

PANTHER: A Library of Protein Families and Subfamilies

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Citation Report

#	ARTICLE	IF	CITATIONS
1	PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. <i>Nucleic Acids Research</i> , 2003, 31, 334-341.	6.5	578
2	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40
3	Mouse Brain Organization Revealed Through Direct Genome-Scale TF Expression Analysis. <i>Science</i> , 2004, 306, 2255-2257.	6.0	390
4	FlyBase: genes and gene models. <i>Nucleic Acids Research</i> , 2004, 33, D390-D395.	6.5	319
5	FunShift: a database of function shift analysis on protein subfamilies. <i>Nucleic Acids Research</i> , 2004, 33, D197-D200.	6.5	39
6	The PANTHER database of protein families, subfamilies, functions and pathways. <i>Nucleic Acids Research</i> , 2004, 33, D284-D288.	6.5	686
7	Coding single-nucleotide polymorphisms associated with complex vs. Mendelian disease: Evolutionary evidence for differences in molecular effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15398-15403.	3.3	258
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9	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
10	Research resources for <i>Drosophila</i> : the expanding universe. <i>Nature Reviews Genetics</i> , 2005, 6, 179-193.	7.7	106
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14	Fly Six-type homeodomain proteins <i>Sine oculis</i> and <i>Optix</i> partner with different cofactors during eye development. <i>Developmental Dynamics</i> , 2005, 234, 497-504.	0.8	58
15	A genome-wide in situ hybridization map of RNA-binding proteins reveals anatomically restricted expression in the developing mouse brain. <i>BMC Developmental Biology</i> , 2005, 5, 14.	2.1	160
16	Large-scale prediction of function shift in protein families with a focus on enzymatic function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 758-768.	1.5	29
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20	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
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28	SSADH Variation in Primates: Intra- and Interspecific Data on a Gene with a Potential Role in Human Cognitive Functions. <i>Journal of Molecular Evolution</i> , 2006, 63, 54-68.	0.8	16
29	Transforming omics data into context: Bioinformatics on genomics and proteomics raw data. <i>Electrophoresis</i> , 2006, 27, 2659-2675.	1.3	33
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1535	Regional sequence expansion or collapse in heterozygous genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1008104.	1.5	31
1536	Label-free quantitative proteomic analysis of gingival crevicular fluid to identify potential early markers for root resorption. <i>BMC Oral Health</i> , 2020, 20, 256.	0.8	7
1537	In-gel digestion coupled with mass spectrometry (GeLC-MS/MS)-based salivary proteomic profiling of canine oral tumors. <i>BMC Veterinary Research</i> , 2020, 16, 335.	0.7	9
1538	Quantitative Protein Corona Composition and Dynamics on Carbon Nanotubes in Biological Environments. <i>Angewandte Chemie</i> , 2020, 132, 23876-23885.	1.6	16

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1541	Applications of Proteomic Tools to Study Insect Vectorâ€‘Plant Virus Interactions. <i>Life</i> , 2020, 10, 143.	1.1	5
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1553	<i>Twist1</i> -Reprogrammed Endothelial Cell Transplantation Potentiates Neovascularization-Mediated Diabetic Wound Tissue Regeneration. <i>Diabetes</i> , 2020, 69, 1232-1247.	0.3	21
1554	Identifying Therapies to Combat Epithelial Mesenchymal Plasticity-Associated Chemoresistance to Conventional Breast Cancer Therapies Using An shRNA Library Screen. <i>Cancers</i> , 2020, 12, 1123.	1.7	7
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1561	Antigenic membrane proteins of virulent variant of <i>Entamoeba histolytica</i> HM-1:IMSS. <i>Pathogens and Global Health</i> , 2020, 114, 333-342.	1.0	1
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1566	The ATGL lipase cooperates with ABHD5 to mobilize lipids for hepatitis C virus assembly. <i>PLoS Pathogens</i> , 2020, 16, e1008554.	2.1	25
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