

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006396	RNA processing	654	35	14.21	6.80e-07	0.0001
GO:0006397	mRNA processing	363	23	7.89	4.30e-06	0.0001
GO:0006412	translation	501	28	10.89	4.30e-06	0.0001
GO:0008380	RNA splicing	292	20	6.35	5.80e-06	0.0001
GO:0043604	amide biosynthetic process	576	30	12.52	7.90e-06	0.0001
GO:0043043	peptide biosynthetic process	518	28	11.26	8.10e-06	0.0001
GO:0016071	mRNA metabolic process	438	24	9.52	3.00e-05	0.0004
GO:0006518	peptide metabolic process	607	29	13.19	5.50e-05	0.0007
GO:0043603	cellular amide metabolic process	715	32	15.54	7.80e-05	0.0009
GO:0000377	RNA splicing, via transesterification re...	174	13	3.78	1.10e-04	0.0010
GO:0000398	mRNA splicing, via spliceosome	174	13	3.78	1.10e-04	0.0010
GO:0000375	RNA splicing, via transesterification re...	175	13	3.80	1.20e-04	0.0010
GO:0033119	negative regulation of RNA splicing	27	5	0.59	2.50e-04	0.0019
GO:0043414	macromolecule methylation	196	13	4.26	3.50e-04	0.0025
GO:0006413	translational initiation	91	8	1.98	8.00e-04	0.0053
GO:0010467	gene expression	3512	100	76.33	9.00e-04	0.0056
GO:1901566	organonitrogen compound biosynthetic pro...	896	34	19.47	1.00e-03	0.0059
GO:0032259	methylation	256	14	5.56	1.43e-03	0.0079
GO:0006807	nitrogen compound metabolic process	4431	119	96.30	2.18e-03	0.0115
GO:0034641	cellular nitrogen compound metabolic pro...	4262	115	92.63	2.34e-03	0.0117
GO:0016576	histone dephosphorylation	4	2	0.09	2.74e-03	0.0129
GO:0007067	mitotic nuclear division	368	17	8.00	2.84e-03	0.0129
GO:0000387	spliceosomal snRNP assembly	29	4	0.63	3.38e-03	0.0147
GO:0030638	polyketide metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0030647	aminoglycoside antibiotic metabolic proc...	5	2	0.11	4.51e-03	0.0154
GO:0043985	histone H4-R3 methylation	5	2	0.11	4.51e-03	0.0154
GO:0044597	daunorubicin metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0044598	doxorubicin metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0046607	positive regulation of centrosome cycle	5	2	0.11	4.51e-03	0.0154
GO:0070507	regulation of microtubule cytoskeleton o...	120	8	2.61	4.63e-03	0.0154
GO:0050686	negative regulation of mRNA processing	32	4	0.70	4.86e-03	0.0157
GO:0032071	regulation of endodeoxyribonuclease acti...	6	2	0.13	6.66e-03	0.0202
GO:0043615	astrocyte cell migration	6	2	0.13	6.66e-03	0.0202
GO:0016571	histone methylation	103	7	2.24	7.13e-03	0.0207
GO:0016570	histone modification	339	15	7.37	7.26e-03	0.0207
GO:0016070	RNA metabolic process	2927	81	63.61	7.97e-03	0.0214
GO:0006479	protein methylation	132	8	2.87	8.13e-03	0.0214
GO:0008213	protein alkylation	132	8	2.87	8.13e-03	0.0214
GO:0016569	covalent chromatin modification	345	15	7.50	8.47e-03	0.0217
GO:1903312	negative regulation of mRNA metabolic pr...	38	4	0.83	9.01e-03	0.0217
GO:0032070	regulation of deoxyribonuclease activity	7	2	0.15	9.19e-03	0.0217
GO:0034969	histone arginine methylation	7	2	0.15	9.19e-03	0.0217