

Shao-Wu Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

2,312
citations

236925

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254184

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all docs

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docs citations

94
times ranked

2269
citing authors

#	ARTICLE	IF	CITATIONS
1	Extracting ROI-Based Contourlet Subband Energy Feature From the sMRI Image for Alzheimer's Disease Classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1627-1639.	3.0	10
2	deepMDDI: A deep graph convolutional network framework for multi-label prediction of drug-drug interactions. <i>Analytical Biochemistry</i> , 2022, 646, 114631.	2.4	18
3	Detection of Alzheimer's disease using features of brain region-of-interest-based individual network constructed with the sMRI image. <i>Computerized Medical Imaging and Graphics</i> , 2022, 98, 102057.	5.8	9
4	mAexpress-Reader: Prediction of m6A regulated expression genes by integrating m6A sites and reader binding information in specific- context. <i>Methods</i> , 2022, , .	3.8	2
5	Prediction of the transcription factor binding sites with meta-learning. <i>Methods</i> , 2022, , .	3.8	2
6	m6Acancer-Net: Identification of m6A-mediated cancer driver genes from gene-site heterogeneous network. <i>Methods</i> , 2022, , .	3.8	1
7	Prediction of Drug-Drug Interaction Using an Attention-Based Graph Neural Network on Drug Molecular Graphs. <i>Molecules</i> , 2022, 27, 3004.	3.8	13
8	kngMap: Sensitive and Fast Mapping Algorithm for Noisy Long Reads Based on the K-Mer Neighborhood Graph. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	5
9	<i>m</i> <i>6</i> ÂÃ<i>Aexpress-BHM</i>: predicting m6A regulation of gene expression in multiple-groups context by a Bayesian hierarchical mixture model. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
10	An Integrative Framework for Combining Sequence and Epigenomic Data to Predict Transcription Factor Binding Sites Using Deep Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 355-364.	3.0	19
11	Alzheimer's disease classification using features extracted from nonsubsamped contourlet subband-based individual networks. <i>Neurocomputing</i> , 2021, 421, 260-272.	5.9	23
12	Recent advances in functional annotation and prediction of the epitranscriptome. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3015-3026.	4.1	13
13	Network controllability-based algorithm to target personalized driver genes for discovering combinatorial drugs of individual patients. <i>Nucleic Acids Research</i> , 2021, 49, e37-e37.	14.5	32
14	Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644012.	3.5	21
15	Funm6AViewer: a web server and R package for functional analysis of context-specific m6A RNA methylation. <i>Bioinformatics</i> , 2021, 37, 4277-4279.	4.1	4
16	Resilience function uncovers the critical transitions in cancer initiation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	3
17	Performance assessment of sample-specific network control methods for bulk and single-cell biological data analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1008962.	3.2	15
18	Identifying driver genes for individual patients through inductive matrix completion. <i>Bioinformatics</i> , 2021, 37, 4477-4484.	4.1	17

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19	<i>m6A-express</i> : uncovering complex and condition-specific m6A regulation of gene expression. <i>Nucleic Acids Research</i> , 2021, 49, e116-e116.	14.5	24
20	Network control principles for identifying personalized driver genes in cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 1641-1662.	6.5	29
21	DPDDI: a deep predictor for drug-drug interactions. <i>BMC Bioinformatics</i> , 2020, 21, 419.	2.6	91
22	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1587-1604.	4.1	38
23	lncRNA_Mdeep: An Alignment-Free Predictor for Distinguishing Long Non-Coding RNAs from Protein-Coding Transcripts by Multimodal Deep Learning. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5222.	4.1	12
24	smsMap: mapping single molecule sequencing reads by locating the alignment starting positions. <i>BMC Bioinformatics</i> , 2020, 21, 341.	2.6	7
25	Identification of Alzheimer's disease based on wavelet transformation energy feature of the structural MRI image and NN classifier. <i>Artificial Intelligence in Medicine</i> , 2020, 108, 101940.	6.5	12
26	Prediction of enhancer-promoter interactions using the cross-cell type information and domain adversarial neural network. <i>BMC Bioinformatics</i> , 2020, 21, 507.	2.6	15
27	LPI-CNNCP: Prediction of lncRNA-protein interactions by using convolutional neural network with the copy-padding trick. <i>Analytical Biochemistry</i> , 2020, 601, 113767.	2.4	28
28	Prediction of the RBP binding sites on lncRNAs using the high-order nucleotide encoding convolutional neural network. <i>Analytical Biochemistry</i> , 2019, 583, 113364.	2.4	18
29	FunDMDep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019, 35, i90-i98.	4.1	34
30	LPI-BLS: Predicting lncRNA-protein interactions with a broad learning system-based stacked ensemble classifier. <i>Neurocomputing</i> , 2019, 370, 88-93.	5.9	48
31	DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. <i>Frontiers in Genetics</i> , 2019, 10, 266.	2.3	32
32	DMSC: A Dynamic Multi-Seeds Method for Clustering 16S rRNA Sequences Into OTUs. <i>Frontiers in Microbiology</i> , 2019, 10, 428.	3.5	12
33	Prediction of lncRNA-disease associations by integrating diverse heterogeneous information sources with RWR algorithm and positive pointwise mutual information. <i>BMC Bioinformatics</i> , 2019, 20, 87.	2.6	49
34	A novel network control model for identifying personalized driver genes in cancer. <i>PLoS Computational Biology</i> , 2019, 15, e1007520.	3.2	50
35	Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. <i>PLoS Computational Biology</i> , 2019, 15, e1006663.	3.2	41
36	Prediction of drug-target interaction by integrating diverse heterogeneous information source with multiple kernel learning and clustering methods. <i>Computational Biology and Chemistry</i> , 2019, 78, 460-467.	2.3	44

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37	Advances in the Prediction of Protein Subcellular Locations with Machine Learning. <i>Current Bioinformatics</i> , 2019, 14, 406-421.	1.5	13
38	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
39	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
40	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
41	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
42	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
43	A novel algorithm for finding optimal driver nodes to target control complex networks and its applications for drug targets identification. <i>BMC Genomics</i> , 2018, 19, 924.	2.8	29
44	Discovering personalized driver mutation profiles of single samples in cancer by network control strategy. <i>Bioinformatics</i> , 2018, 34, 1893-1903.	4.1	108
45	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. <i>Nucleic Acids Research</i> , 2018, 46, D281-D287.	14.5	115
46	Viral and cellular N6-methyladenosine and N6,2â€²-O-dimethyladenosine epitranscriptomes in the KSHV life cycle. <i>Nature Microbiology</i> , 2018, 3, 108-120.	13.3	137
47	NPBSS: a new PacBio sequencing simulator for generating the continuous long reads with an empirical model. <i>BMC Bioinformatics</i> , 2018, 19, 177.	2.6	31
48	trumpet: transcriptome-guided quality assessment of m6A-seq data. <i>BMC Bioinformatics</i> , 2018, 19, 260.	2.6	10
49	Identifying Drug-Target Interactions with Decision Templates. <i>Current Protein and Peptide Science</i> , 2018, 19, 498-506.	1.4	9
50	DBH: A de Bruijn graph-based heuristic method for clustering large-scale 16S rRNA sequences into OTUs. <i>Journal of Theoretical Biology</i> , 2017, 425, 80-87.	1.7	13
51	DMclust, a Densityâ€based Modularity Method for Accurate OTU Picking of 16S rRNA Sequences. <i>Molecular Informatics</i> , 2017, 36, 1600059.	2.5	15
52	Prediction of metabolic fluxes from gene expression data with Huber penalty convex optimization function. <i>Molecular BioSystems</i> , 2017, 13, 901-909.	2.9	6
53	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017, 2017, 063402.	2.3	24
54	Gene Prediction in Metagenomic Fragments with Deep Learning. <i>BioMed Research International</i> , 2017, 2017, 1-9.	1.9	18

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55	QNB: differential RNA methylation analysis for count-based small-sample sequencing data with a quad-negative binomial model. <i>BMC Bioinformatics</i> , 2017, 18, 387.	2.6	40
56	Some Remarks on Prediction of Drug-Target Interaction with Network Models. <i>Current Topics in Medicinal Chemistry</i> , 2017, 17, 2456-2468.	2.1	4
57	Computational Methods for Predicting ncRNA-protein Interactions. <i>Medicinal Chemistry</i> , 2017, 13, 515-525.	1.5	14
58	Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	95
59	p12CDK2-AP1 interacts with CD82 to regulate the proliferation and survival of human oral squamous cell carcinoma cells. <i>Oncology Reports</i> , 2016, 36, 737-744.	2.6	3
60	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005287.	3.2	38
61	Inference of Gene Regulatory Network Based on Local Bayesian Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005024.	3.2	114
62	Exploring the interaction patterns among taxa and environments from marine metagenomic data. <i>Quantitative Biology</i> , 2016, 4, 84-91.	0.5	7
63	Prediction of drug-target interaction by label propagation with mutual interaction information derived from heterogeneous network. <i>Molecular BioSystems</i> , 2016, 12, 520-531.	2.9	43
64	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016, 499, 15-23.	2.4	18
65	A general method of community detection by identifying community centers with affinity propagation. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 447, 508-519.	2.6	19
66	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. <i>BioMed Research International</i> , 2015, 2015, 1-12.	1.9	11
67	MtHc: a motif-based hierarchical method for clustering massive 16S rRNA sequences into OTUs. <i>Molecular BioSystems</i> , 2015, 11, 1907-1913.	2.9	21
68	Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , .		0
69	lncRNA-MFDL: identification of human long non-coding RNAs by fusing multiple features and using deep learning. <i>Molecular BioSystems</i> , 2015, 11, 892-897.	2.9	82
70	Decomposition of RNA methylome reveals co-methylation patterns induced by latent enzymatic regulators of the epitranscriptome. <i>Molecular BioSystems</i> , 2015, 11, 262-274.	2.9	26
71	Some Remarks on Prediction of Protein-Protein Interaction with Machine Learning. <i>Medicinal Chemistry</i> , 2015, 11, 254-264.	1.5	18
72	Prediction of Protein-Protein Interaction with Pairwise Kernel Support Vector Machine. <i>International Journal of Molecular Sciences</i> , 2014, 15, 3220-3233.	4.1	51

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73	Mining Seasonal Marine Microbial Pattern with Greedy Heuristic Clustering and Symmetrical Nonnegative Matrix Factorization. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	2
74	Prediction of Signal Peptide Cleavage Sites with Subsite-Coupled and Template Matching Fusion Algorithm. <i>Molecular Informatics</i> , 2014, 33, 230-239.	2.5	7
75	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , .		2
76	MSLoc-DT: A new method for predicting the protein subcellular location of multispecies based on decision templates. <i>Analytical Biochemistry</i> , 2014, 449, 164-171.	2.4	21
77	Prioritization of candidate disease genes by enlarging the seed set and fusing information of the network topology and gene expression. <i>Molecular BioSystems</i> , 2014, 10, 1400-1408.	2.9	18
78	Identification of protein-RNA interaction sites using the information of spatial adjacent residues. <i>Proteome Science</i> , 2011, 9, S16.	1.7	7
79	Prediction of protein-protein interaction types with amino acid index distribution and pairwise kernel SVM. , 2011, , .		1
80	PPLook: an automated data mining tool for protein-protein interaction. <i>BMC Bioinformatics</i> , 2010, 11, 326.	2.6	14
81	Prediction of protein-protein interaction types using the decision templates based on multiple classifier fusion. <i>Mathematical and Computer Modelling</i> , 2010, 52, 2075-2084.	2.0	11
82	Prediction of protein-protein interaction types using the decision templates. , 2009, , .		1
83	Using the concept of Chou's pseudo amino acid composition to predict protein subcellular localization: an approach by incorporating evolutionary information and von Neumann entropies. <i>Amino Acids</i> , 2008, 34, 565-572.	2.7	138
84	Using Chou's pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. <i>Amino Acids</i> , 2008, 35, 591-598.	2.7	87
85	Classification of protein quaternary structure with support vector machine. <i>Bioinformatics</i> , 2003, 19, 2390-2396.	4.1	75