

term_ID	description	frequency	uniqueness	dispensability	coeff	odds.ratio	FDR
GO:0006415	translational termination	0.18%	0.71	0	-0.217915	0.258139	3.7999E-40
GO:0006414	translational elongation	0.72%	0.831	0.517	0.127091	2.203007	0.00945602
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.00%	0.863	0.109	-0.084067	0.593071	1.10901E-11
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	0.10%	0.717	0.454	0.057315	1.427876	0.004317515
GO:0006413	translational initiation	0.27%	0.843	0.536	0.031417	1.215606	0.012955231
GO:0019083	viral transcription	0.06%	0.863	0.218	-0.164582	0.359582	8.00223E-05
GO:0044033	multi-organism metabolic process	0.23%	0.956	0.519	0.130969	2.256745	0.011128276
GO:0006401	RNA catabolic process	0.27%	0.827	0.559	0.071396	1.558464	0.014430233
GO:0006412	translation	4.70%	0.808	0.555	-0.086026	0.585892	0.014430233
GO:0019058	viral life cycle	1.21%	0.926	0.677	-0.096962	0.547399	0.045947348
GO:0022411	cellular component disassembly	0.29%	0.824	0.496	0.055954	1.415856	0.007163257
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.06%	0.876	0	-0.228241	0.242094	9.92176E-41
GO:0006521	regulation of cellular amino acid metabolic process	0.00%	0.812	0.056	-0.150988	0.39128	2.23692E-26
GO:1902578	single-organism localization	12.73%	0.862	0.465	0.053062	1.390635	0.005304078
GO:1902580	single-organism cellular localization	0.30%	0.812	0.634	-0.070826	0.643938	0.036309258
GO:0016072	rRNA metabolic process	0.76%	0.876	0.281	0.044965	1.322391	0.000204803
GO:0042254	ribosome biogenesis	1.03%	0.865	0.53	-0.106463	0.516011	0.012926408
GO:0033238	regulation of cellular amine metabolic process	0.00%	0.832	0.478	0.096498	1.821566	0.005524617
GO:0051340	regulation of ligase activity	0.00%	0.829	0.184	0.121842	2.132299	5.22295E-08
GO:0016192	vesicle-mediated transport	0.38%	0.918	0	-0.187752	0.31136	1.09854E-32
GO:0008089	anterograde axon cargo transport	0.00%	0.823	0.589	-0.099828	0.537732	0.028807201
GO:0030490	maturation of SSU-rRNA	0.00%	0.838	0.562	0.095974	1.815642	0.014551977
GO:0006901	vesicle coating	0.01%	0.78	0.544	0.083626	1.681527	0.013265465
GO:0032446	protein modification by small protein conjugation	0.12%	0.794	0.34	-0.065626	0.665084	0.000775658
GO:0001775	cell activation	0.05%	0.933	0.072	-0.100327	0.536068	5.90736E-18
GO:0043086	negative regulation of catalytic activity	0.24%	0.781	0.597	-0.080436	0.606605	0.029405972
GO:0006986	response to unfolded protein	0.01%	0.873	0.614	0.077096	1.614656	0.032562304
GO:0046700	heterocycle catabolic process	6.22%	0.86	0.462	0.039358	1.277106	0.005211196
GO:0035966	response to topologically incorrect protein	0.01%	0.879	0	-0.190602	0.305894	1.99152E-32
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.00%	0.651	0.294	0.083142	1.676475	0.000277474
GO:0009068	aspartate family amino acid catabolic process	0.07%	0.849	0.272	0.049073	1.356604	0.93803E-05
GO:0034660	ncRNA metabolic process	3.21%	0.868	0.412	0.156291	2.641348	0.002070202
GO:0070647	protein modification by small protein conjugation or removal	0.13%	0.832	0.516	0.049159	1.357312	0.009370167
GO:0015949	nucleobase-containing small molecule interconversion	0.01%	0.911	0.114	0.115563	2.050689	7.20493E-10
GO:0006508	proteolysis	3.71%	0.858	0.578	-0.029813	0.830876	0.023018913
GO:0032007	negative regulation of TOR signaling	0.00%	0.745	0.416	-0.097459	0.545709	0.002492775
GO:0015980	energy derivation by oxidation of organic compounds	2.41%	0.871	0.1	-0.10222	0.529799	2.5231E-15
GO:0006952	defense response	0.57%	0.88	0.425	0.03927	1.276408	0.002926642
GO:0006091	generation of precursor metabolites and energy	3.22%	0.944	0.058	-0.129928	0.445994	1.37645E-21
GO:0090322	regulation of superoxide metabolic process	0.00%	0.843	0.185	0.090503	1.754951	3.84325E-05
GO:0031929	TOR signaling	0.01%	0.783	0.335	0.094808	1.802534	0.000734041
GO:0042060	wound healing	0.03%	0.893	0.454	0.074367	1.587499	0.004317515
GO:0016071	mRNA metabolic process	0.49%	0.886	0.337	-0.143521	0.409865	0.000774699
GO:1902600	hydrogen ion transmembrane transport	1.80%	0.832	0.301	0.080605	1.650256	0.00032948
GO:0045838	positive regulation of membrane potential	0.00%	0.877	0.14	0.135648	2.323331	7.20493E-10
GO:0010565	regulation of cellular ketone metabolic process	0.04%	0.795	0.566	0.094982	1.804482	0.016944403
GO:0018196	peptidyl-asparagine modification	0.00%	0.864	0.396	0.031153	1.213612	0.001935827
GO:0006887	exocytosis	0.03%	0.776	0.625	0.093471	1.787619	0.034309109
GO:0050817	coagulation	0.02%	0.925	0.038	-0.170696	0.346177	8.77865E-32
GO:0050900	leukocyte migration	0.01%	0.795	0.618	-0.114163	0.491901	0.033924053
GO:0032069	regulation of nuclease activity	0.01%	0.775	0.645	0.031824	1.218685	0.037995385
GO:0042542	response to hydrogen peroxide	0.06%	0.881	0.487	-0.133665	0.435755	0.006483893
GO:0032075	positive regulation of nuclease activity	0.00%	0.794	0.439	0.132812	2.282741	0.004176849
GO:0002181	cytoplasmic translation	0.00%	0.879	0.346	0.134179	2.302208	0.001651123
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	0.00%	0.796	0.512	0.079063	1.634512	0.008826439
GO:0051640	organelle localization	0.03%	0.86	0.539	0.035178	1.244358	0.013069846
GO:0018279	protein N-linked glycosylation via asparagine	0.00%	0.818	0.452	0.068023	1.526129	0.004187233
GO:0044106	cellular amine metabolic process	0.48%	0.924	0.654	-0.112787	0.496124	0.039918869
GO:0009308	amine metabolic process	0.52%	0.95	0.156	-0.074894	0.627862	6.47434E-09
GO:0002431	Fc receptor mediated stimulatory signaling pathway	0.00%	0.713	0.525	0.042081	1.298895	0.012681742
GO:0051247	positive regulation of protein metabolic process	0.11%	0.699	0.538	0.067696	1.523036	0.012981833
GO:0098602	single organism cell adhesion	0.02%	0.959	0.608	0.082331	1.668049	0.031827635
GO:0031960	response to corticosteroid	0.00%	0.89	0.603	0.061658	1.466945	0.03077843
GO:0045321	leukocyte activation	0.04%	0.823	0.662	-0.112656	0.496529	0.040116661
GO:0042554	superoxide anion generation	0.00%	0.951	0.588	0.060007	1.451969	0.024874868
GO:0031400	negative regulation of protein modification process	0.08%	0.655	0.677	0.101751	1.882011	0.044096344
GO:0009250	glucan biosynthetic process	0.15%	0.834	0.227	0.127366	2.206764	8.92772E-05
GO:0016337	single organismal cell-cell adhesion	0.02%	0.959	0.038	-0.164477	0.359816	8.86871E-30
GO:0030239	myofibril assembly	0.00%	0.816	0.366	-0.128217	0.45076	0.001678145
GO:0009611	response to wounding	0.11%	0.891	0.511	0.05878	1.440937	0.008229598
GO:0016050	vesicle organization	0.04%	0.859	0.515	0.029741	1.20301	0.009151008
GO:0050878	regulation of body fluid levels	0.02%	0.814	0.563	0.05849	1.438346	0.014551977
GO:2000377	regulation of reactive oxygen species metabolic process	0.01%	0.83	0.606	0.103427	1.90172	0.031827635
GO:0045725	positive regulation of glycogen biosynthetic process	0.00%	0.723	0.667	0.081119	1.655536	0.043153048
GO:0006909	phagocytosis	0.01%	0.852	0.651	-0.112787	0.496124	0.039918869
GO:0042752	regulation of circadian rhythm	0.01%	0.878	0.154	-0.074894	0.627862	6.47434E-09
GO:0006984	ER-nucleus signaling pathway	0.01%	0.79	0.295	-0.035982	0.799625	0.000280257
GO:0051084	'de novo' posttranslational protein folding	0.01%	0.874	0.291	0.045807	1.329326	0.000277474
GO:0006457	protein folding	0.86%	0.839	0.568	0.040345	1.28496	0.021048476
GO:0035987	endodermal cell differentiation	0.00%	0.895	0.624	0.127103	2.203168	0.034216338
GO:0015804	neutral amino acid transport	0.11%	0.882	0.49	0.081	1.654305	0.007163257
GO:0051129	negative regulation of cellular component organization	0.06%	0.72	0.479	0.083261	1.677721	0.006023515
GO:0006693	prostaglandin metabolic process	0.00%	0.912	0.195	0.04234	1.300994	4.30569E-05

GO:0061024	membrane organization	1.01%	0.868	0.601	0.088205	1.730069	0.03077843
GO:0042770	signal transduction in response to DNA damage	0.01%	0.777	0.364	0.035089	1.24367	0.00166111
GO:0009064	glutamine family amino acid metabolic process	1.29%	0.869	0.518	0.041581	1.29487	0.010873008
GO:0006458	'de novo' protein folding	0.01%	0.874	0.529	0.05095	1.372499	0.012926408
GO:0031330	negative regulation of cellular catabolic process	0.07%	0.715	0.685	-0.073609	0.632894	0.047238048
GO:0090382	phagosome maturation	0.00%	0.881	0.433	-0.105014	0.520679	0.004074487
GO:0010950	positive regulation of endopeptidase activity	0.01%	0.738	0.643	-0.102115	0.530145	0.03759253
GO:0007029	endoplasmic reticulum organization	0.01%	0.872	0.526	-0.100049	0.536995	0.012728344
GO:0031333	negative regulation of protein complex assembly	0.01%	0.731	0.596	0.087219	1.719499	0.028807201
GO:0055072	iron ion homeostasis	0.14%	0.843	0.386	-0.05604	0.705911	0.001836724
GO:2000177	regulation of neural precursor cell proliferation	0.01%	0.852	0.167	-0.120506	0.472887	9.50984E-09
GO:0035020	regulation of Rac protein signal transduction	0.00%	0.781	0.554	0.060737	1.458569	0.013895672
GO:0045055	regulated secretory pathway	0.00%	0.802	0.551	-0.136868	0.427167	0.013265465
GO:0035725	sodium ion transmembrane transport	0.06%	0.865	0.647	-0.074509	0.629364	0.03855751
GO:0055006	cardiac cell development	0.00%	0.892	0.65	0.109417	1.973843	0.039731132
GO:0046903	secretion	0.63%	0.878	0.398	-0.050758	0.729468	0.001979438
GO:0043010	camera-type eye development	0.02%	0.914	0.574	0.110869	1.991734	0.021966811
GO:0070542	response to fatty acid	0.00%	0.895	0.692	-0.032821	0.815486	0.048647971
GO:0034369	plasma lipoprotein particle remodeling	0.00%	0.761	0.508	0.071817	1.562542	0.007765876
GO:0034367	macromolecular complex remodeling	0.00%	0.9	0.509	0.059922	1.451201	0.007835927
GO:0097503	sialylation	0.01%	0.907	0.346	0.040205	1.283845	0.001348678
GO:0042180	cellular ketone metabolic process	0.41%	0.901	0.159	-0.130383	0.444734	8.49851E-09
GO:0007492	endoderm development	0.00%	0.965	0.428	-0.040489	0.777539	0.003347716
GO:0002444	myeloid leukocyte mediated immunity	0.00%	0.899	0.567	-0.119175	0.476816	0.016991145
GO:0009066	aspartate family amino acid metabolic process	0.86%	0.873	0.663	0.050822	1.371412	0.041460185
GO:0006090	pyruvate metabolic process	0.73%	0.884	0.467	0.081188	1.656243	0.005507935
GO:0055114	oxidation-reduction process	15.04%	0.929	0.2	0.14174	2.412978	6.36651E-05