

term_ID	description	frequency	uniqueness	dispensabil	n.genes	coeff	odds.ratio	FDR
GO:002290	electron tra	1.16%	0.836	0.072	114	-0.32677	0.131236	3.95E-12
GO:000609	generation	3.22%	0.929	0	92	-0.5004	0.044609	3.85E-27
GO:000641	translation	0.72%	0.811	0.068	366	0.181267	3.084849	2.55E-12
GO:000641	translation	0.18%	0.685	0.517	283	-0.11496	0.489469	0.003272
GO:000661	SRP-depen	0.10%	0.739	0	319	-0.30031	0.154693	3.65E-25
GO:007064	protein mo	0.13%	0.853	0.384	887	-0.08213	0.600265	0.000135
GO:005511	oxidation-r	15.04%	0.861	0.21	210	0.192492	3.307722	1.48E-08
GO:004277	mitochond	0.11%	0.74	0.591	100	0.154139	2.606245	0.00874
GO:190260	hydrogen i	1.80%	0.786	0.33	856	0.086348	1.710216	0.000022
GO:005160	proteolysis	0.22%	0.799	0.687	213	0.102896	1.89545	0.017362
GO:000018	nuclear-tra	0.00%	0.827	0.119	280	0.187672	3.210111	1.53E-10
GO:003016	protein cat	0.36%	0.829	0.516	14	0.347574	8.671475	0.002968
GO:001656	protein ubi	0.11%	0.831	0.511	99	0.169449	2.866409	0.002772
GO:004363	modificatic	0.14%	0.842	0.699	33	-0.25113	0.209998	0.024186
GO:001908	viral transc	0.06%	0.822	0.243	117	-0.26163	0.196728	2E-07
GO:000639	mRNA proc	0.37%	0.82	0.676	911	0.054977	1.407286	0.014172
GO:004471	single-orga	12.46%	0.827	0.283	469	0.122095	2.135654	1.75E-06
GO:005127	chromosom	0.34%	0.841	0.477	682	-0.07988	0.608711	0.001649
GO:000681	hydrogen t	1.98%	0.843	0.456	81	-0.2273	0.243514	0.000668
GO:000037	RNA splicin	0.04%	0.853	0.232	168	-0.22511	0.246853	1.76E-07
GO:002241	cellular cor	0.29%	0.808	0.523	394	-0.09754	0.545434	0.003408
GO:004403	multi-orga	0.23%	0.979	0.519	327	-0.10698	0.514346	0.00337
GO:000915	purine ribo	1.38%	0.66	0.305	104	0.215113	3.806998	8.01E-06
GO:000838	RNA splicin	0.10%	0.85	0.469	643	0.080315	1.64728	0.001053
GO:004277	mitochond	0.00%	0.73	0.525	793	-0.06973	0.648356	0.003727
GO:000639	RNA proces	2.78%	0.812	0.35	113	-0.22438	0.247978	4.01E-05
GO:190156	organonitro	9.30%	0.827	0.394	688	0.085154	1.697569	0.000229
GO:000681	ion transpo	5.99%	0.824	0.537	99	-0.18248	0.32173	0.004515
GO:007252	purine-con	1.59%	0.798	0.55	51	0.209556	3.677765	0.005574
GO:002261	ribonucleo	0.11%	0.863	0.683	28	-0.2806	0.174854	0.015739
GO:005121	cartilage de	0.01%	0.799	0.036	37	-0.53691	0.035555	1.27E-14
GO:000609	gluconeoge	0.27%	0.815	0.358	706	-0.09669	0.548334	4.12E-05
GO:009040	organophos	4.46%	0.789	0.505	391	0.094118	1.79482	0.002598
GO:007182	ribonucleo	0.11%	0.868	0.683	496	-0.07385	0.631929	0.017102
GO:002240	cell cycle p	0.53%	0.864	0.104	152	-0.27554	0.180432	1.04E-10
GO:000650	proteolysis	3.71%	0.861	0.446	29	-0.35172	0.112389	0.000472
GO:001605	carbohydr	1.54%	0.791	0.636	190	0.114384	2.035727	0.010581
GO:001060	posttranscr	0.54%	0.832	0.293	791	-0.10164	0.531704	3.25E-06
GO:004343	oxoacid me	9.21%	0.75	0.698	117	-0.14229	0.413007	0.02356
GO:000608	organic aci	9.36%	0.763	0.363	716	-0.09581	0.55133	4.35E-05
GO:003437	high-densit	0.00%	0.732	0.465	921	0.070015	1.545139	0.000813
GO:004820	COPII vesic	0.00%	0.741	0.65	16	-0.36029	0.10656	0.011526
GO:000641	translation	0.27%	0.825	0.536	129	0.146469	2.48494	0.004405
GO:000300	system pro	0.20%	0.809	0.637	361	-0.0906	0.569465	0.010964
GO:000150	skeletal sys	0.03%	0.799	0.676	169	0.115916	2.055193	0.015065
GO:000911	nucleotide	9.83%	0.668	0.688	19	-0.32306	0.134298	0.018279

GO:000644 regulation of	0.02%	0.793	0.428	566	0.090148	1.751078	0.000393
GO:000027 mitotic cell	0.09%	0.88	0.684	176	-0.12143	0.470186	0.017102
GO:004369 reverse cho	0.00%	0.884	0.415	948	-0.07539	0.625932	0.000393
GO:005508 nucleobase	10.84%	0.739	0.526	103	0.162165	2.739545	0.004005
GO:190304 mitotic cell	0.08%	0.874	0.677	36	0.220183	3.928877	0.01515
GO:000906 glutamine f	1.29%	0.782	0.128	970	-0.11885	0.477792	4.02E-10
GO:000988 tissue deve	0.13%	0.896	0.557	16	0.316267	7.138289	0.006549
GO:000906 cellular am	0.75%	0.748	0.555	434	-0.0884	0.577316	0.00607
GO:000695 immune re	0.38%	0.938	0	99	-0.45377	0.059606	2.89E-23
GO:007252 purine-con	8.06%	0.831	0.536	82	0.177394	3.011479	0.004256
GO:000609 pyruvate m	0.73%	0.809	0.471	682	-0.07988	0.608711	0.001649
GO:000625 DNA metak	6.34%	0.811	0.403	11	-0.50861	0.042392	0.000351
GO:004304 ATP-depen	0.00%	0.85	0.587	546	-0.07664	0.621099	0.00868
GO:004887 cell motility	0.40%	0.806	0.227	361	-0.16335	0.362352	8.96E-08
GO:005167 localization	0.40%	0.919	0.256	266	0.163818	2.767829	2.33E-07
GO:190268 positive reg	0.20%	0.738	0.368	13	0.410608	12.82975	9.63E-05
GO:000635 DNA-templ	0.12%	0.823	0.323	48	-0.33352	0.125847	1.17E-05
GO:000718 adenylate c	0.01%	0.837	0.687	472	-0.07551	0.625474	0.017329
GO:000635 regulation of	0.21%	0.758	0.378	613	-0.09872	0.54144	0.000103
GO:000718 G-protein c	0.01%	0.837	0.688	84	-0.17071	0.34614	0.018279
GO:003278 monocarbo	2.31%	0.787	0.539	125	-0.16248	0.364316	0.00494
GO:000697 cellular res	1.98%	0.9	0.466	830	-0.07641	0.621987	0.000837
GO:004477 cell cycle pl	0.03%	0.883	0.683	50	0.192011	3.297851	0.016505
GO:003247 regulation of	0.00%	0.799	0.497	924	0.065728	1.504516	0.002002
GO:003260 type I inter	0.00%	0.847	0.637	127	0.1358	2.32552	0.010964
GO:000660 NLS-bearin	0.00%	0.862	0.658	237	-0.10892	0.5082	0.012964
GO:001905 viral life cy	1.21%	0.95	0.677	16	-0.35165	0.112437	0.015073
GO:000718 G-protein c	0.37%	0.796	0.545	650	-0.07407	0.631077	0.005188
GO:003436 macromole	0.00%	0.896	0.33	110	0.206226	3.602452	1.51E-05
GO:004001 locomotor	1.44%	0.994	0	533	0.175522	2.97665	7.07E-16
GO:004001 regulation of	0.06%	0.897	0.642	215	-0.11585	0.486781	0.011287
GO:000662 lipid metab	3.09%	0.864	0.144	545	0.139502	2.379638	6.78E-10
GO:000698 response to	0.01%	0.937	0.288	433	-0.13505	0.432009	2.72E-06
GO:000635 DNA-templ	0.20%	0.817	0.338	705	0.09268	1.778858	2.92E-05
GO:000007 DNA dama	0.01%	0.855	0.586	83	0.167113	2.825089	0.008452
GO:000918 cyclic nucle	0.11%	0.786	0.378	176	-0.17473	0.337615	0.000128
GO:005164 organelle lo	0.03%	0.893	0.539	412	-0.09285	0.561559	0.004636
GO:000861 lipid biosyn	2.21%	0.806	0.45	655	-0.08753	0.580444	0.000548
GO:000611 energy rese	0.13%	0.862	0.6	90	-0.17892	0.328931	0.0092
GO:000919 cyclic nucle	0.11%	0.73	0.628	145	0.129657	2.238418	0.009927
GO:004259 homeostat	0.97%	0.901	0.328	365	-0.13772	0.424904	1.33E-05
GO:190165 glycosyl co	8.26%	0.794	0.663	266	-0.1029	0.527567	0.013011
GO:000165 urogenital	0.02%	0.803	0.68	11	0.335985	8.068902	0.015201
GO:000905 macromole	1.64%	0.866	0.304	138	-0.22011	0.254644	6.33E-06
GO:000703 Golgi organ	0.01%	0.874	0.609	541	-0.07638	0.622095	0.009336
GO:004887 chemical ho	0.26%	0.907	0.664	67	-0.19658	0.294747	0.013011
GO:003136 N-terminal	0.04%	0.864	0.477	774	0.071402	1.558516	0.001845

GO:007182 protein-DN	0.03%	0.878	0.62	98	0.153789	2.60059	0.009709
GO:000726 cell-cell sig	0.06%	0.898	0.085	420	0.168033	2.841288	8.83E-12
GO:009013 tissue migr	0.01%	0.838	0.538	179	0.126923	2.2007	0.004515
GO:007200 renal syste	0.02%	0.804	0.654	16	-0.36029	0.10656	0.011526
GO:000698 ER-nucleus	0.01%	0.845	0.364	10	-0.5608	0.030648	7.02E-05
GO:002261 biological a	1.21%	0.994	0	106	-0.3845	0.091673	1.49E-16
GO:005134 regulation i	0.00%	0.92	0.005	431	-0.21075	0.269894	1.77E-15
GO:001605 carbohydra	1.35%	0.865	0.519	17	-0.38703	0.090243	0.003374
GO:000715 cell adhesio	0.56%	0.991	0	89	-0.46298	0.056292	2.93E-22
GO:005081 negative re	0.00%	0.8	0.561	92	0.162963	2.753158	0.00688
GO:003596 response to	0.01%	0.94	0.614	110	0.146602	2.486997	0.00964
GO:004227 ribosomal s	0.08%	0.901	0.392	47	0.259009	5.001008	0.000194
GO:003112 RNA 3'-end	0.09%	0.851	0.501	89	-0.20267	0.283794	0.002192
GO:004428 small mole	1.35%	0.793	0.503	296	-0.11492	0.489606	0.002495
GO:003051 intracellula	0.01%	0.843	0.37	150	-0.18994	0.307162	0.000102
GO:001820 peptidyl-lys	0.06%	0.858	0.49	68	-0.22954	0.240149	0.001991
GO:000738 pattern spe	0.04%	0.8	0.69	33	0.222708	3.991004	0.019228
GO:003285 positive reg	0.00%	0.697	0.471	47	0.237125	4.365104	0.001348
GO:003052 intracellula	0.12%	0.814	0.489	107	0.168025	2.841148	0.001923
GO:000705 chromosom	0.37%	0.898	0.1	333	0.181045	3.080605	2.49E-11
GO:190257 single-orga	12.73%	0.827	0.58	104	-0.16897	0.349917	0.008421
GO:190258 single-orga	0.30%	0.829	0.634	32	-0.27649	0.179376	0.010581
GO:005508 transmemk	9.40%	0.77	0.699	10	-0.3999	0.083305	0.025869
GO:001571 organic ani	1.43%	0.827	0.64	718	-0.06543	0.665911	0.010964
GO:004694 fatty-acyl-C	0.05%	0.868	0.145	66	-0.35316	0.111384	9.03E-09
GO:003533 long-chain	0.00%	0.911	0.674	27	-0.28811	0.166881	0.014011
GO:007182 protein-lipi	0.00%	0.894	0.523	927	-0.06541	0.665998	0.003395
GO:000679 sulfur comp	1.67%	0.934	0.076	456	0.163273	2.758471	7.06E-12
GO:004428 small mole	5.87%	0.762	0.548	110	-0.17139	0.344696	0.00524
GO:003080 regulation i	0.01%	0.738	0.625	88	0.16053	2.71185	0.009873
GO:007147 cellular res	0.02%	0.933	0.312	56	-0.31508	0.141123	1.05E-05
GO:003225 methylatio	2.78%	0.986	0.01	42	-0.5152	0.04069	8.17E-15
GO:007132 cellular res	0.01%	0.917	0.619	19	-0.34343	0.118326	0.009678
GO:000695 defense res	0.57%	0.944	0.673	127	0.132817	2.282809	0.013568
GO:003158 cell-substra	0.02%	0.991	0.64	361	-0.0906	0.569465	0.010964
GO:002261 ribonucleo	1.06%	0.885	0.57	655	-0.07095	0.643458	0.008128
GO:005508 anion hom	0.03%	0.918	0.543	76	-0.20379	0.28183	0.00494
GO:004348 regulation i	0.00%	0.866	0.547	758	-0.06887	0.651817	0.00524
GO:000752 neuromusc	0.00%	0.854	0.352	302	0.131504	2.264261	4.12E-05
GO:003592 cellular res	0.00%	0.924	0.578	136	-0.14931	0.395385	0.008322
GO:000628 regulation i	0.04%	0.758	0.623	181	-0.12808	0.451154	0.009742
GO:004864 anatomical	0.13%	0.894	0.655	26	-0.29766	0.157265	0.011714
GO:003529 tube devel	0.04%	0.798	0.693	37	0.211264	3.717018	0.021135
GO:190113 carbohydra	3.92%	0.84	0.505	540	0.081739	1.661924	0.002541
GO:000007 cell cycle cl	0.02%	0.891	0.611	26	-0.30456	0.150661	0.009471
GO:004544 fat cell diff	0.01%	0.844	0.469	64	-0.2466	0.215984	0.000945
GO:000908 branched-c	0.01%	0.817	0.628	125	-0.15196	0.388935	0.010049

GO:007180 protein tra	0.53%	0.801	0.668	91	0.153292	2.592575	0.013473
GO:004341 macromole	1.18%	0.86	0.511	99	0.169449	2.866409	0.002772
GO:004348 regulation	0.00%	0.866	0.549	808	0.063992	1.488376	0.005475
GO:004427 sulfur comp	1.34%	0.886	0.676	166	-0.12727	0.45341	0.014554
GO:001591 phospholip	0.02%	0.858	0.691	115	0.132732	2.281605	0.020485
GO:003163 plasminoge	0.01%	0.902	0.257	14	-0.57358	0.028309	4.72E-07