO:0070300 p=1.3E-03 | n=13 p=2.4E-03 | n=3 p=3.1E-03 | n=2 p=3.1E-03 | n=2 fg=0.33 | bg=0.06 | fg=0.08 | bg=0.01 fg=0.05 bg=0.00 fg=0.05 bg=0.00 p=3.1E-03 n=2 p=4.0E-03 n=3 p=5.7E-03 n=2 p=9.6E-03 n=2 p=9.9E-03 n=1 fğ=0.08 bg=0.01 fg=0.05 bg=0.00 bg=0.00 bg=0.00 fg=0.05 fg=0.03 p=1.5E-02 n=1 p=1.5E-02 n=1 fg=0.03 fg=0.03 bg=0.00 bg=0.00 fg=0.03 fg=0.03 p=2.0E-02 bg=0.00 bg=0.00 bg=0.00 p=2.0F-02n=1fg=0.03 fg=0.03 p=2.0E-02 bg=0.00 bg=0.00 p=2.5F-02n=1p=2.5E-02 fg=0.03 fg=0.13 fg=0.03 p=2.9E-02n=5bg=0.02 bg=0.00 n=1fg=0.03 fg=0.03 bg=0.00 bg=0.00 p=2.9E-02n=1n=1fg=0.03 p=2.9E-02 p=3.4E-02 bg=0.00 bg=0.00 n=1fg=0.03 n=1fg=0.03 p=3.4E-02 p=3.9E-02 bg=0.00 bg=0.00 n=1fg=0.03 n=1p=4.6E-02 p=4.6E-02 fg=0.10 fg=0.10 bg=0.03 n=4bg=0.03 n=4p=4.8E-02 p=4.9E-02 p=5.3E-02 p=5.8E+02 n=2fg=0.05 bg=0.01 fg=0.03 bg=0.00 bg=0.00 n=1 fg=0.03 fg=0.03 n=1 guanylate cyclase activity GO:0004383 phosphatidic acid binding GO:0070300 bq = 0.00n=1p=5.8E-02 fg=0.03 bg=0.00 0 1 2 3 0.0 0.2 5 0.4 0.6 0.8 1.0 fraction -log(p)

n=39/134 input genes with annotations

GO:CC gc018 fraction genes in fg and expected value

plasma membrane GO:0005886
sperm head GO:0061827
junctional membrane complex GO:0030314
sperm flagellum GO:0036126
Schaffer collateral – CA1 synapse GO:0098685
9+2 motile cilium GO:0097729
sperm connecting piece GO:0097224
sperm midpiece GO:0097225
outer kinetochore GO:0000940
motile cilium GO:0031514
sperm head plasma membrane GO:1990913
cytoplasmic dynein complex GO:0005929
sperm plasma membrane GO:0007524 p=5.9E-04 | n=20 p=2.3E-03 | n=3 bg=0.25 bg=0.01 fg=0.07 p=5.0E-03 n=1 p=1.8E-02 n=3 fg=0.03 bg=0.00 fg=0.07 bg=0.01 p=1.8E-02 p=2.3E-02 n=3 fg=0.07 bg=0.01 fg=0.07 bg=0.02 bg=0.00 n=3p=3.0E-02 p=3.1E-02 fg=0.03 fg=0.05 n=1 bg=0.01 n=2p=4.5E-02 p=5.1E-02 fg=0.03 fg=0.07 n=1 bg=0.00 bg=0.02 n=3p=6.4E-02 p=8.7E-02 fg=0.03 bg=0.00 bg=0.00 bg=0.06 fa=0.03 n=1p=8.9E-02 p=9.2E-02 fg = 0.12bg=0.00 bg=0.03 fg=0.03 fg=0.07 sperm plasma membrane GO:0097524 membrane raft GO:0045121 n=1p=1.1E-01fg=0.07 fg=0.03 membrane microdomain GO:0098857 apoptosome GO:0043293 p=1.1E-01n=3bg=0.03 p=1.5E-01 bg=0.00 n=1fg=0.03 fg=0.03 sarcoplasmic reticulum GO:0016529 p=1.5E-01n=1bg=0.00 p=1.8E-01 bg=0.00 n=1trans-Golgi network membrane GO:0032588 male germ cell nucleus GO:001673
photoreceptor outer segment GO:001675
basolateral plasma membrane GO:0016323
endoplasmic reticulum–Golgi intermediate... GO:0005793 fg=0.03 fg=0.03 p=1.8E-01 n=1bg=0.01 p=1.8E-01 bg=0.01 n=1fg=0.05 p=1.9E-01n=2bg=0.02 bg=0.01 p=2.0E -01 n=1p=2.0E-01 cell projection GO:0042995 n=9=0.23bg=0.16 secretory granule GO:0030141 basal plasma membrane GO:0009925 p=2.0E-01 fg=0.05 bg=0.02 n=2fg=0.05 p=2.0E-01 n=2bg=0.02 dynein complex GO:0030286 glutamatergic synapse GO:0098978 p=2.0E-01 fg=0.03 bg=0.01 n=1p=2.1E-01 p=2.1E-01 n=3 fg=0.07 bg=0.04 germ cell nucleus GO:0043073 cell surface GO:0009986 fg=0.03 bg=0.01 n=1 p=2.1E-01 fg=0.07 bg=0.04 0 2 3 0.0 1 5 0.2 0.4 0.6 0.8 1.0 fraction -log(p) n=40/134 input genes with annotations