

The PANTHER database of protein families, subfamilies

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Understanding Complex Regulatory Systems: Integrating Molecular Biology and Systems Analysis. <i>Transfusion Medicine and Hemotherapy</i> , 2005, 32, 304-321.	0.7	9
2	Proteomic identification of proteins conjugated to ISG15 in mouse and human cells. <i>Biochemical and Biophysical Research Communications</i> , 2005, 336, 496-506.	1.0	211
3	Using process diagrams for the graphical representation of biological networks. <i>Nature Biotechnology</i> , 2005, 23, 961-966.	9.4	429
4	Avoiding inconsistencies over time and tracking difficulties in Applied Biosystems AB1700/Panther probe-to-gene annotations. <i>BMC Bioinformatics</i> , 2005, 6, 307.	1.2	30
6	InterProScan: protein domains identifier. <i>Nucleic Acids Research</i> , 2005, 33, W116-W120.	6.5	2,556
7	Genome-wide localization of histone 4 arginine 3 methylation in a differentiation primed myeloid leukemia cell line. <i>Immunobiology</i> , 2005, 210, 141-152.	0.8	11
8	A comprehensive pathway map of epidermal growth factor receptor signaling. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0010.	3.2	902
9	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. <i>Genome Biology</i> , 2006, 7, R83.	13.9	50
10	Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools. <i>Nucleic Acids Research</i> , 2006, 34, W645-W650.	6.5	487
11	Bioinformatics database infrastructure for biotechnology research. <i>Journal of Biotechnology</i> , 2006, 124, 629-639.	1.9	15
12	A Computational Framework for the Topological Analysis and Targeted Disruption of Signal Transduction Networks. <i>Biophysical Journal</i> , 2006, 91, 382-398.	0.2	48
13	Pathway analysis of kidney cancer using proteomics and metabolic profiling. <i>Molecular Cancer</i> , 2006, 5, 64.	7.9	205
14	Identification and comparative analysis of accessory gland proteins in Orthoptera. <i>Genome</i> , 2006, 49, 1069-1080.	0.9	89
15	Automated protein function prediction—the genomic challenge. <i>Briefings in Bioinformatics</i> , 2006, 7, 225-242.	3.2	307
16	Proteomic identification of processes and pathways characteristic of osmoregulatory tissues in spiny dogfish shark (<i>Squalus acanthias</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2006, 1, 328-343.	0.4	16
17	Identification and pathway analysis of immediate hyperosmotic stress responsive molecular mechanisms in tilapia (<i>Oreochromis mossambicus</i>) gill. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2006, 1, 344-356.	0.4	44
18	Possible implication of ciliary neurotrophic factor (CNTF) and β -synuclein in the ammonia effect on cultured rat astroglial cells: A study using DNA and protein microarrays. <i>Neurochemistry International</i> , 2006, 48, 729-738.	1.9	15
19	PANTHER: Protein families and subfamilies modeled on the divergence of function. , 2006, , .		1

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20	An integrated approach to mapping the proteome of the human bone marrow stromal cell. <i>Proteomics</i> , 2006, 6, 5169-5182.	1.3	50
21	Molecular signature of mice T lymphocytes following tolerance induction by allogeneic BMT and CD40-CD40L costimulation blockade. <i>Transplant International</i> , 2006, 19, 146-157.	0.8	7
22	Protein biomarkers associated with acute renal failure and chronic kidney disease. <i>European Journal of Clinical Investigation</i> , 2006, 36, 753-763.	1.7	52
23	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006, 38, 431-440.	9.4	2,162
24	A subtype of multiple sclerosis defined by an activated immune defense program. <i>Genes and Immunity</i> , 2006, 7, 522-531.	2.2	84
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26	Using high-throughput SNP technologies to study cancer. <i>Oncogene</i> , 2006, 25, 1594-1601.	2.6	116
27	Creating hierarchical models of protein families based on Expressed Sequence Tags: The "Sprockets" analysis pipeline. <i>Analytica Chimica Acta</i> , 2006, 564, 123-132.	2.6	0
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29	ProFAT: a web-based tool for the functional annotation of protein sequences. <i>BMC Bioinformatics</i> , 2006, 7, 466.	1.2	9
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31	NovelFam3000 " Uncharacterized human protein domains conserved across model organisms. <i>BMC Genomics</i> , 2006, 7, 48.	1.2	5
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39	Genetic Reclassification of Histologic Grade Delineates New Clinical Subtypes of Breast Cancer. <i>Cancer Research</i> , 2006, 66, 10292-10301.	0.4	606
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42	Contrasting evolution of expression differences in the testis between species and subspecies of the house mouse. <i>Genome Research</i> , 2006, 17, 42-49.	2.4	67
43	Sequence Analysis and Organization of the Neodiprion abietis Nucleopolyhedrovirus Genome. <i>Journal of Virology</i> , 2006, 80, 6952-6963.	1.5	38
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64	Gene expression profiles in rat brain disclose CNS signature genes and regional patterns of functional specialisation. <i>BMC Genomics</i> , 2007, 8, 94.	1.2	36
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75	A domain-based approach to predict protein-protein interactions. <i>BMC Bioinformatics</i> , 2007, 8, 199.	1.2	68
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80	Computational protein function prediction: Are we making progress?. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 2505-2511.	2.4	46
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