

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0071826	ribonucleoprotein complex subunit organi...	168	12	2.60	0.000011	0.0011
GO:0022618	ribonucleoprotein complex assembly	161	11	2.49	0.000040	0.0014
GO:0022613	ribonucleoprotein complex biogenesis	328	16	5.07	0.000049	0.0014
GO:0000377	RNA splicing, via transesterification re...	174	11	2.69	0.000081	0.0014
GO:0000398	mRNA splicing, via spliceosome	174	11	2.69	0.000081	0.0014
GO:0000375	RNA splicing, via transesterification re...	175	11	2.71	0.000085	0.0014
GO:0090304	nucleic acid metabolic process	3317	75	51.30	0.000100	0.0014
GO:0032877	positive regulation of DNA endoreduplica...	2	2	0.03	0.000240	0.0030
GO:0016071	mRNA metabolic process	438	17	6.77	0.000450	0.0050
GO:0008380	RNA splicing	292	13	4.52	0.000610	0.0061
GO:0010467	gene expression	3512	75	54.31	0.000690	0.0061
GO:0006139	nucleobase-containing compound metabolic...	3697	78	57.17	0.000730	0.0061
GO:0034641	cellular nitrogen compound metabolic pro...	4262	87	65.91	0.000860	0.0066
GO:0034622	cellular macromolecular complex assembly	604	20	9.34	0.001070	0.0074
GO:0016070	RNA metabolic process	2927	64	45.26	0.001180	0.0074
GO:0006807	nitrogen compound metabolic process	4431	89	68.52	0.001250	0.0074
GO:0001825	blastocyst formation	31	4	0.48	0.001260	0.0074
GO:0031860	telomeric 3' overhang formation	4	2	0.06	0.001400	0.0074
GO:0060718	chorionic trophoblast cell differentiati...	4	2	0.06	0.001400	0.0074
GO:0006397	mRNA processing	363	14	5.61	0.001530	0.0076
GO:0046483	heterocycle metabolic process	3793	78	58.66	0.001640	0.0078
GO:0006725	cellular aromatic compound metabolic pro...	3809	78	58.90	0.001870	0.0085
GO:0032466	negative regulation of cytokinesis	5	2	0.08	0.002310	0.0091
GO:0070365	hepatocyte differentiation	5	2	0.08	0.002310	0.0091
GO:0019827	stem cell population maintenance	118	7	1.82	0.002350	0.0091
GO:0044260	cellular macromolecule metabolic process	5398	103	83.48	0.002360	0.0091
GO:0098727	maintenance of cell number	120	7	1.86	0.002590	0.0093
GO:0043170	macromolecule metabolic process	5740	108	88.77	0.002720	0.0093
GO:0006396	RNA processing	654	20	10.11	0.002740	0.0093
GO:0051171	regulation of nitrogen compound metaboli...	2734	59	42.28	0.002800	0.0093
GO:1901360	organic cyclic compound metabolic proces...	3933	79	60.82	0.003070	0.0099
GO:0060717	chorion development	6	2	0.09	0.003420	0.0101
GO:1902074	response to salt	6	2	0.09	0.003420	0.0101
GO:1903867	extraembryonic membrane development	6	2	0.09	0.003420	0.0101
GO:0000245	spliceosomal complex assembly	41	4	0.63	0.003590	0.0103
GO:0051172	negative regulation of nitrogen compound...	1077	28	16.66	0.004340	0.0118
GO:0010468	regulation of gene expression	2670	57	41.29	0.004370	0.0118
GO:0043038	amino acid activation	44	4	0.68	0.004640	0.0119
GO:0043039	tRNA aminoacylation	44	4	0.68	0.004640	0.0119
GO:0060255	regulation of macromolecule metabolic pr...	3694	74	57.13	0.004980	0.0124
GO:0009059	macromolecule biosynthetic process	3224	66	49.86	0.005370	0.0131
GO:0000086	G2/M transition of mitotic cell cycle	75	5	1.16	0.006040	0.0140
GO:0001824	blastocyst development	75	5	1.16	0.006040	0.0140
GO:0032875	regulation of DNA endoreduplication	8	2	0.12	0.006260	0.0142
GO:0044839	cell cycle G2/M phase transition	78	5	1.21	0.007120	0.0150
GO:0017148	negative regulation of translation	110	6	1.70	0.007170	0.0150
GO:0060706	cell differentiation involved in embryon...	26	3	0.40	0.007280	0.0150
GO:0034645	cellular macromolecule biosynthetic proc...	3149	64	48.70	0.007470	0.0150
GO:0002829	negative regulation of type 2 immune res...	9	2	0.14	0.007970	0.0150
GO:0042023	DNA endoreduplication	9	2	0.14	0.007970	0.0150
GO:0045056	transcytosis	9	2	0.14	0.007970	0.0150
GO:0071786	endoplasmic reticulum tubular network or...	9	2	0.14	0.007970	0.0150
GO:2000105	positive regulation of DNA-dependent DNA...	9	2	0.14	0.007970	0.0150
GO:0080090	regulation of primary metabolic process	3713	73	57.42	0.008770	0.0161
GO:0034249	negative regulation of cellular amide me...	115	6	1.78	0.008840	0.0161
GO:0031326	regulation of cellular biosynthetic proc...	2645	55	40.90	0.009120	0.0162
GO:0031327	negative regulation of cellular biosynth...	1035	26	16.01	0.009220	0.0162