	CO torm	Candidates	n valua	a valua
	GO term	contained	p-value	q-value
GO:0022804	active transmembrane transporter activity	21 (9.9%)	0.000204	0.02
GO:0031224	intrinsic component of membrane	160 (5.3%)	0.000235	0.00947
GO:0005509	calcium ion binding	33 (8.0%)	0.00025	0.0202
GO:0071944	cell periphery	148 (5.3%)	0.000321	0.00947
GO:0005886	plasma membrane	144 (5.3%)	0.0004	0.00947
GO:0016021	integral component of membrane	156 (5.3%)	0.000462	0.0498
GO:0008015	blood circulation	22 (8.7%)	0.000931	0.269
GO:0004857	enzyme inhibitor activity	19 (9.2%)	0.00103	0.0504
GO:0003013	circulatory system process	22 (8.6%)	0.00103	0.385
GO:0004888	transmembrane signaling receptor activity	28 (7.7%)	0.00119	0.105
GO:0034341	response to interferon-gamma	11 (12.2%)	0.00123	0.269
GO:0034097	response to cytokine	33 (7.3%)	0.00135	0.385
GO:0031526	brush border membrane	<u>5 (23.8%)</u>	0.00143	0.164
GO:0021834	chemorepulsion involved in embryonic olfactory	2 (100.0%)	0.00173	0.269
GO:0044057	regulation of system process	21 (8.4%)	0.00177	0.385
GO:0021537	telencephalon development	16 (9.4%)	0.00193	0.445
GO:0021954	central nervous system neuron development	8 (14.3%)	0.00207	0.269
GO:0004866	endopeptidase inhibitor activity	9 (12.7%)	0.0026	0.0788
GO:0051101	regulation of DNA binding	9 (12.5%)	0.00287	0.469
GO:0004896	cytokine receptor activity	6 (17.1%)	0.00292	0.0788
GO:0030414	peptidase inhibitor activity	9 (12.3%)	0.00315	0.105
GO:0015643	toxic substance binding	3 (37.5%)	0.00342	0.0726
GO:0043023	ribosomal large subunit binding	3 (37.5%)	0.00342	0.105
GO:0072376	protein activation cascade	5 (19.2%)	0.00389	0.168
GO:0061135	endopeptidase regulator activity	9 (11.8%)	0.00415	0.105
GO:0015399	primary active transmembrane transporter activit	9 (11.7%)	0.00453	0.105
3O:0015405	P-P-bond-hydrolysis-driven transmembrane trans	9 (11.7%)	0.00453	0.0917
GO:0038023	signaling receptor activity	29 (6.9%)	0.00487	0.145
GO:0004872	receptor activity	35 (6.6%)	0.00488	0.0726
GO:0072378	blood coagulation, fibrin clot formation	3 (33.3%)	0.00498	0.642
GO:0042613	MHC class II protein complex	3 (33.3%)	0.00498	0.174
GO:0048630	skeletal muscle tissue growth	2 (66.7%)	0.00504	0.445
GO:0061364	apoptotic process involved in luteolysis	2 (66.7%)	0.00504	0.445
GO:0048495	Roundabout binding	2 (66.7%)	0.00504	0.105
GO:0045338	farnesyl diphosphate metabolic process	2 (66.7%)	0.00504	0.41
GO:0022857	transmembrane transporter activity	37 (6.5%)	0.00507	0.0726
GO:0043392	negative regulation of DNA binding	6 (15.4%)	0.0051	0.41
GO:0006955	immune response	52 (6.0%)	0.00535	0.168
GO:0044700	single organism signaling	187 (4.8%)	0.0062	0.168
GO:0030198	extracellular matrix organization	20 (7.6%)	0.0066	0.642
GO:0043062	extracellular structure organization	20 (7.6%)	0.00687	0.445
3O:0002544	chronic inflammatory response	3 (30.0%)	0.00689	0.41

GO:0022891	substrate-specific transmembrane transporter ac	34 (6.5%)	0.00714	0.145
GO:0030276	clathrin binding	6 (14.3%)	0.00738	0.145
GO:0005887	integral component of plasma membrane	45 (6.0%)	0.00768	0.429
GO:0021543	pallium development	11 (9.6%)	0.00781	0.445
GO:0030900	forebrain development	<u>19 (7.6%)</u>	0.0087	0.445
GO:0007154	cell communication	<u>193 (4.8%)</u>	0.009	0.445
GO:0031226	intrinsic component of plasma membrane	46 (5.9%)	0.00935	0.38
GO:0005615	extracellular space	38 (6.2%)	0.00938	0.167
GO:0001134	transcription factor activity, transcription factor re	2 (50.0%)	0.0098	0.157
GO:0045341	MHC class I biosynthetic process	2 (50.0%)	0.0098	0.41