

PANTHER in 2013: modeling the evolution of gene function in the context of phylogenetic trees

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Citation Report

#	ARTICLE	IF	CITATIONS
1	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. BMC Genomics, 2013, 14, 204.	2.8	61
2	Large-scale gene function analysis with the PANTHER classification system. Nature Protocols, 2013, 8, 1551-1566.	12.0	2,276
3	Proteomic techniques for characterisation of mesenchymal stem cell secretome. Biochimie, 2013, 95, 2196-2211.	2.6	231
4	The evolution of lineage-specific clusters of single nucleotide substitutions in the human genome. Molecular Phylogenetics and Evolution, 2013, 69, 276-285.	2.7	3
5	Tethering preferences of domain families co-occurring in multi-domain proteins. Molecular BioSystems, 2013, 9, 1708.	2.9	1
6	On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks. , 2013, , .		1
7	Exploring the role of post-translational modifications on protein-protein interactions with survivin. Archives of Biochemistry and Biophysics, 2013, 538, 64-70.	3.0	25
8	Web Apollo: a web-based genomic annotation editing platform. Genome Biology, 2013, 14, R93.	9.6	329
9	Role of genomic architecture in the expression dynamics of long noncoding RNAs during differentiation of human neuroblastoma cells. BMC Systems Biology, 2013, 7, S11.	3.0	24
10	Conversion of KEGG metabolic pathways to SBGN maps including automatic layout. BMC Bioinformatics, 2013, 14, 250.	2.6	13
11	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. BMC Genomics, 2013, 14, 798.	2.8	76
12	Gene variants associated with antisocial behaviour: a latent variable approach. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2013, 54, 1074-1085.	5.2	16
13	Crosstalk between B16 melanoma cells and B-1 lymphocytes induces global changes in tumor cell gene expression. Immunobiology, 2013, 218, 1293-1303.	1.9	11
14	Differential in Gel Electrophoresis (DIGE) Comparative Proteomic Analysis of Macrophages Cell Cultures in Response to Perthamide C Treatment. Marine Drugs, 2013, 11, 1288-1299.	4.6	7
15	Oxidative Bioactivation of Abacavir in Subcellular Fractions of Human Antigen Presenting Cells. Chemical Research in Toxicology, 2013, 26, 1064-1072.	3.3	12
16	Pathway Databases: Making Chemical and Biological Sense of the Genomic Data Flood. Chemistry and Biology, 2013, 20, 629-635.	6.0	20
17	HMPAS: Human Membrane Protein Analysis System. Proteome Science, 2013, 11, S7.	1.7	10
18	SILAC-based phosphoproteomics reveals an inhibitory role of KSR1 in p53 transcriptional activity via modulation of DBC1. British Journal of Cancer, 2013, 109, 2675-2684.	6.4	16

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19	In-depth bioinformatic analysis of lung cancer-associated microRNA targets. <i>Oncology Reports</i> , 2013, 30, 2945-2956.	2.6	4
20	Epigenome-wide profiling identifies significant differences in DNA methylation between matched-pairs of T- and B-lymphocytes from healthy individuals. <i>Epigenetics</i> , 2013, 8, 1188-1197.	2.7	42
21	Genome-wide identification of genes regulated in <i>trans</i> by transposable element small interfering RNAs. <i>RNA Biology</i> , 2013, 10, 1379-1395.	3.1	91
22	TATN-1 Mutations Reveal a Novel Role for Tyrosine as a Metabolic Signal That Influences Developmental Decisions and Longevity in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013, 9, e1004020.	3.5	41
23	Linking Transcriptional Changes over Time in Stimulated Dendritic Cells to Identify Gene Networks Activated during the Innate Immune Response. <i>PLoS Computational Biology</i> , 2013, 9, e1003323.	3.2	24
24	Systemically Circulating Viral and Tumor-Derived MicroRNAs in KSHV-Associated Malignancies. <i>PLoS Pathogens</i> , 2013, 9, e1003484.	4.7	140
25	Integrated virus-host methylome analysis in head and neck squamous cell carcinoma. <i>Epigenetics</i> , 2013, 8, 953-961.	2.7	31
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147	Runs of homozygosity reveal signatures of positive selection for reproduction traits in breed and non-breed horses. <i>BMC Genomics</i> , 2015, 16, 764.	2.8	125
148	A human 3'UTR clone collection to study post-transcriptional gene regulation. <i>BMC Genomics</i> , 2015, 16, 1036.	2.8	7
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