

term_ID	description	frequency	uniqueness	dispensability	ngenes	coeff	odds.ratio	FDR
GO:0045333	cellular respiration	2.26%	0.82	0	128	-0.518292	0.039916	1.63E-34
GO:0006415	translational termination	0.18%	0.612	0.099	89	-0.570456	0.028864	1.91E-32
GO:0006091	generation of precursor metabolites and energy	3.22%	0.921	0.079	320	-0.351257	0.112712	6.76E-31
GO:0006414	translational elongation	0.72%	0.784	0.517	99	-0.526762	0.037869	1.31E-29
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	0.10%	0.663	0.454	106	-0.479174	0.050901	4.92E-25
GO:0055114	oxidation-reduction process	15.04%	0.865	0.21	431	-0.27791	0.177798	4.33E-24
GO:0042775	mitochondrial ATP synthesis coupled electron transport	0.11%	0.735	0.687	42	-0.605466	0.02322	4.34E-20
GO:1902600	hydrogen ion transmembrane transport	1.80%	0.786	0.129	37	-0.620467	0.021153	4.68E-19
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.00%	0.797	0.109	114	-0.413354	0.076625	9.13E-19
GO:0051276	chromosome organization	0.34%	0.76	0.501	545	0.190419	3.265399	1.66E-16
GO:0019083	viral transcription	0.06%	0.779	0.218	152	-0.351384	0.112622	2.29E-16
GO:0006413	translational initiation	0.27%	0.8	0.536	150	-0.327023	0.131031	1.4E-13
GO:0044033	multi-organism metabolic process	0.23%	0.962	0.519	168	-0.310333	0.145352	2.51E-13
GO:0006818	hydrogen transport	1.98%	0.849	0.456	66	-0.424136	0.071659	3.72E-12
GO:0070647	protein modification by small protein conjugation or removal	0.13%	0.831	0.342	533	0.164051	2.771836	1.2E-11
GO:0044711	single-organism biosynthetic process	12.46%	0.824	0.312	971	-0.130809	0.443559	1.72E-10
GO:0006397	mRNA processing	0.37%	0.771	0.676	280	0.202111	3.511494	1.85E-10
GO:0006412	translation	4.70%	0.745	0.555	369	-0.198973	0.290387	2.66E-10
GO:0006082	organic acid metabolic process	9.36%	0.763	0.332	717	-0.142847	0.411586	1.35E-09
GO:0032446	protein modification by small protein conjugation	0.12%	0.816	0.516	455	0.152736	2.583635	1.12E-08
GO:0019058	viral life cycle	1.21%	0.927	0.677	283	-0.204917	0.279856	1.32E-08
GO:0042776	mitochondrial ATP synthesis coupled proton transport	0.00%	0.711	0.525	14	-0.640516	0.018675	1.46E-08
GO:0006357	regulation of transcription from RNA polymerase II promoter	0.21%	0.736	0.319	925	0.112329	2.009888	1.97E-08
GO:0045893	positive regulation of transcription, DNA-templated	0.19%	0.707	0.365	734	0.123424	2.15337	2.01E-08
GO:0022411	cellular component disassembly	0.29%	0.76	0.523	361	-0.180329	0.32606	2.81E-08
GO:0009142	nucleoside triphosphate biosynthetic process	0.67%	0.694	0.287	35	-0.455125	0.059106	3.79E-08
GO:0008380	RNA splicing	0.10%	0.811	0.24	266	0.18108	3.081273	7.85E-08
GO:0000375	RNA splicing, via transesterification reactions	0.04%	0.809	0.469	210	0.198952	3.443218	7.85E-08
GO:0006094	gluconeogenesis	0.27%	0.815	0.334	48	-0.388477	0.089436	3.09E-07
GO:0051603	proteolysis involved in cellular protein catabolic process	0.22%	0.783	0.687	366	0.153216	2.591352	3.13E-07
GO:1901566	organonitrogen compound biosynthetic process	9.30%	0.803	0.403	433	-0.15279	0.386922	4.77E-07
GO:0030163	protein catabolic process	0.36%	0.812	0.516	456	0.137212	2.346015	5.39E-07
GO:0043632	modification-dependent macromolecule catabolic process	0.14%	0.827	0.699	333	0.15315	2.590279	1.09E-06
GO:0072522	purine-containing compound biosynthetic process	1.59%	0.776	0.344	138	-0.246489	0.216139	1.16E-06
GO:0006811	ion transport	5.99%	0.83	0.537	791	-0.111124	0.501279	1.69E-06
GO:0046390	ribose phosphate biosynthetic process	1.82%	0.756	0.66	122	-0.256237	0.203434	1.8E-06
GO:0022402	cell cycle process	0.53%	0.875	0.111	855	0.100625	1.868888	2.17E-06
GO:0016051	carbohydrate biosynthetic process	1.54%	0.789	0.636	113	-0.256384	0.203428	4.96E-06
GO:0009063	cellular amino acid catabolic process	0.75%	0.735	0.312	81	-0.292942	0.161942	5.46E-06
GO:0006396	RNA processing	2.78%	0.771	0.352	469	0.125025	2.174896	6.42E-06
GO:0006259	DNA metabolic process	6.34%	0.774	0.403	643	0.108768	1.965895	7.2E-06
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	0.54%	0.763	0.389	706	0.102423	1.889886	1.16E-05
GO:0046034	ATP metabolic process	5.37%	0.65	0.675	282	-0.164663	0.359402	1.35E-05
GO:0090407	organophosphate biosynthetic process	4.46%	0.788	0.461	365	-0.143098	0.410944	2.31E-05
GO:0071824	protein-DNA complex subunit organization	0.03%	0.811	0.62	92	0.231048	4.203323	2.36E-05
GO:0042274	ribosomal small subunit biogenesis	0.08%	0.845	0.409	19	-0.475962	0.051927	2.63E-05
GO:0055086	nucleobase-containing small molecule metabolic process	10.84%	0.721	0.526	947	-0.089038	0.575027	5.16E-05
GO:1902578	single-organism localization	12.73%	0.833	0.58	361	-0.13825	0.423513	5.68E-05
GO:1902580	single-organism cellular localization	0.30%	0.814	0.634	361	-0.13825	0.423513	5.68E-05
GO:0048208	COPII vesicle coating	0.00%	0.659	0.65	13	0.420529	13.64572	8.72E-05
GO:0010608	posttranscriptional regulation of gene expression	0.54%	0.819	0.393	302	0.135424	2.320094	8.91E-05
GO:0000278	mitotic cell cycle	0.09%	0.891	0.684	687	0.094997	1.804652	8.91E-05
GO:0019693	ribose phosphate metabolic process	7.90%	0.773	0.696	784	-0.094148	0.557053	9.3E-05
GO:0034375	high-density lipoprotein particle remodeling	0.00%	0.755	0.494	10	-0.562093	0.030404	0.000132
GO:0043044	ATP-dependent chromatin remodeling	0.00%	0.77	0.587	47	0.276443	5.573303	0.000138
GO:0006336	DNA replication-independent nucleosome assembly	0.00%	0.693	0.641	31	0.316461	7.146918	0.000158
GO:0007005	mitochondrion organization	0.05%	0.787	0.693	225	-0.162267	0.364793	0.000184
GO:0072521	purine-containing compound metabolic process	8.06%	0.803	0.536	829	-0.088267	0.577791	0.000193
GO:0006839	mitochondrial transport	0.02%	0.83	0.699	140	-0.200519	0.287611	0.000198
GO:0033108	mitochondrial respiratory chain complex assembly	0.00%	0.79	0.581	21	-0.426978	0.070405	0.000207
GO:1903047	mitotic cell cycle process	0.08%	0.885	0.677	565	0.098959	1.849635	0.000207
GO:0022618	ribonucleoprotein complex assembly	0.11%	0.787	0.683	104	0.198062	3.424239	0.000336
GO:0003008	system process	0.20%	0.922	0.535	615	-0.098165	0.543319	0.000345
GO:0044282	small molecule catabolic process	1.35%	0.795	0.512	182	-0.17259	0.342125	0.000368
GO:0097031	mitochondrial respiratory chain complex I biogenesis	0.00%	0.871	0.314	16	-0.452187	0.060195	0.000535
GO:0010257	NADH dehydrogenase complex assembly	0.00%	0.83	0.539	16	-0.452187	0.060195	0.000535
GO:0043488	regulation of mRNA stability	0.00%	0.864	0.179	36	0.286903	5.947602	0.000538
GO:0071826	ribonucleoprotein complex subunit organization	0.11%	0.796	0.683	110	0.186867	3.194099	0.000683
GO:0043487	regulation of RNA stability	0.00%	0.863	0.505	37	0.276536	5.576495	0.001001
GO:0010212	response to ionizing radiation	0.01%	0.964	0	71	0.217703	3.86878	0.001006
GO:0043691	reverse cholesterol transport	0.00%	0.889	0.232	11	-0.5	0.044721	0.001025
GO:0018205	peptidyl-lysine modification	0.06%	0.837	0.49	145	0.162721	2.749022	0.001086
GO:1901605	alpha-amino acid metabolic process	4.27%	0.739	0.638	127	-0.189066	0.308828	0.001272
GO:0051640	organelle localization	0.03%	0.877	0.539	180	0.14672	2.488811	0.001328
GO:0032787	monocarboxylic acid metabolic process	2.31%	0.782	0.505	297	-0.125862	0.457407	0.001545
GO:0006323	DNA packaging	0.17%	0.695	0.475	84	0.19809	3.42482	0.00171
GO:0051052	regulation of DNA metabolic process	0.16%	0.779	0.351	173	0.146786	2.489845	0.001757
GO:0030518	intracellular steroid hormone receptor signaling pathway	0.01%	0.853	0.237	88	0.193735	3.333389	0.001813
GO:0016072	rRNA metabolic process	0.76%	0.803	0.406	60	-0.256417	0.203207	0.001851

GO:0030521	androgen receptor signaling pathway	0.00%	0.86	0.674	52	0.236188	4.339733	0.001959
GO:0006998	nuclear envelope organization	0.00%	0.781	0.648	50	0.239066	4.418053	0.002051
GO:0006282	regulation of DNA repair	0.04%	0.747	0.623	50	0.238712	4.408352	0.002104
GO:0008202	steroid metabolic process	0.04%	0.879	0.097	144	-0.171346	0.344781	0.002356
GO:0006974	cellular response to DNA damage stimulus	1.98%	0.909	0.387	539	0.08741	1.721539	0.002356
GO:0032109	positive regulation of response to nutrient levels	0.00%	0.886	0.566	14	0.362756	9.529427	0.00242
GO:0071103	DNA conformation change	0.90%	0.805	0.463	129	0.1622	2.740139	0.002526
GO:0009083	branched-chain amino acid catabolic process	0.01%	0.808	0.628	19	-0.390018	0.088583	0.003085
GO:0006090	pyruvate metabolic process	0.73%	0.805	0.445	65	-0.239733	0.225407	0.003086
GO:0006482	protein demethylation	0.00%	0.825	0.412	17	0.336227	8.081046	0.003412
GO:0008214	protein dealkylation	0.00%	0.863	0.412	17	0.336227	8.081046	0.003412
GO:0034367	macromolecular complex remodeling	0.00%	0.839	0.509	17	-0.402075	0.082188	0.003621
GO:0006790	sulfur compound metabolic process	1.67%	0.926	0.072	237	-0.131009	0.443006	0.003777
GO:0031123	RNA 3'-end processing	0.09%	0.811	0.501	98	0.175504	2.976319	0.004259
GO:0006112	energy reserve metabolic process	0.13%	0.86	0.698	125	-0.1732	0.34083	0.00496
GO:0008610	lipid biosynthetic process	2.21%	0.798	0.579	412	-0.097485	0.545622	0.005721
GO:0016125	sterol metabolic process	0.01%	0.858	0.401	67	-0.22551	0.246238	0.006086
GO:0061024	membrane organization	1.01%	0.814	0.586	653	-0.077912	0.616193	0.006202
GO:0010745	negative regulation of macrophage derived foam cell differentiation	0.00%	0.867	0.522	12	-0.4402	0.06485	0.00636
GO:0071825	protein-lipid complex subunit organization	0.00%	0.835	0.523	26	-0.329992	0.128636	0.006794
GO:0006997	nucleus organization	0.01%	0.807	0.61	69	0.194952	3.358686	0.007252
GO:0051216	cartilage development	0.01%	0.928	0.637	57	-0.236766	0.229602	0.00803
GO:0009064	glutamine family amino acid metabolic process	1.29%	0.77	0.684	29	-0.312749	0.143186	0.00803
GO:0006352	DNA-templated transcription, initiation	0.46%	0.768	0.383	200	0.123194	2.150289	0.008323
GO:0043543	protein acylation	0.06%	0.84	0.491	147	0.140691	2.397285	0.008442
GO:0006302	double-strand break repair	0.06%	0.786	0.65	115	0.155948	2.635714	0.008645
GO:0016052	carbohydrate catabolic process	1.35%	0.852	0.519	91	-0.18834	0.310224	0.010509
GO:2000463	positive regulation of excitatory postsynaptic membrane potential	0.00%	0.884	0.317	12	0.350154	8.81161	0.011588
GO:0007059	chromosome segregation	0.37%	0.904	0.107	127	0.146106	2.479332	0.011596
GO:0031060	regulation of histone methylation	0.00%	0.629	0.69	17	0.313796	7.029534	0.011596
GO:0044770	cell cycle phase transition	0.03%	0.895	0.683	390	0.088451	1.73271	0.012342
GO:0006629	lipid metabolic process	3.09%	0.862	0.155	793	-0.066353	0.662088	0.013472
GO:0030397	membrane disassembly	0.00%	0.817	0.597	36	0.239364	4.426266	0.013487
GO:1901361	organic cyclic compound catabolic process	6.34%	0.803	0.61	956	-0.059915	0.689115	0.015892
GO:0015711	organic anion transport	1.43%	0.827	0.64	215	-0.121093	0.471165	0.016066
GO:0044283	small molecule biosynthetic process	5.87%	0.761	0.465	266	-0.108679	0.508954	0.01699
GO:0006446	regulation of translational initiation	0.02%	0.789	0.549	47	0.211838	3.730317	0.017729
GO:0071322	cellular response to carbohydrate stimulus	0.01%	0.932	0.272	27	-0.302617	0.152492	0.017731
GO:0006749	glutathione metabolic process	0.12%	0.802	0.443	30	-0.288142	0.166845	0.019031
GO:0051028	mRNA transport	0.05%	0.894	0.532	68	0.181637	3.091954	0.019031
GO:1901685	glutathione derivative metabolic process	0.00%	0.937	0.062	23	-0.317853	0.138715	0.020744
GO:1901687	glutathione derivative biosynthetic process	0.00%	0.907	0.062	23	-0.317853	0.138715	0.020744
GO:0055085	transmembrane transport	9.40%	0.771	0.699	717	-0.065988	0.66359	0.021842
GO:0006354	DNA-templated transcription, elongation	0.12%	0.791	0.34	107	0.147532	2.501403	0.023104
GO:0006936	muscle contraction	0.02%	0.932	0.652	180	-0.126034	0.456916	0.024176
GO:0046949	fatty-acyl-CoA biosynthetic process	0.05%	0.865	0.563	16	-0.359681	0.106963	0.024615
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.00%	0.91	0.674	16	-0.359681	0.106963	0.024615
GO:0030522	intracellular receptor signaling pathway	0.12%	0.827	0.489	190	0.1139	2.029612	0.024634
GO:0001941	postsynaptic membrane organization	0.00%	0.829	0.629	13	0.323828	7.481742	0.025089
GO:0006508	proteolysis	3.71%	0.84	0.578	703	0.062879	1.478117	0.025849
GO:0009081	branched-chain amino acid metabolic process	0.48%	0.791	0.502	22	-0.31441	0.141715	0.028113
GO:0043414	macromolecule methylation	1.18%	0.831	0.511	115	0.138742	2.368437	0.030816
GO:0001503	ossification	0.03%	0.932	0.667	169	0.116355	2.060813	0.033067
GO:0006955	immune response	0.38%	0.954	0.466	923	0.054135	1.399941	0.033599
GO:0001649	osteoblast differentiation	0.01%	0.898	0.638	118	0.135849	2.326234	0.033739
GO:0006816	calcium ion transport	0.05%	0.875	0.532	186	-0.119132	0.476944	0.034052
GO:0061641	CENP-A containing chromatin organization	0.00%	0.795	0.609	21	0.267446	5.270228	0.03629
GO:0002446	neutrophil mediated immunity	0.00%	0.988	0.602	10	0.341131	8.33109	0.036432
GO:1901137	carbohydrate derivative biosynthetic process	3.92%	0.833	0.185	472	-0.075053	0.627243	0.037753