

Wei-Sheng Wu

List of Publications by Year in descending order

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59
papers

935
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567281

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526287

27
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62
all docs

62
docs citations

62
times ranked

1100
citing authors

#	ARTICLE	IF	CITATIONS
1	LCMD: Lung Cancer Metabolome Database. Computational and Structural Biotechnology Journal, 2022, 20, 65-78.	4.1	8
2	CLASH Analyst: A Web Server to Identify In Vivo RNA-RNA Interactions from CLASH Data. Non-coding RNA, 2022, 8, 6.	2.6	2
3	KDmarkers: A biomarker database for investigating epigenetic methylation and gene expression levels in Kawasaki disease. Computational and Structural Biotechnology Journal, 2022, 20, 1295-1305.	4.1	2
4	Systematic Analysis of Phosphatidylinositol-5-phosphate-Interacting Proteins Using Yeast Proteome Microarrays. Analytical Chemistry, 2021, 93, 868-877.	6.5	5
5	YPIBP: A repository for phosphoinositide-binding proteins in yeast. Computational and Structural Biotechnology Journal, 2021, 19, 3692-3707.	4.1	3
6	Cancer DEIso: An integrative analysis platform for investigating differentially expressed gene-level and isoform-level human cancer markers. Computational and Structural Biotechnology Journal, 2021, 19, 5149-5159.	4.1	5
7	Malignant transformation of oral potentially malignant disorders in Taiwan. Medicine (United Tj ETQq1 1 0.784314 rgt /Overlock 10 T	1.6	16
8	A tool for analyzing and visualizing ribo-seq data at the isoform level. BMC Bioinformatics, 2021, 22, 271.	2.6	0
9	OrchidBase 4.0: a database for orchid genomics and molecular biology. BMC Plant Biology, 2021, 21, 371.	3.6	10
10	Taxonomic and Functional Dysregulation in Salivary Microbiomes During Oral Carcinogenesis. Frontiers in Cellular and Infection Microbiology, 2021, 11, 663068.	3.9	7
11	Identifying piRNA targets on mRNAs in C. elegans using a deep multi-head attention network. BMC Bioinformatics, 2021, 22, 503.	2.6	7
12	Elucidating the regulatory mechanism of Swi1 prion in global transcription and stress responses. Scientific Reports, 2020, 10, 21838.	3.3	5
13	YQFC: a web tool to compare quantitative biological features between two yeast gene lists. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	1
14	Analysis and Prediction of Overloaded Extra-Heavy Vehicles for Highway Safety Using Machine Learning. Mobile Information Systems, 2020, 2020, 1-20.	0.6	2
15	Systematical Analysis of the Protein Targets of Lactoferricin B and Histatin-5 Using Yeast Proteome Microarrays. International Journal of Molecular Sciences, 2019, 20, 4218.	4.1	8
16	piRTarBase: a database of piRNA targeting sites and their roles in gene regulation. Nucleic Acids Research, 2019, 47, D181-D187.	14.5	46
17	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. Science, 2018, 359, 587-592.	12.6	198
18	YHMI: a web tool to identify histone modifications and histone/chromatin regulators from a gene list in yeast. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	1

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19	HRPDviewer: human ribosome profiling data viewer. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	8
20	YARG: A repository for arsenic-related genes in yeast. PLoS ONE, 2018, 13, e0201204.	2.5	7
21	pirScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in <i>C. elegans</i> . Nucleic Acids Research, 2018, 46, W43-W48.	14.5	41
22	MVIAeval: a web tool for comprehensively evaluating the performance of a new missing value imputation algorithm. BMC Bioinformatics, 2017, 18, 31.	2.6	11
23	Chronic treatment with cisplatin induces chemoresistance through the TIP60-mediated Fanconi anemia and homologous recombination repair pathways. Scientific Reports, 2017, 7, 3879.	3.3	12
24	YGMD: a repository for yeast cooperative transcription factor sets and their target gene modules. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	3
25	CSmiRTar: Condition-Specific microRNA targets database. PLoS ONE, 2017, 12, e0181231.	2.5	21
26	Detecting Cooperativity between Transcription Factors Based on Functional Coherence and Similarity of Their Target Gene Sets. PLoS ONE, 2016, 11, e0162931.	2.5	5
27	CoopTFD: a repository for predicted yeast cooperative transcription factor pairs. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw092.	3.0	3
28	Combined Interactions of Plant Homeodomain and Chromodomain Regulate NuA4 Activity at DNA Double-Strand Breaks. Genetics, 2016, 202, 77-92.	2.9	6
29	A Computational Method for Identifying Yeast Cell Cycle Transcription Factors. Methods in Molecular Biology, 2016, 1342, 209-219.	0.9	0
30	YCRD: Yeast Combinatorial Regulation Database. PLoS ONE, 2016, 11, e0159213.	2.5	3
31	Properly defining the targets of a transcription factor significantly improves the computational identification of cooperative transcription factor pairs in yeast. BMC Genomics, 2015, 16, S10.	2.8	8
32	PCTFPeval: a web tool for benchmarking newly developed algorithms for predicting cooperative transcription factor pairs in yeast. BMC Bioinformatics, 2015, 16, S2.	2.6	6
33	YAGM: a web tool for mining associated genes in yeast based on diverse biological associations. BMC Systems Biology, 2015, 9, S1.	3.0	8
34	Functional redundancy of transcription factors explains why most binding targets of a transcription factor are not affected when the transcription factor is knocked out. BMC Systems Biology, 2015, 9, S2.	3.0	22
35	YTRP: a repository for yeast transcriptional regulatory pathways. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau014-bau014.	3.0	19
36	IMDE: An easy-to-use web server for missing data estimation. , 2014, , .		1

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37	A comprehensive performance evaluation on the prediction results of existing cooperative transcription factors identification algorithms. <i>BMC Systems Biology</i> , 2014, 8, S9.	3.0	9
38	Identifying cooperative transcription factors in yeast using multiple data sources. <i>BMC Systems Biology</i> , 2014, 8, S2.	3.0	11
39	A regulatory similarity measure using the location information of transcription factor binding sites in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2014, 8, S9.	3.0	2
40	YGA: Identifying distinct biological features between yeast gene sets. <i>Gene</i> , 2013, 518, 26-34.	2.2	6
41	Missing value imputation for microarray data: a comprehensive comparison study and a web tool. <i>BMC Systems Biology</i> , 2013, 7, S12.	3.0	35
42	Shrinkage regression-based methods for microarray missing value imputation. <i>BMC Systems Biology</i> , 2013, 7, S11.	3.0	8
43	Fuzzy Logic Applications in Control Theory and Systems Biology. <i>Advances in Fuzzy Systems</i> , 2013, 2013, 1-1.	0.9	0
44	Identifying Functional Transcription Factor Binding Sites in Yeast by Considering Their Positional Preference in the Promoters. <i>PLoS ONE</i> , 2013, 8, e83791.	2.5	2
45	Identifying biologically interpretable transcription factor knockout targets by jointly analyzing the transcription factor knockout microarray and the ChIP-chip data. <i>BMC Systems Biology</i> , 2012, 6, 102.	3.0	22
46	Yeast cell cycle transcription factors identification by variable selection criteria. <i>Gene</i> , 2011, 485, 172-176.	2.2	8
47	Different Functional Gene Clusters in Yeast have Different Spatial Distributions of the Transcription Factor Binding Sites. <i>Bioinformatics and Biology Insights</i> , 2011, 5, BBI.S6362.	2.0	6
48	YPA: an integrated repository of promoter features in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2011, 39, D647-D652.	14.5	36
49	The spatial distribution of cis regulatory elements in yeast promoters and its implications for transcriptional regulation. <i>BMC Genomics</i> , 2010, 11, 581.	2.8	42
50	Identification of yeast cell cycle transcription factors using dynamic system model. , 2010, , .		0
51	Systematic identification of yeast cell cycle transcription factors using multiple data sources. <i>BMC Bioinformatics</i> , 2008, 9, 522.	2.6	37
52	Identifying gene regulatory modules of heat shock response in yeast. <i>BMC Genomics</i> , 2008, 9, 439.	2.8	42
53	Robust filtering circuit design for stochastic gene networks under intrinsic and extrinsic molecular noises. <i>Mathematical Biosciences</i> , 2008, 211, 342-355.	1.9	39
54	Reconstructing a Network of Stress-Response Regulators via Dynamic System Modeling of Gene Regulation. <i>Gene Regulation and Systems Biology</i> , 2008, 2, GRSB.S558.	2.3	2

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55	Underlying Principles of Natural Selection in Network Evolution: Systems Biology Approach. Evolutionary Bioinformatics, 2007, 3, 117693430700300.	1.2	7
56	Identifying Stress Transcription Factors Using Gene Expression and TF-Gene Association Data. Bioinformatics and Biology Insights, 2007, 1, BBI.S292.	2.0	13
57	Identifying regulatory targets of cell cycle transcription factors using gene expression and CHIP-chip data. BMC Bioinformatics, 2007, 8, 188.	2.6	35
58	Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. BMC Bioinformatics, 2006, 7, 421.	2.6	59
59	Stability analysis of the turbo decoding algorithm using Max-Log-MAP. , 0, , .		0