

Wei-Sheng Wu

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

935
citations

567281

15
h-index

526287

27
g-index

62
all docs

62
docs citations

62
times ranked

1100
citing authors

#	ARTICLE	IF	CITATIONS
1	The piRNA targeting rules and the resistance to piRNA silencing in endogenous genes. <i>Science</i> , 2018, 359, 587-592.	12.6	198
2	Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. <i>BMC Bioinformatics</i> , 2006, 7, 421.	2.6	59
3	piRTarBase: a database of piRNA targeting sites and their roles in gene regulation. <i>Nucleic Acids Research</i> , 2019, 47, D181-D187.	14.5	46
4	Identifying gene regulatory modules of heat shock response in yeast. <i>BMC Genomics</i> , 2008, 9, 439.	2.8	42
5	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
6	pirScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2018, 46, W43-W48.	14.5	41
7	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
8	Systematic identification of yeast cell cycle transcription factors using multiple data sources. <i>BMC Bioinformatics</i> , 2008, 9, 522.	2.6	37
9	YPA: an integrated repository of promoter features in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2011, 39, D647-D652.	14.5	36
10	Identifying regulatory targets of cell cycle transcription factors using gene expression and ChIP-chip data. <i>BMC Bioinformatics</i> , 2007, 8, 188.	2.6	35
11	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
12	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
13	Functional redundancy of transcription factors explains why most binding targets of a transcription factor are not affected when the transcription factor is knocked out. <i>BMC Systems Biology</i> , 2015, 9, S2.	3.0	22
14	CSmiRTar: Condition-Specific microRNA targets database. <i>PLoS ONE</i> , 2017, 12, e0181231.	2.5	21
15	YTRP: a repository for yeast transcriptional regulatory pathways. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau014-bau014.	3.0	19
16	Malignant transformation of oral potentially malignant disorders in Taiwan. <i>Medicine (United Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142</i>	1.0	16
17	Identifying Stress Transcription Factors Using Gene Expression and TF-Gene Association Data. <i>Bioinformatics and Biology Insights</i> , 2007, 1, BBI.S292.	2.0	13
18	Chronic treatment with cisplatin induces chemoresistance through the TIP60-mediated Fanconi anemia and homologous recombination repair pathways. <i>Scientific Reports</i> , 2017, 7, 3879.	3.3	12

#	ARTICLE	IF	CITATIONS
19	Identifying cooperative transcription factors in yeast using multiple data sources. <i>BMC Systems Biology</i> , 2014, 8, S2.	3.0	11
20	MVIAeval: a web tool for comprehensively evaluating the performance of a new missing value imputation algorithm. <i>BMC Bioinformatics</i> , 2017, 18, 31.	2.6	11
21	OrchidBase 4.0: a database for orchid genomics and molecular biology. <i>BMC Plant Biology</i> , 2021, 21, 371.	3.6	10
22	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
23	Yeast cell cycle transcription factors identification by variable selection criteria. <i>Gene</i> , 2011, 485, 172-176.	2.2	8
24	Shrinkage regression-based methods for microarray missing value imputation. <i>BMC Systems Biology</i> , 2013, 7, S11.	3.0	8
25	Properly defining the targets of a transcription factor significantly improves the computational identification of cooperative transcription factor pairs in yeast. <i>BMC Genomics</i> , 2015, 16, S10.	2.8	8
26	YAGM: a web tool for mining associated genes in yeast based on diverse biological associations. <i>BMC Systems Biology</i> , 2015, 9, S1.	3.0	8
27	HRPDviewer: human ribosome profiling data viewer. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	8
28	Systematical Analysis of the Protein Targets of Lactoferricin B and Histatin-5 Using Yeast Proteome Microarrays. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4218.	4.1	8
29	LCMD: Lung Cancer Metabolome Database. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 65-78.	4.1	8
30	Underlying Principles of Natural Selection in Network Evolution: Systems Biology Approach. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	1.2	7
31	YARG: A repository for arsenic-related genes in yeast. <i>PLoS ONE</i> , 2018, 13, e0201204.	2.5	7
32	Taxonomic and Functional Dysregulation in Salivary Microbiomes During Oral Carcinogenesis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663068.	3.9	7
33	Identifying piRNA targets on mRNAs in <i>C. elegans</i> using a deep multi-head attention network. <i>BMC Bioinformatics</i> , 2021, 22, 503.	2.6	7
34	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
35	YGA: Identifying distinct biological features between yeast gene sets. <i>Gene</i> , 2013, 518, 26-34.	2.2	6
36	PCTFPeval: a web tool for benchmarking newly developed algorithms for predicting cooperative transcription factor pairs in yeast. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	6

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37	Combined Interactions of Plant Homeodomain and Chromodomain Regulate NuA4 Activity at DNA Double-Strand Breaks. <i>Genetics</i> , 2016, 202, 77-92.	2.9	6
38	Detecting Cooperativity between Transcription Factors Based on Functional Coherence and Similarity of Their Target Gene Sets. <i>PLoS ONE</i> , 2016, 11, e0162931.	2.5	5
39	Elucidating the regulatory mechanism of Swi1 prion in global transcription and stress responses. <i>Scientific Reports</i> , 2020, 10, 21838.	3.3	5
40	Systematic Analysis of Phosphatidylinositol-5-phosphate-Interacting Proteins Using Yeast Proteome Microarrays. <i>Analytical Chemistry</i> , 2021, 93, 868-877.	6.5	5
41	Cancer DEIso: An integrative analysis platform for investigating differentially expressed gene-level and isoform-level human cancer markers. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5149-5159.	4.1	5
42	CoopTFD: a repository for predicted yeast cooperative transcription factor pairs. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw092.	3.0	3
43	YGMD: a repository for yeast cooperative transcription factor sets and their target gene modules. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	3
44	YPIBP: A repository for phosphoinositide-binding proteins in yeast. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3692-3707.	4.1	3
45	YCRD: Yeast Combinatorial Regulation Database. <i>PLoS ONE</i> , 2016, 11, e0159213.	2.5	3
46	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
47	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
48	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
49	Analysis and Prediction of Overloaded Extra-Heavy Vehicles for Highway Safety Using Machine Learning. <i>Mobile Information Systems</i> , 2020, 2020, 1-20.	0.6	2
50	CLASH Analyst: A Web Server to Identify In Vivo RNA-RNA Interactions from CLASH Data. <i>Non-coding RNA</i> , 2022, 8, 6.	2.6	2
51	KDmarkers: A biomarker database for investigating epigenetic methylation and gene expression levels in Kawasaki disease. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1295-1305.	4.1	2
52	IMDE: An easy-to-use web server for missing data estimation. , 2014, , .		1
53	YHMI: a web tool to identify histone modifications and histone/chromatin regulators from a gene list in yeast. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	1
54	YQFC: a web tool to compare quantitative biological features between two yeast gene lists. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	1

#	ARTICLE	IF	CITATIONS
55	Stability analysis of the turbo decoding algorithm using Max-Log-MAP. , 0, , .		0
56	Identification of yeast cell cycle transcription factors using dynamic system model. , 2010, , .		0
57	Fuzzy Logic Applications in Control Theory and Systems Biology. Advances in Fuzzy Systems, 2013, 2013, 1-1.	0.9	0
58	A Computational Method for Identifying Yeast Cell Cycle Transcription Factors. Methods in Molecular Biology, 2016, 1342, 209-219.	0.9	0
59	A tool for analyzing and visualizing ribo-seq data at the isoform level. BMC Bioinformatics, 2021, 22, 271.	2.6	0