Shao-Wu Zhang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7806003/publications.pdf

Version: 2024-02-01

		236925	254184
85	2,312	25	43
papers	citations	h-index	g-index

94	94	94	2269
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Using the concept of Chouâ€™s pseudo amino acid composition to predict protein subcellular localization: an approach by incorporating evolutionary information and von Neumann entropies. Amino Acids, 2008, 34, 565-572.	2.7	138
2	Viral and cellular N6-methyladenosine and N6,2â€²-O-dimethyladenosine epitranscriptomes in the KSHV life cycle. Nature Microbiology, 2018, 3, 108-120.	13.3	137
3	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287.	14.5	115
4	Inference of Gene Regulatory Network Based on Local Bayesian Networks. PLoS Computational Biology, 2016, 12, e1005024.	3.2	114
5	Discovering personalized driver mutation profiles of single samples in cancer by network control strategy. Bioinformatics, 2018, 34, 1893-1903.	4.1	108
6	Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. BioMed Research International, 2016, 2016, 1-8.	1.9	95
7	DPDDI: a deep predictor for drug-drug interactions. BMC Bioinformatics, 2020, 21, 419.	2.6	91
8	Using Chouâ€™s pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. Amino Acids, 2008, 35, 591-598.	2.7	87
9	lncRNA-MFDL: identification of human long non-coding RNAs by fusing multiple features and using deep learning. Molecular BioSystems, 2015, 11, 892-897.	2.9	82
10	Classification of protein quaternary structure with support vector machine. Bioinformatics, 2003, 19, 2390-2396.	4.1	75
11	Prediction of Proteinâ€“Protein Interaction with Pairwise Kernel Support Vector Machine. International Journal of Molecular Sciences, 2014, 15, 3220-3233.	4.1	51
12	A novel network control model for identifying personalized driver genes in cancer. PLoS Computational Biology, 2019, 15, e1007520.	3.2	50
13	Prediction of lncRNA-disease associations by integrating diverse heterogeneous information sources with RWR algorithm and positive pointwise mutual information. BMC Bioinformatics, 2019, 20, 87.	2.6	49
14	LPI-BLS: Predicting lncRNAâ€“protein interactions with a broad learning system-based stacked ensemble classifier. Neurocomputing, 2019, 370, 88-93.	5.9	48
15	Prediction of drug-target interaction by integrating diverse heterogeneous information source with multiple kernel learning and clustering methods. Computational Biology and Chemistry, 2019, 78, 460-467.	2.3	44
16	Prediction of drugâ€“target interaction by label propagation with mutual interaction information derived from heterogeneous network. Molecular BioSystems, 2016, 12, 520-531.	2.9	43
17	Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. PLoS Computational Biology, 2019, 15, e1006663.	3.2	41
18	QNB: differential RNA methylation analysis for count-based small-sample sequencing data with a quad-negative binomial model. BMC Bioinformatics, 2017, 18, 387.	2.6	40

#	Article	IF	Citations
19	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. PLoS Computational Biology, 2016, 12, e1005287.	3.2	38
20	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. Computational and Structural Biotechnology Journal, 2020, 18, 1587-1604.	4.1	38
21	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. Bioinformatics, 2019, 35, i90-i98.	4.1	34
22	DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. Frontiers in Genetics, 2019, 10, 266.	2.3	32
23	Network controllability-based algorithm to target personalized driver genes for discovering combinatorial drugs of individual patients. Nucleic Acids Research, 2021, 49, e37-e37.	14.5	32
24	NPBSS: a new PacBio sequencing simulator for generating the continuous long reads with an empirical model. BMC Bioinformatics, 2018, 19, 177.	2.6	31
25	A novel algorithm for finding optimal driver nodes to target control complex networks and its applications for drug targets identification. BMC Genomics, 2018, 19, 924.	2.8	29
26	Network control principles for identifying personalized driver genes in cancer. Briefings in Bioinformatics, 2020, 21, 1641-1662.	6.5	29
27	LPI-CNNCP: Prediction of lncRNA-protein interactions by using convolutional neural network with the copy-padding trick. Analytical Biochemistry, 2020, 601, 113767.	2.4	28
28	Decomposition of RNA methylome reveals co-methylation patterns induced by latent enzymatic regulators of the epitranscriptome. Molecular BioSystems, 2015, 11, 262-274.	2.9	26
29	Constrained target controllability of complex networks. Journal of Statistical Mechanics: Theory and Experiment, 2017, 2017, 063402.	2.3	24
30	m6A-express: uncovering complex and condition-specific m6A regulation of gene expression. Nucleic Acids Research, 2021, 49, e116-e116.	14.5	24
31	Alzheimerâ€™s disease classification using features extracted from nonsubsampled contourlet subband-based individual networks. Neurocomputing, 2021, 421, 260-272.	5.9	23
32	MSLoc-DT: A new method for predicting the protein subcellular location of multispecies based on decision templates. Analytical Biochemistry, 2014, 449, 164-171.	2.4	21
33	MtHc: a motif-based hierarchical method for clustering massive 16S rRNA sequences into OTUs. Molecular BioSystems, 2015, 11, 1907-1913.	2.9	21
34	Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. Frontiers in Microbiology, 2021, 12, 644012.	3.5	21
35	A general method of community detection by identifying community centers with affinity propagation. Physica A: Statistical Mechanics and Its Applications, 2016, 447, 508-519.	2.6	19
36	An Integrative Framework for Combining Sequence and Epigenomic Data to Predict Transcription Factor Binding Sites Using Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 355-364.	3.0	19

#	Article	IF	Citations
37	Prioritization of candidate disease genes by enlarging the seed set and fusing information of the network topology and gene expression. Molecular BioSystems, 2014, 10, 1400-1408.	2.9	18
38	DRME: Count-based differential RNA methylation analysis at small sample size scenario. Analytical Biochemistry, 2016, 499, 15-23.	2.4	18
39	Gene Prediction in Metagenomic Fragments with Deep Learning. BioMed Research International, 2017, 2017, 1-9.	1.9	18
40	Prediction of the RBP binding sites on lncRNAs using the high-order nucleotide encoding convolutional neural network. Analytical Biochemistry, 2019, 583, 113364.	2.4	18
41	Some Remarks on Prediction of Protein-Protein Interaction with Machine Learning. Medicinal Chemistry, 2015, 11, 254-264.	1.5	18
42	deepMDDI: A deep graph convolutional network framework for multi-label prediction of drug-drug interactions. Analytical Biochemistry, 2022, 646, 114631.	2.4	18
43	Identifying driver genes for individual patients through inductive matrix completion. Bioinformatics, 2021, 37, 4477-4484.	4.1	17
44	DMclust, a Densityâ€based Modularity Method for Accurate OTU Picking of 16S rRNA Sequences. Molecular Informatics, 2017, 36, 1600059.	2.5	15
45	Prediction of enhancerâ€“promoter interactions using the cross-cell type information and domain adversarial neural network. BMC Bioinformatics, 2020, 21, 507.	2.6	15
46	Performance assessment of sample-specific network control methods for bulk and single-cell biological data analysis. PLoS Computational Biology, 2021, 17, e1008962.	3.2	15
47	PPLook: an automated data mining tool for protein-protein interaction. BMC Bioinformatics, 2010, 11, 326.	2.6	14
48	Computational Methods for Predicting ncRNA-protein Interactions. Medicinal Chemistry, 2017, 13, 515-525.	1.5	14
49	DBH: A de Bruijn graph-based heuristic method for clustering large-scale 16S rRNA sequences into OTUs. Journal of Theoretical Biology, 2017, 425, 80-87.	1.7	13
50	Recent advances in functional annotation and prediction of the epitranscriptome. Computational and Structural Biotechnology Journal, 2021, 19, 3015-3026.	4.1	13
51	Advances in the Prediction of Protein Subcellular Locations with Machine Learning. Current Bioinformatics, 2019, 14, 406-421.	1.5	13
52	Prediction of Drug-Drug Interaction Using an Attention-Based Graph Neural Network on Drug Molecular Graphs. Molecules, 2022, 27, 3004.	3.8	13
53	DMSC: A Dynamic Multi-Seeds Method for Clustering 16S rRNA Sequences Into OTUs. Frontiers in Microbiology, 2019, 10, 428.	3.5	12
54	lncRNA_Mdeep: An Alignment-Free Predictor for Distinguishing Long Non-Coding RNAs from Protein-Coding Transcripts by Multimodal Deep Learning. International Journal of Molecular Sciences, 2020, 21, 5222.	4.1	12

#	Article	IF	Citations
55	Identification of Alzheimer's disease based on wavelet transformation energy feature of the structural MRI image and NN classifier. Artificial Intelligence in Medicine, 2020, 108, 101940.	6.5	12
56	Prediction of proteinâ€“protein interaction types using the decision templates based on multiple classier fusion. Mathematical and Computer Modelling, 2010, 52, 2075-2084.	2.0	11
57	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. BioMed Research International, 2015, 2015, 1-12.	1.9	11
58	trumpet: transcriptome-guided quality assessment of m6A-seq data. BMC Bioinformatics, 2018, 19, 260.	2.6	10
59	Extracting ROI-Based Contourlet Subband Energy Feature From the sMRI Image for Alzheimerâ€™s Disease Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1627-1639.	3.0	10
60	Identifying Drug-Target Interactions with Decision Templates. Current Protein and Peptide Science, 2018, 19, 498-506.	1.4	9
61	Detection of Alzheimerâ€™s disease using features of brain region-of-interest-based individual network constructed with the sMRI image. Computerized Medical Imaging and Graphics, 2022, 98, 102057.	5.8	9
62	Identification of protein-RNA interaction sites using the information of spatial adjacent residues. Proteome Science, 2011, 9, S16.	1.7	7
63	Prediction of Signal Peptide Cleavage Sites with Subsiteâ€Coupled and Template Matching Fusion Algorithm. Molecular Informatics, 2014, 33, 230-239.	2.5	7
64	Exploring the interaction patterns among taxa and environments from marine metagenomic data. Quantitative Biology, 2016, 4, 84-91.	0.5	7
65	smsMap: mapping single molecule sequencing reads by locating the alignment starting positions. BMC Bioinformatics, 2020, 21, 341.	2.6	7
66	Prediction of metabolic fluxes from gene expression data with Huber penalty convex optimization function. Molecular BioSystems, 2017, 13, 901-909.	2.9	6
67	kngMap: Sensitive and Fast Mapping Algorithm for Noisy Long Reads Based on the K-Mer Neighborhood Graph. Frontiers in Genetics, 2022, 13, .	2.3	5
68	Funm6AViewer: a web server and R package for functional analysis of context-specific m6A RNA methylation. Bioinformatics, 2021, 37, 4277-4279.	4.1	4
69	Some Remarks on Prediction of Drug-Target Interaction with Network Models. Current Topics in Medicinal Chemistry, 2017, 17, 2456-2468.	2.1	4
70	p12CDK2-AP1 interacts with CD82 to regulate the proliferation and survival of human oral squamous cell carcinoma cells. Oncology Reports, 2016, 36, 737-744.	2.6	3
71	Resilience function uncovers the critical transitions in cancer initiation. Briefings in Bioinformatics, 2021, 22, .	6.5	3
72	Mining Seasonal Marine Microbial Pattern with Greedy Heuristic Clustering and Symmetrical Nonnegative Matrix Factorization. BioMed Research International, 2014, 2014, 1-9.	1.9	2

#	Article	IF	Citations
73	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , .		2
74	mAexpress-Reader: Prediction of m6A regulated expression genes by integrating m6A sites and reader binding information in specific- context. Methods, 2022, , .	3.8	2
75	Prediction of the transcription factor binding sites with meta-learning. Methods, 2022, , .	3.8	2
76	Prediction of protein-protein interaction types using the decision templates. , 2009, , .		1
77	Prediction of protein-protein interaction types with amino acid index distribution and pairwise kernel SVM. , 2011, , .		1
78	m6Acancer-Net: Identification of m6A-mediated cancer driver genes from gene-site heterogeneous network. Methods, 2022, , .	3.8	1
79	m 6 ÂAexpress-BHM: predicting m6A regulation of gene expression in multiple-groups context by a Bayesian hierarchical mixture model. Briefings in Bioinformatics, 2022, 23, .	6.5	1
80	Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , .		0
81	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
82	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
83	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
84	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0
85	A novel network control model for identifying personalized driver genes in cancer. , 2019, 15, e1007520.		0