

Jijun Tang

List of Publications by Year in descending order

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Version: 2024-02-01

111
papers

3,350
citations

159585

30
h-index

161849

54
g-index

113
all docs

113
docs citations

113
times ranked

2109
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , 2018, 117, 212-217.	4.1	184
2	Identification of drug-side effect association via multiple information integration with centered kernel alignment. <i>Neurocomputing</i> , 2019, 325, 211-224.	5.9	182
3	Identification of drug-target interactions via multiple information integration. <i>Information Sciences</i> , 2017, 418-419, 546-560.	6.9	168
4	Pretata: predicting TATA binding proteins with novel features and dimensionality reduction strategy. <i>BMC Systems Biology</i> , 2016, 10, 114.	3.0	143
5	Identification of protein subcellular localization via integrating evolutionary and physicochemical information into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 462, 230-239.	1.7	135
6	Enhancing Hi-C data resolution with deep convolutional neural network HiCPlus. <i>Nature Communications</i> , 2018, 9, 750.	12.8	132
7	Predicting protein-protein interactions via multivariate mutual information of protein sequences. <i>BMC Bioinformatics</i> , 2016, 17, 398.	2.6	130
8	Identification of Drug-Target Interactions via Dual Laplacian Regularized Least Squares with Multiple Kernel Fusion. <i>Knowledge-Based Systems</i> , 2020, 204, 106254.	7.1	106
9	Identification of membrane protein types via multivariate information fusion with Hilbert-Schmidt Independence Criterion. <i>Neurocomputing</i> , 2020, 383, 257-269.	5.9	105
10	Steps toward accurate reconstructions of phylogenies from gene-order data. <i>Journal of Computer and System Sciences</i> , 2002, 65, 508-525.	1.2	90
11	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , 2017, 18, 742.	2.8	85
12	Identification of Protein-Protein Interactions via a Novel Matrix-Based Sequence Representation Model with Amino Acid Contact Information. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1623.	4.1	83
13	Identification of drug-target interactions via fuzzy bipartite local model. <i>Neural Computing and Applications</i> , 2020, 32, 10303-10319.	5.6	83
14	MDA-SKF: Similarity Kernel Fusion for Accurately Discovering miRNA-Disease Association. <i>Frontiers in Genetics</i> , 2018, 9, 618.	2.3	74
15	MK-FSVM-SVDD: A Multiple Kernel-based Fuzzy SVM Model for Predicting DNA-binding Proteins via Support Vector Data Description. <i>Current Bioinformatics</i> , 2021, 16, 274-283.	1.5	71
16	Identification of Drug-Side Effect Association via Semisupervised Model and Multiple Kernel Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 2619-2632.	6.3	70
17	DeepAVP: A Dual-Channel Deep Neural Network for Identifying Variable-Length Antiviral Peptides. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3012-3019.	6.3	69
18	Identification of Protein-Ligand Binding Sites by Sequence Information and Ensemble Classifier. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 3149-3161.	5.4	67

#	ARTICLE	IF	CITATIONS
19	Improved detection of DNA-binding proteins via compression technology on PSSM information. PLoS ONE, 2017, 12, e0185587.	2.5	63
20	Genome Reduction by Deletion of Paralogs in the Marine Cyanobacterium Prochlorococcus. Molecular Biology and Evolution, 2011, 28, 2751-2760.	8.9	62
21	Human protein subcellular localization identification via fuzzy model on Kernelized Neighborhood Representation. Applied Soft Computing Journal, 2020, 96, 106596.	7.2	54
22	Exploring associations of non-coding RNAs in human diseases via three-matrix factorization with hypergraph-regular terms on center kernel alignment. Briefings in Bioinformatics, 2021, 22, .	6.5	51
23	Discovering Cancer Subtypes via an Accurate Fusion Strategy on Multiple Profile Data. Frontiers in Genetics, 2019, 10, 20.	2.3	49
24	An Ameliorated Prediction of Drug-Target Interactions Based on Multi-Scale Discrete Wavelet Transform and Network Features. International Journal of Molecular Sciences, 2017, 18, 1781.	4.1	46
25	FKL-Spa-LapRLS: an accurate method for identifying human microRNA-disease association. BMC Genomics, 2018, 19, 911.	2.8	46
26	Critical evaluation of web-based prediction tools for human protein subcellular localization. Briefings in Bioinformatics, 2020, 21, 1628-1640.	6.5	45
27	Excess of non-conservative amino acid changes in marine bacterioplankton lineages with reduced genomes. Nature Microbiology, 2017, 2, 17091.	13.3	41
28	Protein Crystallization Identification via Fuzzy Model on Linear Neighborhood Representation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1986-1995.	3.0	41
29	A Novel Computational Method for Detecting DNA Methylation Sites with DNA Sequence Information and Physicochemical Properties. International Journal of Molecular Sciences, 2018, 19, 511.	4.1	38
30	Identification of drug-target interactions via multiple kernel-based triple collaborative matrix factorization. Briefings in Bioinformatics, 2022, 23, .	6.5	38
31	Identification of DNA-protein Binding Sites through Multi-Scale Local Average Blocks on Sequence Information. Molecules, 2017, 22, 2079.	3.8	32
32	AIEpred: An Ensemble Predictive Model of Classifier Chain to Identify Anti-Inflammatory Peptides. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1831-1840.	3.0	31
33	Probabilistic Reconstruction of Ancestral Gene Orders with Insertions and Deletions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 667-672.	3.0	28
34	Multivariate Information Fusion With Fast Kernel Learning to Kernel Ridge Regression in Predicting LncRNA-Protein Interactions. Frontiers in Genetics, 2018, 9, 716.	2.3	28
35	Identification of Protein-Protein Interactions by Detecting Correlated Mutation at the Interface. Journal of Chemical Information and Modeling, 2015, 55, 2042-2049.	5.4	27
36	FKRR-MVSF: A Fuzzy Kernel Ridge Regression Model for Identifying DNA-Binding Proteins by Multi-View Sequence Features via Chou's Five-Step Rule. International Journal of Molecular Sciences, 2019, 20, 4175.	4.1	26

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37	Identification of Highest-Affinity Binding Sites of Yeast Transcription Factor Families. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1876-1883.	5.4	26
38	Phylogenetic analysis of genome rearrangements among five mammalian orders. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 871-882.	2.7	23
39	MAXIMUM LIKELIHOOD PHYLOGENETIC RECONSTRUCTION FROM HIGH-RESOLUTION WHOLE-GENOME DATA AND A TREE OF 68 EUKARYOTES. , 2012, , .		22
40	Identification of human microRNA-disease association via hypergraph embedded bipartite local model. <i>Computational Biology and Chemistry</i> , 2020, 89, 107369.	2.3	21
41	Inferring human microbe-drug associations via multiple kernel fusion on graph neural network. <i>Knowledge-Based Systems</i> , 2022, 238, 107888.	7.1	21
42	LightCpG: a multi-view CpG sites detection on single-cell whole genome sequence data. <i>BMC Genomics</i> , 2019, 20, 306.	2.8	20
43	Maximum likelihood phylogenetic reconstruction from high-resolution whole-genome data and a tree of 68 eukaryotes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 285-96.	0.7	20
44	Identification of 14-3-3 Proteins Phosphopeptide-Binding Specificity Using an Affinity-Based Computational Approach. <i>PLoS ONE</i> , 2016, 11, e0147467.	2.5	19
45	Detecting complexes from edge-weighted PPI networks via genes expression analysis. <i>BMC Systems Biology</i> , 2018, 12, 40.	3.0	18
46	CrystalM: a multi-view fusion approach for protein crystallization prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	17
47	Kernel Fusion Method for Detecting Cancer Subtypes via Selecting Relevant Expression Data. <i>Frontiers in Genetics</i> , 2020, 11, 979.	2.3	17
48	A Novel Triple Matrix Factorization Method for Detecting Drug-Side Effect Association Based on Kernel Target Alignment. <i>BioMed Research International</i> , 2020, 2020, 1-11.	1.9	17
49	Identify RNA-associated subcellular localizations based on multi-label learning using Chou's 5-steps rule. <i>BMC Genomics</i> , 2021, 22, 56.	2.8	17
50	Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data. <i>Scientific Reports</i> , 2017, 7, 15209.	3.3	16
51	Identification of Inhibitors of MMPS Enzymes via a Novel Computational Approach. <i>International Journal of Biological Sciences</i> , 2018, 14, 863-871.	6.4	16
52	Granular multiple kernel learning for identifying RNA-binding protein residues via integrating sequence and structure information. <i>Neural Computing and Applications</i> , 2021, 33, 11387.	5.6	16
53	Analysis of Co-Associated Transcription Factors via Ordered Adjacency Differences on Motif Distribution. <i>Scientific Reports</i> , 2017, 7, 43597.	3.3	15
54	Finding pathway-modulating genes from a novel Ontology Fingerprint-derived gene network. <i>Nucleic Acids Research</i> , 2014, 42, e138-e138.	14.5	14

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55	Reconstruction of Ancestral Gene Orders Using Probabilistic and Gene Encoding Approaches. PLoS ONE, 2014, 9, e108796.	2.5	13
56	An Efficient Multiple Kernel Support Vector Regression Model for Assessing Dry Weight of Hemodialysis Patients. Current Bioinformatics, 2021, 16, 284-293.	1.5	13
57	Identification of DNA-Binding Proteins by Multiple Kernel Support Vector Machine and Sequence Information. Current Proteomics, 2020, 17, 302-310.	0.3	13
58	Predicting S-sulenylation Sites Using Physicochemical Properties Differences. Letters in Organic Chemistry, 2017, 14, .	0.5	11
59	Predicting subcellular location of protein with evolution information and sequence-based deep learning. BMC Bioinformatics, 2021, 22, 515.	2.6	11
60	Res2Unet: A multi-scale channel attention network for retinal vessel segmentation. Neural Computing and Applications, 2022, 34, 12001-12015.	5.6	11
61	Multi-Omics Data Fusion via a Joint Kernel Learning Model for Cancer Subtype Discovery and Essential Gene Identification. Frontiers in Genetics, 2021, 12, 647141.	2.3	10
62	Multivariate Information Fusion for Identifying Antifungal Peptides with Hilbert-Schmidt Independence Criterion. Current Bioinformatics, 2022, 17, 89-100.	1.5	10
63	PHYLOGENETIC RECONSTRUCTION FROM COMPLETE GENE ORDERS OF WHOLE GENOMES. , 2007, , .		10
64	Reconstructing Ancestral Genomic Orders Using Binary Encoding and Probabilistic Models. Lecture Notes in Computer Science, 2013, , 17-27.	1.3	9
65	A Multichannel Deep Neural Network for Retina Vessel Segmentation via a Fusion Mechanism. Frontiers in Bioengineering and Biotechnology, 2021, 9, 697915.	4.1	9
66	Identification of protein-nucleotide binding residues via graph regularized k-local hyperplane distance nearest neighbor model. Applied Intelligence, 2022, 52, 6598-6612.	5.3	9
67	The Computational Models of Drug-target Interaction Prediction. Protein and Peptide Letters, 2020, 27, 348-358.	0.9	9
68	Exemplar or matching: modeling DCJ problems with unequal content genome data. Journal of Combinatorial Optimization, 2016, 32, 1165-1181.	1.3	8
69	SMDB: pivotal somatic sequence alterations reprogramming regulatory cascades. NAR Cancer, 2020, 2, zcaa030.	3.1	8
70	A sequence-based multiple kernel model for identifying DNA-binding proteins. BMC Bioinformatics, 2021, 22, 291.	2.6	7
71	Multi-Task Deep Supervision on Attention R2U-Net for Brain Tumor Segmentation. Frontiers in Oncology, 2021, 11, 704850.	2.8	7
72	Ancestral Genome Reconstruction on Whole Genome Level. Current Genomics, 2017, 18, 306-315.	1.6	7

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73	AN EXACT SOLVER FOR THE DCJ MEDIAN PROBLEM. , 2008, , .		6
74	Predicting MHC class I binder: existing approaches and a novel recurrent neural network solution. Briefings in Bioinformatics, 2021, 22, .	6.5	6
75	EditPredict: Prediction of RNA editable sites with convolutional neural network. Genomics, 2021, 113, 3864-3871.	2.9	6
76	Improving Genome Rearrangement Phylogeny Using Sequence-Style Parsimony. , 0, , .		5
77	A Divide-and-Conquer Implementation of Three Sequence Alignment and Ancestor Inference. , 2007, , .		5
78	A Novel Peptide Binding Prediction Approach for HLA-DR Molecule Based on Sequence and Structural Information. BioMed Research International, 2016, 2016, 1-10.	1.9	5
79	Analysis of gene copy number changes in tumor phylogenetics. Algorithms for Molecular Biology, 2016, 11, 26.	1.2	5
80	A Median Solver and Phylogenetic Inference Based on Double-Cut-and-Join Sorting. Journal of Computational Biology, 2018, 25, 302-312.	1.6	5
81	Diagnosis of Brain Diseases via Multi-Scale Time-Series Model. Frontiers in Neuroscience, 2019, 13, 197.	2.8	5
82	Inferring gene regulatory network via fusing gene expression image and RNA-seq data. Bioinformatics, 2022, 38, 1716-1723.	4.1	5
83	Emulating Insertion and Deletion Events in Genome Rearrangement Analysis. , 2011, , .		4
84	A Cooperative Co-Evolutionary Genetic Algorithm for Tree Scoring and Ancestral Genome Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1248-1254.	3.0	4
85	Down syndrome prediction/screening model based on deep learning and illumina genotyping array. , 2017, , .		4
86	Phylogeny analysis from gene-order data with massive duplications. BMC Genomics, 2017, 18, 760.	2.8	4
87	Machine and Deep Learning for Prediction of Subcellular Localization. Methods in Molecular Biology, 2021, 2361, 249-261.	0.9	4
88	A Zero-Shot Method for 3D Medical Image Segmentation. , 2021, , .		4
89	Identification of DNA N4-methylcytosine Sites via Multiview Kernel Sparse Representation Model. IEEE Transactions on Artificial Intelligence, 2023, 4, 1236-1245.	4.7	4
90	Genome3D: A viewer-model framework for integrating and visualizing multi-scale epigenomic information within a three-dimensional genome. , 2011, , .		3

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91	Utilizing Deep Learning and Oversampling Methods to Identify Children's Emotional and Behavioral Risk. <i>Journal of Psychoeducational Assessment</i> , 2021, 39, 227-241.	1.5	3
92	Exploring effectiveness of <i>ab-initio</i> protein-protein docking methods on a novel antibacterial protein complex dataset. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	3
93	Identifying potential association on gene-disease network via dual hypergraph regularized least squares. <i>BMC Genomics</i> , 2021, 22, 605.	2.8	3
94	A New Approach for Tree Alignment Based on Local Re-Optimization. , 2008, , .		2
95	Matching a Set of Patterns with Wildcards. , 2010, , .		2
96	Maximum likelihood phylogenetic reconstruction using gene order encodings. , 2011, , .		2
97	Isolating - a new resampling method for gene order data. , 2011, , .		2
98	Assessing ancestral genome reconstruction methods by resampling. , 2014, , .		2
99	Phylogenetic Reconstruction for Copy-Number Evolution Problems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 694-699.	3.0	2
100	Complex Detection in PPI Network Using Genes Expression Information. <i>Current Proteomics</i> , 2018, 15, 119-127.	0.3	2
101	An two-layer predictive model of ensemble classifier chain for detecting antimicrobial peptides. , 2020, , .		2
102	Identification of DNA N4-methylcytosine sites via fuzzy model on self representation. <i>Applied Soft Computing Journal</i> , 2022, 122, 108840.	7.2	2
103	Ancestral reconstruction under weighted maximum matching. , 2015, , .		1
104	Improvement of phylogenetic method to analyze compositional heterogeneity. <i>BMC Systems Biology</i> , 2017, 11, 79.	3.0	1
105	Ancestral Genome Reconstruction. <i>Computational Biology</i> , 2019, , 193-203.	0.2	1
106	Global Autozygosity Is Associated with Cancer Risk, Mutational Signature and Prognosis. <i>Cancers</i> , 2020, 12, 3646.	3.7	1
107	Serum Metabolites Associated with Blood Pressure in Chronic Kidney Disease Patients. <i>Metabolites</i> , 2022, 12, 281.	2.9	1
108	Phylogenetic reconstruction with disk-covering and Bayesian approaches. , 2008, , .		0

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109	Guest Editorial for the 14 th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 396-397.	3.0	0
110	Achieving large and distant ancestral genome inference by using an improved discrete quantum-behaved particle swarm optimization algorithm. BMC Bioinformatics, 2020, 21, 516.	2.6	0
111	An Accurate Tool for Uncovering Cancer Subtypes by Fast Kernel Learning Method to Integrate Multiple Profile Data. Frontiers in Cell and Developmental Biology, 2021, 9, 615747.	3.7	0