

Large-scale gene function analysis with the PANTHER c

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. PLoS ONE, 2014, 9, e94816.	1.1	249
4	SILAC-Based Proteomic Profiling of the Human MDA-MB-231 Metastatic Breast Cancer Cell Line in Response to the Two Antitumoral Lactoferrin Isoforms: The Secreted Lactoferrin and the Intracellular Delta-Lactoferrin. PLoS ONE, 2014, 9, e104563.	1.1	11
5	Identification of Protein Network Alterations upon Retinal Ischemia-Reperfusion Injury by Quantitative Proteomics Using a Rattus norvegicus Model. PLoS ONE, 2014, 9, e116453.	1.1	9
6	MicroRNA responses to focal cerebral ischemia in male and female mouse brain. Frontiers in Molecular Neuroscience, 2014, 7, 11.	1.4	39
7	A highly efficient tumor-infiltrating MDSC differentiation system for discovery of anti-neoplastic targets, which circumvents the need for tumor establishment in mice. Oncotarget, 2014, 5, 7843-7857.	0.8	62
8	Plasma proteomic changes during hypothermic and normothermic cardiopulmonary bypass in aortic surgeries. International Journal of Molecular Medicine, 2014, 34, 947-56.	1.8	9
9	Structure Based Functional Annotation of Putative Conserved Proteins from Treponema pallidum: Search for a Potential Drug Target. Letters in Drug Design and Discovery, 2014, 12, 46-59.	0.4	13
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11	Next-generation sequencing identifies equine cartilage and subchondral bone miRNAs and suggests their involvement in osteochondrosis physiopathology. BMC Genomics, 2014, 15, 798.	1.2	31
12	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau022.	1.4	62
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16	An Unbiased Proteomic Screen Reveals Caspase Cleavage Is Positively and Negatively Regulated by Substrate Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 1184-1197.	2.5	39
17	Characterization and <i>In Vivo</i> Functional Analysis of the <i>Schizosaccharomyces pombe</i> ICLN Gene. Molecular and Cellular Biology, 2014, 34, 595-605.	1.1	13
18	Chronic exposure to TGF β 1 regulates myeloid cell inflammatory response in an IRF7 β -dependent manner. EMBO Journal, 2014, 33, 2906-2921.	3.5	95
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40	Single-step Enrichment by Ti4+-IMAC and Label-free Quantitation Enables In-depth Monitoring of Phosphorylation Dynamics with High Reproducibility and Temporal Resolution. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2426-2434.	2.5	89
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