

Juan Liu

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

1,296
citations

394421

19
h-index

377865

34
g-index

81
all docs

81
docs citations

81
times ranked

1754
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel computational framework for simultaneous integration of multiple types of genomic data to identify microRNA-gene regulatory modules. <i>Bioinformatics</i> , 2011, 27, i401-i409.	4.1	212
2	Construction and investigation of breast cancer-specific ceRNA network based on the mRNA and miRNA expression data. <i>IET Systems Biology</i> , 2014, 8, 96-103.	1.5	110
3	Prediction of conformational B-cell epitopes from 3D structures by random forests with a distance-based feature. <i>BMC Bioinformatics</i> , 2011, 12, 341.	2.6	92
4	An accurate feature-based method for identifying DNA-binding residues on protein surfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 509-517.	2.6	68
5	Computational Prediction of Conformational B-Cell Epitopes from Antigen Primary Structures by Ensemble Learning. <i>PLoS ONE</i> , 2012, 7, e43575.	2.5	52
6	Edge-group sparse PCA for network-guided high dimensional data analysis. <i>Bioinformatics</i> , 2018, 34, 3479-3487.	4.1	43
7	Deciphering early development of complex diseases by progressive module network. <i>Methods</i> , 2014, 67, 334-343.	3.8	42
8	CytoBrain: Cervical Cancer Screening System Based on Deep Learning Technology. <i>Journal of Computer Science and Technology</i> , 2021, 36, 347-360.	1.5	38
9	Interpretable Machine Learning for Early Prediction of Prognosis in Sepsis: A Discovery and Validation Study. <i>Infectious Diseases and Therapy</i> , 2022, 11, 1117-1132.	4.0	37
10	Prediction of heme binding residues from protein sequences with integrative sequence profiles. <i>Proteome Science</i> , 2012, 10, S20.	1.7	36
11	CSCD2: an integrated interactivational database of cancer-specific circular RNAs. <i>Nucleic Acids Research</i> , 2022, 50, D1179-D1183.	14.5	35
12	A Bayesian regression approach to the prediction of MHC-II binding affinity. <i>Computer Methods and Programs in Biomedicine</i> , 2008, 92, 1-7.	4.7	33
13	Mixture classification model based on clinical markers for breast cancer prognosis. <i>Artificial Intelligence in Medicine</i> , 2010, 48, 129-137.	6.5	33
14	Exploiting a Reduced Set of Weighted Average Features to Improve Prediction of DNA-Binding Residues from 3D Structures. <i>PLoS ONE</i> , 2011, 6, e28440.	2.5	30
15	Computer-Based Image Studies on Tumor Nests Mathematical Features of Breast Cancer and Their Clinical Prognostic Value. <i>PLoS ONE</i> , 2013, 8, e82314.	2.5	25
16	Segmentation of Hematoxylin-Eosin stained breast cancer histopathological images based on pixel-wise SVM classifier. <i>Science China Information Sciences</i> , 2015, 58, 1-13.	4.3	24
17	Prediction of drug-disease associations based on ensemble meta paths and singular value decomposition. <i>BMC Bioinformatics</i> , 2019, 20, 134.	2.6	24
18	Predicting drug-disease interactions by semi-supervised graph cut algorithm and three-layer data integration. <i>BMC Medical Genomics</i> , 2017, 10, 79.	1.5	23

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19	Predicting linear B-cell epitopes by using sequence-derived structural and physicochemical features. International Journal of Data Mining and Bioinformatics, 2012, 6, 557.	0.1	22
20	Quantum dots-based double imaging combined with organic dye imaging to establish an automatic computerized method for cancer Ki67 measurement. Scientific Reports, 2016, 6, 20564.	3.3	20
21	Identification of single-stranded and double-stranded dna binding proteins based on protein structure. BMC Bioinformatics, 2014, 15, S4.	2.6	18
22	Quantitative prediction of MHC-II binding affinity using particle swarm optimization. Artificial Intelligence in Medicine, 2010, 50, 127-132.	6.5	16
23	Review of Machine Learning Methods for the Prediction and Reconstruction of Metabolic Pathways. Frontiers in Molecular Biosciences, 2021, 8, 634141.	3.5	15
24	Two-step segmentation of Hematoxylin-Eosin stained histopathological images for prognosis of breast cancer. , 2014, , .		14
25	A computational model to predict bone metastasis in breast cancer by integrating the dysregulated pathways. BMC Cancer, 2014, 14, 618.	2.6	14
26	Local network component analysis for quantifying transcription factor activities. Methods, 2017, 124, 25-35.	3.8	14
27	Selecting informative genes using a multiobjective evolutionary algorithm. , 0, , .		11
28	Analysis and classification of DNA-binding sites in single-stranded and double-stranded DNA-binding proteins using protein information. IET Systems Biology, 2014, 8, 176-183.	1.5	11
29	Improved Diagnostic Accuracy of Ameloblastoma and Odontogenic Keratocyst on Cone-Beam CT by Artificial Intelligence. Frontiers in Oncology, 2021, 11, 793417.	2.8	11
30	Quantitative prediction of MHC-II peptide binding affinity using relevance vector machine. Applied Intelligence, 2009, 31, 180-187.	5.3	10
31	Predicting immunogenic T-cell epitopes by combining various sequence-derived features. , 2013, , .		10
32	Surface shapes and surrounding environment analysis of single-stranded and double-stranded DNA-binding proteins in protein-DNA interface. Proteins: Structure, Function and Bioinformatics, 2016, 84, 979-989.	2.6	10
33	A Two-Stage Method to Identify Joint Modules From Matched MicroRNA and mRNA Expression Data. IEEE Transactions on Nanobioscience, 2016, 15, 362-370.	3.3	10
34	Link Prediction Only With Interaction Data and its Application on Drug Repositioning. IEEE Transactions on Nanobioscience, 2020, 19, 547-555.	3.3	10
35	Pre-Clinical Drug Prioritization via Prognosis-Guided Genetic Interaction Networks. PLoS ONE, 2010, 5, e13937.	2.5	9
36	Inferring Gene Dependency Network Specific to Phenotypic Alteration Based on Gene Expression Data and Clinical Information of Breast Cancer. PLoS ONE, 2014, 9, e92023.	2.5	9

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37	Measuring the quality of linear patterns in biclusters. <i>Methods</i> , 2015, 83, 18-27.	3.8	8
38	Comparative network stratification analysis for identifying functional interpretable network biomarkers. <i>BMC Bioinformatics</i> , 2017, 18, 48.	2.6	7
39	Discovering large conserved functional components in global network alignment by graph matching. <i>BMC Genomics</i> , 2018, 19, 670.	2.8	6
40	Sparse Weighted Canonical Correlation Analysis. <i>Chinese Journal of Electronics</i> , 2018, 27, 459-466.	1.5	6
41	Group-sparse SVD Models via L_1 - and L_0 -norm Penalties and Their Applications in Biological Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019, , 1-1.	5.7	6
42	Databases for B-Cell Epitopes. <i>Methods in Molecular Biology</i> , 2014, 1184, 135-148.	0.9	5
43	TransMixNet: An Attention Based Double-Branch Model for White Blood Cell Classification and Its Training with the Fuzzified Training Data. , 2021, , .		5
44	Distinct interfacial biclique patterns between ssDNA-binding proteins and those with dsDNAs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 598-610.	2.6	4
45	Integration of a prognostic gene module with a drug sensitivity module to identify drugs that could be repurposed for breast cancer therapy. <i>Computers in Biology and Medicine</i> , 2015, 61, 163-171.	7.0	4
46	Integration of multiple heterogeneous omics data. , 2016, , .		4
47	Predicting Drug-Disease Treatment Associations Based on Topological Similarity and Singular Value Decomposition. , 2019, , .		4
48	DeepRF: A deep learning method for predicting metabolic pathways in organisms based on annotated genomes. <i>Computers in Biology and Medicine</i> , 2022, 147, 105756.	7.0	4
49	A concept learning method based on a hybrid genetic algorithm. <i>Science in China Series D: Earth Sciences</i> , 1998, 41, 488-495.	0.9	3
50	Prediction of Linear B-Cell Epitopes Using AAT Scale. , 2009, , .		3
51	Predicting Response to Preoperative Chemotherapy Agents by Identifying Drug Action on Modeled MicroRNA Regulation Networks. <i>PLoS ONE</i> , 2014, 9, e98140.	2.5	3
52	A modified Polak-Ribière-Polyak descent method for unconstrained optimization. <i>Optimization Methods and Software</i> , 2014, 29, 177-188.	2.4	3
53	Differential function analysis: identifying structure and activation variations in dysregulated pathways. <i>Science China Information Sciences</i> , 2017, 60, 1.	4.3	3
54	Prediction of drug-disease treatment relations based on positive and unlabeled samples. <i>Journal of Intelligent and Fuzzy Systems</i> , 2018, 35, 1363-1373.	1.4	3

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55	Tumor classification based on gene microarray data and hybrid learning method. , 0, , .		2
56	BiodMHC: an online server for the prediction of MHC class II-peptide binding affinity. Journal of Genetics and Genomics, 2009, 36, 289-296.	3.9	2
57	Context-specific miRNA regulation network predicts cancer prognosis. , 2011, , .		2
58	Predicting distant metastasis in breast cancer using ensemble classifier based on context-specific miRNA regulation modules. , 2012, , .		2
59	Integrating peptides' sequence and energy of contact residues information improves prediction of peptide and HLA-I binding with unknown alleles. BMC Bioinformatics, 2013, 14, S1.	2.6	2
60	Semi-supervised graph cut algorithm for drug repositioning by integrating drug, disease and genomic associations. , 2016, , .		2
61	A Novel Sparse Penalty for Singular Value Decomposition. Chinese Journal of Electronics, 2017, 26, 306-312.	1.5	2
62	Network-based cancer genomic data integration for pattern discovery. BMC Genomic Data, 2021, 22, 54.	1.7	2
63	A genetic algorithm applied to optimal gene subset selection. , 0, , .		1
64	A simple method of inferring pairwise gene interactions from microarray time series data. , 2005, , .		1
65	Prediction of $\hat{\Gamma}^2$ -turns using double BP network with novel coding schemes of amino acids. Wuhan University Journal of Natural Sciences, 2009, 14, 119-124.	0.4	1
66	MDAS: An integrated system for metabonomic data analysis. Interdisciplinary Sciences, Computational Life Sciences, 2009, 1, 61-71.	3.6	1
67	A novel locally linear embedding and wavelet transform based encoding method for prediction of MHC-II binding affinity. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 145-150.	3.6	1
68	Network stratification analysis for identifying function-specific network layers. Molecular BioSystems, 2016, 12, 1232-1240.	2.9	1
69	Gene Functional Module Discovery via Integrating Gene Expression and PPI Network Data. Lecture Notes in Computer Science, 2019, , 116-126.	1.3	1
70	COMNA: Core-attachment based protein complex detection via multiple network alignment. , 2021, , .		1
71	The simulated annealing method applied to protein structure prediction. , 0, , .		0
72	Web-Based Parallel Corpora for Statistical Machine Translation. , 2007, , .		0

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73	Web-based parallel corpora for statistical machine translation. , 2007, , .		0
74	Predicting cleavage sites in exogenous antigen using weighted SVM. , 2010, , .		0
75	In silico Genetic Network Models for *Pre-clinical Drug Prioritization. Nature Precedings, 2010, , .	0.1	0
76	Dynamic remodeling of context-specific miRNAs regulation networks facilitate in silico cancer drug screening. , 2011, , .		0
77	The convergence rate of a three-term HS method with restart strategy for unconstrained optimization problems. Optimization, 2014, 63, 1387-1400.	1.7	0
78	GMAlign: A new network aligner for revealing large conserved functional components. , 2017, , .		0
79	A Robust Approach to Locate HER2 and CEN17 Signals in Varied FISH Images. , 2019, , .		0
80	Predicting Binding-Peptide of HLA-I on Unknown Alleles by Integrating Sequence Information and Energies of Contact Residues. Communications in Computer and Information Science, 2012, , 160-165.	0.5	0
81	GPPIAL: A New Global PPI Network Aligner Based on Orthologs. , 2020, , .		0