GO:0006396 RNA processing 964 35 14.21 8.80e-07 0.0001	GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GC:0006412 translation S01 28 10.89 4.30e-06 0.0001	GO:0006396	RNA processing	654	35	14.21	6.80e-07	0.0001
GO:0008380 RNA splicing 292 20 6.35 5.80e-06 0.0001	GO:0006397	mRNA processing	363	23	7.89	4.30e-06	0.0001
GO:0043604	GO:0006412	translation	501	28	10.89	4.30e-06	0.0001
GO:0043043 peptide biosynthetic process 518 28 11.26 8.10e-06 0.0001	GO:0008380	RNA splicing	292	20	6.35	5.80e-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:043603 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:0000378 RNA splicing, via spliceosome 174 13 3.78 1.10e-04 0.0010 GO:000375 RNA splicing, via spliceosome 174 13 3.80 1.20e-04 0.0010 GO:000371 RNA splicing, via spliceosome 175 13 3.80 1.20e-04 0.0010 GO:000371 RNA splicing, via transesterification re 175 13 3.80 1.20e-04 0.0010 GO:000371 macromolecule methylation 27 5 0.59 2.50e-04 0.0019 GO:0043414 macromolecule methylation 196 13 4.26 3.50e-04 0.0025 GO:0044341 macromolecule methylation 196 13 4.26 3.50e-04 0.0025 GO:0010467 gene expression 3512 100 76.33 9.00e-04 0.0025 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 5.66 1.43e-03 0.0079 GO:0038259 mitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GO:0034641 cellular nitrogen compound metabolic proc 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:0007067 mitotic nuclear division 368 17 8.00 2.84e-03 0.0129 GO:000363 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0030647 aminoglycoside antiblotic 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:0044598 doxorubicin 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:0044598 doxorubicin 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:0046670 positive regulation of mRNA processing 32 4 0.70 4.88e-03 0.0154 GO:0046670 positive regulation of mRNA processing 32 4 0.70 4.88e-03 0.0207 GO:0016670 listone modification 33 15 7.37 7.26e-03	GO:0043604	amide biosynthetic process	576	30	12.52	7.90e-06	0.0001
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:0000378 mRNA splicing, via spliceosome 174 13 3.78 1.10e-04 0.0010 GO:0000378 RNA splicing, via spliceosome 174 13 3.78 1.10e-04 0.0010 GO:000375 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:0033119 negative regulation of RNA splicing 27 5 0.59 2.50e-04 0.0025 GO:00043414 macromolecule methylation 196 13 4.26 3.50e-04 0.0025 GO:0006413 translational initiation 91 8 1.98 8.00e-04 0.0025 GO:0006413 translational initiation 91 8 1.98 8.00e-04 0.0056 GO:01901566 organonitrogen compound biosynthetic pro 896 34 19.47 1.00e-03 0.0059 GO:0303259 methylation 256 14 5.56 1.43e-03 0.0079 GO:0003259 methylation 256 14 5.56 1.43e-03 0.0115 GO:0034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GO:0034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GO:0006676 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:000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GO:003638 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0033638 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin metabolic process 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:0044597 histone modification 339 15 7.37 7.26e-03 0.0202 GO:0043616 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GO:0043616 astrocyte cell migration 10 3 7 2.24 7.13e-03 0.0207 GO:0043619 protein methylation 132 8 2.67 8.13e-03 0.0214 GO:0006479 protein methylation 132 8 2.67 8.13e-03 0.0217 GO:0006479 protein	GO:0043043	peptide biosynthetic process	518	28	11.26	8.10e-06	0.0001
GC:0043603 cellular amide metabolic process 715 32 15.54 7.80e-05 0.0009 GC:0000377 RNA splicing, via transesterification re 174 13 3.78 1.10e-04 0.0010 GC:0000398 mRNA splicing, via spliceosome 174 13 3.78 1.10e-04 0.0010 GC:0000375 RNA splicing, via transesterification re 175 13 3.80 1.20e-04 0.0010 GC:000375 RNA splicing, via transesterification re 175 13 3.80 1.20e-04 0.0010 GC:00033119 negative regulation of RNA splicing 27 5 0.59 2.50e-04 0.0019 GC:00043414 macromolecule methylation 196 13 4.26 3.50e-04 0.0025 GC:0006413 translational initiation 91 8 1.98 8.00e-04 0.0053 GC:0010467 gene expression 3512 100 76.33 9.00e-04 0.0056 GC:01001666 organonitrogen compound biosynthetic pro 896 34 19.47 1.00e-03 0.0059 GC:0901660 ritrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:0034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:0034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:0034641 cellular nitrogen compound metabolic process 4431 19 96.30 2.84e-03 0.0112 GC:0003667 mitotic nuclear division 368 17 8.00 2.84e-03 0.0129 GC:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0149 GC:0003687 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0149 GC:0030638 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0030638 histone H4-R3 methylation 5 2 0.11 4.51e-03 0.0154 GC:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0046607 positive regulation of mRNA processing 32 4 0.70 4.86e-03 0.0154 GC:0003671 histone modification 339 15 7.37 7.26e-03 0.0207 GC:0016670 histone modification 339 15 7.37 7.26e-03 0.0207 GC:0016670 histone modification 339 15 7.37 7.26e-03 0.0217 GC:0003679 protein alkylation 132 8 2.87 8.13e-03 0.0217 GC:00036270 regulation of mRNA metabolic process 2927 81 63.66 7.97e-03 0.0217 GC:00036270 regulation of mRNA metabolic process 2927 81 63.67 7.97e-03 0.0217 GC:00036270 regulation of mRNA metabolic proce	GO:0016071	mRNA metabolic process	438	24	9.52	3.00e-05	0.0004
GO:0000377 RNA splicing, via transesterification re 174	GO:0006518	peptide metabolic process	607	29	13.19	5.50e-05	0.0007
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:00033119 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 3612 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 process 4431 119 96.30 2.18e-03 0.0115 GO:0034641 cellular nitrogen compound metabolic process 4462 115 92.63 2.34e-03 0.0112 GO:0007667 histone dephosphorylation 4 2 0.09 2.74e-03 0.0129 GO:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0129 GO:0003083 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GO:0030647 aminoplycoside antiblotic metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0030647 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin metabolic process 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:0044596 doxorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044596 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:0046698 doxorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0046697 regulation of microtubule cytoskeleton 0 120 8 2.61 4.63e-03 0.0157 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:0016570 histone modification 339 15 7.37 7.26e-03 0.0207 GO:0016570 histone modification 345 15 7.50 8.47e-03 0.0217 GO:0006890 covalent chromatin modification 345	GO:0043603	cellular amide metabolic process	715	32	15.54	7.80e-05	0.0009
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:0010467 gene expression 3512 100 76.33 9.00e-04 0.0056 GO:1901666 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:0034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GO:003467 histone dephosphorylation 4 2 0.09 2.74e-03 0.0129 GO:0007667 mitotic nuclear division 368 17 8.00 2.84e-03 0.0149 GO:000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0149	GO:0000377	RNA splicing, via transesterification re	174	13	3.78	1.10e-04	0.0010
GC:0033119 negative regulation of RNA splicing 27 5 0.59 2.50e-04 0.0019 GC:0043414 macromolecule methylation 196 13 4.26 3.50e-04 0.0025 GC:0006413 translational initiation 91 8 1.98 8.00e-04 0.0053 GC:0010467 gene expression 3512 100 76.33 9.00e-04 0.0056 GC:1901566 organonitrogen compound biosynthetic pro 896 34 19.47 1.00e-03 0.0059 GC:0006807 nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:00034641 cellular nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:0006807 nitrogen compound metabolic pro 4262 115 92.63 2.34e-03 0.0117 GC:00016576 histone dephosphorylation 4 2 0.09 2.74e-03 0.0129 GC:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GC:0003638 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0030647 aminoglycoside antibiotic metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0044598 doxorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0044598 doxorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0046607 positive regulation of centrosome cycle 5 2 0.11 4.51e-03 0.0154 GC:005686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0154 GC:005686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0154 GC:005686 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GC:0043615 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GC:0043615 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GC:0043615 astrocyte cell migration 103 7 2.24 7.13e-03 0.0202 GC:0016670 histone methylation 103 7 2.24 7.13e-03 0.0207 GC:0016670 protein methylation 132 8 2.87 8.13e-03 0.0214 GC:0006479 protein methylation 132 8 2.87 8.13e-03 0.0217 GC:0016659 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GC:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GC:0016570 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217 GC:00032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	GO:0000398	mRNA splicing, via spliceosome	174	13	3.78	1.10e-04	0.0010
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:00034641 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:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0129 GO:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GO:0030684 aminoglycoside antibiotic metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0030687 aminoglycoside antibiotic metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin metabolic process 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:005686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0157 GO:005681 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GO:004657 histone modification 339 15 7.37 7.26e-03 0.0207 GO:0016570 protein methylation 132 8 2.87 8.13e-03 0.0217 GO:000649 protein methylation 132 8 2.87 8.13e-03 0.0217 GO:0006569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0006569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0006370 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217 GO:0003270 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	GO:0000375	RNA splicing, via transesterification re	175	13	3.80	1.20e-04	0.0010
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:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GO:000388 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0030638 polyketide metabolic process 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: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:0050686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0157 GO:0032071 fegulation of endodeoxyribonuclease acti 6 2 0.13 6.66e-03 0.0202 GO:0016570 histone methylation 103 7 2.24 7.13e-03 0.0207 GO:0016670 protein methylation 103 7 2.24 7.13e-03 0.0207 GO:0016670 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:0006479 protein methylation 132 8 2.87 8.13e-03 0.0214 GO:0006479 protein methylation 132 8 2.87 8.13e-03 0.0214 GO:0016669 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	GO:0033119	negative regulation of RNA splicing	27	5	0.59	2.50e-04	0.0019
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:0000767 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:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GO:0044597 daunorubicin 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:005686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0157 GO:0032071 regulation of mRNA processing 32 4 0.70 4.86e-03 0.0202 GO:0043615 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GO:0016570 histone methylation 103 7 2.24 7.13e-03 0.0207 GO:0016570 histone medification 339 15 7.37 7.26e-03 0.0207 GO:0016570 histone medification 339 15 7.37 7.26e-03 0.0207 GO:0016570 histone medification 345 15 7.50 8.47e-03 0.0217 GO:0008213 protein alkylation 132 8 2.87 8.13e-03 0.0217 GO:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.	GO:0043414	macromolecule methylation	196	13	4.26	3.50e-04	0.0025
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:0044597 daunorubicin 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:0050686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0157 GO:0032071 regulation of mRNA processing 32 4 0.70 4.86e-03 0.0202 GO:0043615 astrocyte cell migration 6 2 0.13 6.66e-03 0.0202 GO:0045670 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:0016570 histone modification 132 8 2.87 8.13e-03 0.0214 GO:0008213 protein alkylation 132 8 2.87 8.13e-03 0.0217 GO:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	GO:0006413	translational initiation	91	8	1.98	8.00e-04	0.0053
GO:0032259 methylation 256	GO:0010467	gene expression	3512	100	76.33	9.00e-04	0.0056
GC:0006807 nitrogen compound metabolic process 4431 119 96.30 2.18e-03 0.0115 GC:0034641 cellular nitrogen compound metabolic pro 4262 115 92.63 2.34e-03 0.0117 GC:0016576 histone dephosphorylation 4 2 0.09 2.74e-03 0.0129 GC:0007067 mitotic nuclear division 368 17 8.00 2.84e-03 0.0129 GC:0000387 spliceosomal snRNP assembly 29 4 0.63 3.38e-03 0.0147 GC:0030638 polyketide metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0030647 aminoglycoside antibiotic metabolic proc 5 2 0.11 4.51e-03 0.0154 GC:0043985 histone H4-R3 methylation 5 2 0.11 4.51e-03 0.0154 GC:0044597 daunorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0044598 doxorubicin metabolic process 5 2 0.11 4.51e-03 0.0154 GC:0046607 positive regulation of centrosome cycle 5 2 0.11 4.51e-03 0.0154 GC:0050686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0154 GC:0032071 regulation of endodeoxyribonuclease acti 6 2 0.13 6.66e-03 0.0202 GC:0016571 histone methylation 103 7 2.24 7.13e-03 0.0207 GC:0016570 histone modification 339 15 7.37 7.26e-03 0.0207 GC:0016570 histone modification 339 15 7.37 7.26e-03 0.0214 GC:0006479 protein methylation 132 8 2.87 8.13e-03 0.0214 GC:0006213 protein alkylation 132 8 2.87 8.13e-03 0.0214 GC:0006213 protein alkylation 132 8 2.87 8.13e-03 0.0217 GC:01903312 negative regulation of mRNA metabolic pr 38 4 0.83 9.01e-03 0.0217 GC:01903312 negative regulation of mRNA metabolic pr 38 4 0.83 9.01e-03 0.0217 GC:019032070 regulation of mRNA metabolic pr 38 4 0.83 9.01e-03 0.0217	GO:1901566	organonitrogen compound biosynthetic pro	896	34	19.47	1.00e-03	0.0059
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:0050686 negative regulation of mRNA processing 32 4 0.70 4.86e-03 0.0157 GO:0032071 regulation of microtubule cytoskeleton 0 120 8 2.61 4.63e-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:0016570 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:0016609 crovalent chromatin modification 132 8 2.87 8.13e-03 0.0214 GO:0006479 protein methylation 132 8 2.87 8.13e-03 0.0214 GO:0006213 protein alkylation 132 8 2.87 8.13e-03 0.0217 GO:016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:01903312 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:0032259	methylation	256	14	5.56	1.43e-03	0.0079
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:0016570 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:0016670 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:0006479 protein methylation 132 8 2.87 8.13e-03 0.0214 GO:0006213 protein alkylation 132 8 2.87 8.13e-03 0.0214 GO:016569 covalent chromatin modification 345 15 7.50 8.47e-03 0.0217 GO:01903312 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:0006807	nitrogen compound metabolic process	4431	119	96.30	2.18e-03	0.0115
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:0016570 histone modification 339 15 7.37 7.26e-03 0.0207 GO:0016670 RNA metabolic process 2927 81 63.61 7.97e-03 0.0214 GO:0008213 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:0008213 protein alkylation 132 8 2.87 8.13e-03 0.0217 GO:1903312 negative regulation of mRNA metabolic pr 38 4 0.83 9.01e-03 0.0217 GO:01903312 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:0034641	cellular nitrogen compound metabolic pro	4262	115	92.63	2.34e-03	0.0117
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 0 120 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:0016670 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:0016576	histone dephosphorylation	4	2	0.09	2.74e-03	0.0129
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 0 120 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: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:0008213 protein methylation 132 8 2.87 8.13e–03 0.0214 GO:0008213 protein methylation 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:0007067	mitotic nuclear division	368	17	8.00	2.84e-03	0.0129
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:0008213 protein methylation 132 8 2.87 8.13e–03 0.0214 GO:000659 covalent chromatin modification 345 15 7.50 8.47e–03 0.0217 GO:01903312 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:0000387	spliceosomal snRNP assembly	29	4	0.63	3.38e-03	0.0147
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:01903312 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:0030638	polyketide metabolic process	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:00016569 covalent chromatin modification 345 15 7.50 8.47e–03 0.0217 GO:01903312 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:0030647	aminoglycoside antibiotic metabolic proc	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:0043985	histone H4-R3 methylation	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:0044597	daunorubicin metabolic process	5	2	0.11	4.51e-03	0.0154
GO:0070507 regulation of microtubule cytoskeleton o 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 GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	GO:0044598	doxorubicin metabolic process	5	2	0.11	4.51e-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:0046607	positive regulation of centrosome cycle	5	2	0.11	4.51e-03	0.0154
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:0070507	regulation of microtubule cytoskeleton o	120	8	2.61	4.63e-03	0.0154
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:0050686	negative regulation of mRNA processing	32	4	0.70	4.86e-03	0.0157
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:0032071	regulation of endodeoxyribonuclease acti	6	2	0.13	6.66e-03	0.0202
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:0043615	astrocyte cell migration	6	2	0.13	6.66e-03	0.0202
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:0016571	histone methylation	103	7	2.24	7.13e-03	0.0207
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:0016570	histone modification	339	15	7.37	7.26e-03	0.0207
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:0016070	RNA metabolic process	2927	81	63.61	7.97e-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:0006479	protein methylation	132	8	2.87	8.13e-03	0.0214
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:0008213	protein alkylation	132	8	2.87	8.13e-03	0.0214
GO:0032070 regulation of deoxyribonuclease activity 7 2 0.15 9.19e-03 0.0217	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:0034969 histone arginine methylation 7 2 0.15 9.19e–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