Juan Liu

List of Publications by Year
in descending order

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	CSCD2: an integrated interactional database of cancer-specific circular RNAs. Nucleic Acids Research, 2022, 50, D1179-D1183.	14.5	35
2	Interpretable Machine Learning for Early Prediction of Prognosis in Sepsis: A Discovery and Validation Study. Infectious Diseases and Therapy, 2022, 11, 1117-1132.	4.0	37
3	DeepRF: A deep learning method for predicting metabolic pathways in organisms based on annotated genomes. Computers in Biology and Medicine, 2022, 147, 105756.	7.0	4
4	CytoBrain: Cervical Cancer Screening System Based on Deep Learning Technology. Journal of Computer Science and Technology, 2021, 36, 347-360.	1.5	38
5	Review of Machine Learning Methods for the Prediction and Reconstruction of Metabolic Pathways. Frontiers in Molecular Biosciences, 2021, 8, 634141.	3.5	15
6	Improved Diagnostic Accuracy of Ameloblastoma and Odontogenic Keratocyst on Cone-Beam CT by Artificial Intelligence. Frontiers in Oncology, 2021, 11, 793417.	2.8	11
7	Network-based cancer genomic data integration for pattern discovery. BMC Genomic Data, 2021, 22, 54.	1.7	2
8	COMNA: Core-attachment based protein complex detection via multiple network alignment. , 2021, , .		1
9	TransMixNet: An Attention Based Double-Branch Model for White Blood Cell Classification and Its Training with the Fuzzified Training Data. , 2021, , .		5
10	Link Prediction Only With Interaction Data and its Application on Drug Repositioning. IEEE Transactions on Nanobioscience, 2020, 19, 547-555.	3.3	10
11	GPPIAL: A New Global PPI Network Aligner Based on Orthologs. , 2020, , .		0
12	Group-sparse SVD Models via L_1- and L_0-norm Penalties and Their Applications in Biological Data. IEEE Transactions on Knowledge and Data Engineering, 2019, , 1-1.	5.7	6
13	Prediction of drug-disease associations based on ensemble meta paths and singular value decomposition. BMC Bioinformatics, 2019, 20, 134.	2.6	24
14	A Robust Approach to Locate HER2 and CEN17 Signals in Varied FISH Images. , 2019, , .		0
15	Predicting Drug-Disease Treatment Associations Based on Topological Similarity and Singular Value Decomposition. , 2019, , .		4
16	Gene Functional Module Discovery via Integrating Gene Expression and PPI Network Data. Lecture Notes in Computer Science, 2019, , 116-126.	1.3	1
17	Edge-group sparse PCA for network-guided high dimensional data analysis. Bioinformatics, 2018, 34, 3479-3487.	4.1	43
18	Discovering large conserved functional components in global network alignment by graph matching. BMC Genomics, 2018, 19, 670.	2.8	6

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19	Prediction of drug-disease treatment relations based on positive and unlabeled samples. Journal of Intelligent and Fuzzy Systems, 2018, 35, 1363-1373.	1.4	3
20	Sparse Weighted Canonical Correlation Analysis. Chinese Journal of Electronics, 2018, 27, 459-466.	1.5	6
21	Differential function analysis: identifying structure and activation variations in dysregulated pathways. Science China Information Sciences, 2017, 60, 1.	4.3	3
22	Comparative network stratification analysis for identifying functional interpretable network biomarkers. BMC Bioinformatics, 2017, 18, 48.	2.6	7
23	Local network component analysis for quantifying transcription factor activities. Methods, 2017, 124, 25-35.	3.8	14
24	A Novel Sparse Penalty for Singular Value Decomposition. Chinese Journal of Electronics, 2017, 26, 306-312.	1.5	2
25	GMAlign: A new network aligner for revealing large conserved functional components. , 2017, , .		0
26	Predicting drug-disease interactions by semi-supervised graph cut algorithm and three-layer data integration. BMC Medical Genomics, 2017, 10, 79.	1.5	23
27	Surface shapes and surrounding environment analysis of singleâ€•and doubleâ€stranded DNAâ€binding proteins in proteinâ€DNA interface. Proteins: Structure, Function and Bioinformatics, 2016, 84, 979-989.	2.6	10
28	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
29	Semi-supervised graph cut algorithm for drug repositioning by integrating drug, disease and genomic associations. , 2016, , .		2
30	Integration of multiple heterogeneous omics data. , 2016, , .		4
31	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
32	Network stratification analysis for identifying function-specific network layers. Molecular BioSystems, 2016, 12, 1232-1240.	2.9	1
33	Integration of a prognostic gene module with a drug sensitivity module to identify drugs that could be repurposed for breast cancer therapy. Computers in Biology and Medicine, 2015, 61, 163-171.	7.0	4
34	Segmentation of Hematoxylin-Eosin stained breast cancer histopathological images based on pixel-wise SVM classifier. Science China Information Sciences, 2015, 58, 1-13.	4.3	24
35	Measuring the quality of linear patterns in biclusters. Methods, 2015, 83, 18-27.	3.8	8
36	Predicting Response to Preoperative Chemotherapy Agents by Identifying Drug Action on Modeled MicroRNA Regulation Networks. PLoS ONE, 2014, 9, e98140.	2.5	3

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37	The convergence rate of a three-term HS method with restart strategy for unconstrained optimization problems. Optimization, 2014, 63, 1387-1400.	1.7	0
38	Construction and investigation of breastâ€cancerâ€specific ceRNA network based on the mRNA and miRNA expression data. IET Systems Biology, 2014, 8, 96-103.	1.5	110
39	Analysis and classification of DNAâ€binding sites in singleâ€stranded and doubleâ€stranded DNAâ€binding proteins using protein information. IET Systems Biology, 2014, 8, 176-183.	1.5	11
40	Two-step segmentation of Hematoxylin-Eosin stained histopathological images for prognosis of breast cancer. , 2014, , .		14
41	A modified Polakâ€“Ribiâ€˜ereâ€“Polyak descent method for unconstrained optimization. Optimization Methods and Software, 2014, 29, 177-188.	2.4	3
42	A computational model to predict bone metastasis in breast cancer by integrating the dysregulated pathways. BMC Cancer, 2014, 14, 618.	2.6	14
43	Deciphering early development of complex diseases by progressive module network. Methods, 2014, 67, 334-343.	3.8	42
44	Identification of single-stranded and double-stranded dna binding proteins based on protein structure. BMC Bioinformatics, 2014, 15, S4.	2.6	18
45	Databases for B-Cell Epitopes. Methods in Molecular Biology, 2014, 1184, 135-148.	0.9	5
46	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
47	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
48	Predicting immunogenic T-cell epitopes by combining various sequence-derived features. , 2013, , .		10
49	Computer-Based Image Studies on Tumor Nests Mathematical Features of Breast Cancer and Their Clinical Prognostic Value. PLoS ONE, 2013, 8, e82314.	2.5	25
50	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
51	Predicting distant metastasis in breast cancer using ensemble classifier based on context-specific miRNA regulation modules. , 2012, , .		2
52	Computational Prediction of Conformational B-Cell Epitopes from Antigen Primary Structures by Ensemble Learning. PLoS ONE, 2012, 7, e43575.	2.5	52
53	Prediction of heme binding residues from protein sequences with integrative sequence profiles. Proteome Science, 2012, 10, S20.	1.7	36
54	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

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55	Dynamic remodeling of context-specific miRNAs regulation networks facilitate in silico cancer drug screening. , 2011, , .		0
56	Context-specific miRNA regulation network predicts cancer prognosis. , 2011, , .		2
57	A novel computational framework for simultaneous integration of multiple types of genomic data to identify microRNA-gene regulatory modules. Bioinformatics, 2011, 27, i401-i409.	4.1	212
58	Exploiting a Reduced Set of Weighted Average Features to Improve Prediction of DNA-Binding Residues from 3D Structures. PLoS ONE, 2011, 6, e28440.	2.5	30
59	Prediction of conformational B-cell epitopes from 3D structures by random forests with a distance-based feature. BMC Bioinformatics, 2011, 12, 341.	2.6	92
60	An accurate featureâ€based method for identifying DNAâ€binding residues on protein surfaces. Proteins: Structure, Function and Bioinformatics, 2011, 79, 509-517.	2.6	68
61	Distinct interfacial biclique patterns between ssDNAâ€binding proteins and those with dsDNAs. Proteins: Structure, Function and Bioinformatics, 2011, 79, 598-610.	2.6	4
62	Predicting cleavage sites in exogenous antigen using weighted SVM. , 2010, , .		0
63	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
64	Mixture classification model based on clinical markers for breast cancer prognosis. Artificial Intelligence in Medicine, 2010, 48, 129-137.	6.5	33
65	Quantitative prediction of MHC-II binding affinity using particle swarm optimization. Artificial Intelligence in Medicine, 2010, 50, 127-132.	6.5	16
66	In silico Genetic Network Models for *Pre-clinical Drug Prioritization. Nature Precedings, 2010, , .	0.1	0
67	Pre-Clinical Drug Prioritization via Prognosis-Guided Genetic Interaction Networks. PLoS ONE, 2010, 5, e13937.	2.5	9
68	Quantitative prediction of MHC-II peptide binding affinity using relevance vector machine. Applied Intelligence, 2009, 31, 180-187.	5.3	10
69	Prediction of Î²-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
70	MDAS: An integrated system for metabonomic data analysis. Interdisciplinary Sciences, Computational Life Sciences, 2009, 1, 61-71.	3.6	1
71	Prediction of Linear B-Cell Epitopes Using AAT Scale. , 2009, , .		3
72	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

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73	A Bayesian regression approach to the prediction of MHC-II binding affinity. Computer Methods and Programs in Biomedicine, 2008, 92, 1-7.	4.7	33
74	Web-Based Parallel Corpora for Statistical Machine Translation. , 2007, , .		0
75	Web-based parallel corpora for statistical machine translation. , 2007, , .		0
76	A simple method of inferring pairwise gene interactions from microarray time series data. , 2005, , .		1
77	A concept learning method based on a hybrid genetic algorithm. Science in China Series D: Earth Sciences, 1998, 41, 488-495.	0.9	3
78	Selecting informative genes using a multiobjective evolutionary algorithm. , 0, , .		11
79	Tumor classification based on gene microarray data and hybrid learning method. , 0, , .		2
80	The simulated annealing method applied to protein structure prediction. , 0, , .		0
81	A genetic algorithm applied to optimal gene subset selection. , 0, , .		1