

GO term	candidate genes	p-value	q-value
GO:0071944 cell periphery	235 (8.5%)	2.00E-05	0.00127
GO:0005886 plasma membrane	228 (8.5%)	3.43E-05	0.00127
GO:0031224 intrinsic component of membrane	249 (8.3%)	7.45E-05	0.00184
GO:0044700 single organism signaling	309 (8.0%)	7.55E-05	0.00634
GO:0072376 protein activation cascade	8 (30.8%)	0.000209	0.0088
GO:0004888 transmembrane signaling receptor activity	44 (12.2%)	8.82E-05	0.0145
GO:0022804 active transmembrane transporter activity	29 (13.7%)	0.000191	0.02
GO:0038023 signaling receptor activity	47 (11.2%)	0.000327	0.02
GO:0016021 integral component of membrane	243 (8.2%)	0.000167	0.0216
GO:0031226 intrinsic component of plasma membrane	77 (9.9%)	0.0003	0.0216
GO:0004872 receptor activity	56 (10.5%)	0.000495	0.0233
GO:0048495 Roundabout binding	3 (100.0%)	0.000301	0.0248
GO:0003013 circulatory system process	35 (13.7%)	4.38E-05	0.0363
GO:0005615 extracellular space	60 (9.8%)	0.00206	0.0375
GO:0009986 cell surface	44 (10.4%)	0.00253	0.0375
GO:0003008 system process	88 (9.9%)	0.00012	0.0389
GO:0007154 cell communication	317 (7.9%)	0.000245	0.0389
GO:0005887 integral component of plasma membrane	75 (10.0%)	0.000252	0.0389
GO:0007267 cell-cell signaling	73 (10.0%)	0.00033	0.0389
GO:0043062 extracellular structure organization	33 (12.5%)	0.000368	0.0389
GO:0044707 single-multicellular organism process	314 (7.7%)	0.00162	0.0455
GO:0005509 calcium ion binding	46 (11.1%)	0.000466	0.0512
GO:0051716 cellular response to stimulus	342 (7.5%)	0.00295	0.0566
GO:0042221 response to chemical	201 (8.0%)	0.00337	0.0566
GO:0046883 regulation of hormone secretion	24 (14.6%)	0.000242	0.057
GO:0023061 signal release	36 (12.4%)	0.000268	0.057
GO:0009914 hormone transport	27 (13.8%)	0.00028	0.057
GO:0030198 extracellular matrix organization	33 (12.6%)	0.000343	0.057
GO:0008015 blood circulation	34 (13.4%)	8.60E-05	0.0605
GO:0007586 digestion	10 (21.7%)	0.000781	0.066
GO:0021537 telencephalon development	23 (13.5%)	0.000991	0.0699
GO:0006955 immune response	78 (8.9%)	0.0052	0.0728
GO:0042613 MHC class II protein complex	4 (44.4%)	0.00193	0.0794
GO:0034774 secretory granule lumen	7 (23.3%)	0.00311	0.0794
GO:0044057 regulation of system process	31 (12.4%)	0.00067	0.0894
GO:0003012 muscle system process	29 (12.6%)	0.000754	0.0894
GO:0004896 cytokine receptor activity	8 (22.9%)	0.00184	0.0914
GO:0004866 endopeptidase inhibitor activity	12 (16.9%)	0.00251	0.0914
GO:0019958 C-X-C chemokine binding	2 (100.0%)	0.0045	0.0914
GO:0015405 P-P-bond-hydrolysis-driven transmembrane transport	12 (15.6%)	0.00498	0.0914
GO:0004930 G-protein coupled receptor activity	18 (13.0%)	0.00499	0.0914
GO:0004871 signal transducer activity	61 (9.4%)	0.00415	0.0974