

PRINCESS, a Protein Interaction Confidence Evaluation

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Protein Interaction Data Set Highlighted with Human Ras-MAPK/PI3K Signaling Pathways. <i>Journal of Proteome Research</i> , 2008, 7, 3879-3889.	1.8	38
2	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , 2009, 25, 1158-1164.	1.8	111
3	DASMIweb: online integration, analysis and assessment of distributed protein interaction data. <i>Nucleic Acids Research</i> , 2009, 37, W122-W128.	6.5	2
4	Dynamic proteomics in modeling of the living cell. Protein-protein interactions. <i>Biochemistry (Moscow)</i> , 2009, 74, 1586-1607.	0.7	35
5	A mouse protein interactome through combined literature mining with multiple sources of interaction evidence. <i>Amino Acids</i> , 2010, 38, 1237-1252.	1.2	28
6	Proteomics in China: Ready for prime time. <i>Science China Life Sciences</i> , 2010, 53, 22-33.	2.3	5
7	An improved method for scoring protein-protein interactions using semantic similarity within the gene ontology. <i>BMC Bioinformatics</i> , 2010, 11, 562.	1.2	153
8	Protein Interaction Data Resources. , 2010, , 1375-1385.		1
9	Using manifold embedding for assessing and predicting protein interactions from high-throughput experimental data. <i>Bioinformatics</i> , 2010, 26, 2744-2751.	1.8	209
10	Uniformly curated signaling pathways reveal tissue-specific cross-talks and support drug target discovery. <i>Bioinformatics</i> , 2010, 26, 2042-2050.	1.8	72
11	Proteome scanning to predict PDZ domain interactions using support vector machines. <i>BMC Bioinformatics</i> , 2010, 11, 507.	1.2	33
12	HitPredict: a database of quality assessed protein-protein interactions in nine species. <i>Nucleic Acids Research</i> , 2011, 39, D744-D749.	6.5	111
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14	IntScore: a web tool for confidence scoring of biological interactions. <i>Nucleic Acids Research</i> , 2012, 40, W140-W146.	6.5	51
15	Proteomic analysis of trichloroethylene-induced alterations in expression, distribution, and interactions of SET/TAF-III \pm and two SET/TAF-III \pm -binding proteins, eEF1A1 and eEF1A2, in hepatic L-02 cells. <i>Toxicology and Applied Pharmacology</i> , 2012, 263, 259-272.	1.3	9
16	ppiPre - an R package for predicting protein-protein interactions. , 2012, , .		1
17	Domain-mediated protein interaction prediction: From genome to network. <i>FEBS Letters</i> , 2012, 586, 2751-2763.	1.3	48
18	Cluster-based assessment of protein-protein interaction confidence. <i>BMC Bioinformatics</i> , 2012, 13, 262.	1.2	26

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19	The NRF2-related interactome and regulome contain multifunctional proteins and fine-tuned autoregulatory loops. <i>FEBS Letters</i> , 2012, 586, 1795-1802.	1.3	95
20	Signalink 2 – a signaling pathway resource with multi-layered regulatory networks. <i>BMC Systems Biology</i> , 2013, 7, 7.	3.0	169
21	Identification of KAP-1-associated complexes negatively regulating the β -major globin genes in the β -globin locus. <i>Journal of Proteomics</i> , 2013, 80, 132-144.	1.2	2
22	ppiPre: predicting protein-protein interactions by combining heterogeneous features. <i>BMC Systems Biology</i> , 2013, 7, S8.	3.0	17
23	Opportunities for protein interaction network-guided cellular engineering. <i>IUBMB Life</i> , 2013, 65, 17-27.	1.5	3
24	Assessment of high-confidence protein-protein interactome in yeast. <i>Computational Biology and Chemistry</i> , 2013, 45, 1-8.	1.1	12
25	Measuring gene functional similarity based on group-wise comparison of GO terms. <i>Bioinformatics</i> , 2013, 29, 1424-1432.	1.8	83
26	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1689-1700.	2.5	31
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29	Navigating the Multilayered Organization of Eukaryotic Signaling: A New Trend in Data Integration. <i>PLoS Computational Biology</i> , 2014, 10, e1003385.	1.5	9
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31	Network-based identification of key proteins involved in apoptosis and cell cycle regulation. <i>Cell Proliferation</i> , 2014, 47, 356-368.	2.4	2
32	Integrating the interactome and the transcriptome of <i>Drosophila</i> . <i>BMC Bioinformatics</i> , 2014, 15, 177.	1.2	4
33	LSECtin Expressed on Melanoma Cells Promotes Tumor Progression by Inhibiting Antitumor T-cell Responses. <i>Cancer Research</i> , 2014, 74, 3418-3428.	0.4	270
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35	Hsp27 Acts as a Master Molecular Chaperone and Plays an Essential Role in Hepatocellular Carcinoma Progression. <i>Digestion</i> , 2015, 92, 192-202.	1.2	18
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38	SGFSC: speeding the gene functional similarity calculation based on hash tables. <i>BMC Bioinformatics</i> , 2016, 17, 445.	1.2	6
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40	Using prior knowledge from cellular pathways and molecular networks for diagnostic specimen classification. <i>Briefings in Bioinformatics</i> , 2016, 17, 440-452.	3.2	25
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42	protein2vec: Predicting Protein-Protein Interactions Based on LSTM. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	5
43	A Yeast BiFC-seq Method for Genome-wide Interactome Mapping. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 795-807.	3.0	0
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47	Signalogs: Orthology-Based Identification of Novel Signaling Pathway Components in Three Metazoans. <i>PLoS ONE</i> , 2011, 6, e19240.	1.1	22
48	Trichloroethylene induces biphasic concentration-dependent changes in cell proliferation and the expression of SET-associated proteins in human hepatic L-02 cells. <i>Biomedical and Environmental Sciences</i> , 2013, 26, 618-21.	0.2	5
49	ALIŞAN PERFORMANSI –LİTEÄNDEKİ FADELERİN KARAR AÇICI ALGORİTMASI LE BELİRENİMESİ. Mehmet Akif Ersoy Üniversitesi İktisadi Ve İdari Bilimler Fakültesi Dergisi, 0, , .	0.2	0
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