Jialiang Yang

List of Publications by Year
in descending order

93 papers	7,639 citations	172386 29 h-index	64755 79 g-index
95 all docs	95 docs citations	95 times ranked	19177 citing authors

#	Article	IF	Citations
1	Cervical Cancer Metastasis and Recurrence Risk Prediction Based on Deep Convolutional Neural Network. Current Bioinformatics, 2022, 17, 164-173.	0.7	26
2	A weighted bilinear neural collaborative filtering approach for drug repositioning. Briefings in Bioinformatics, 2022, 23, .	3.2	72
3	A multi-omics machine learning framework in predicting the survival of colorectal cancer patients. Computers in Biology and Medicine, 2022, 146, 105516.	3.9	34
4	Migration inhibition and selective cytotoxicity of cobalt hydroxide nanosheets on different cancer cell lines. New Journal of Chemistry, 2022, 46, 10289-10298.	1.4	3
5	Predicting breast cancer recurrence and metastasis risk by integrating color and texture features of histopathological images and machine learning technologies. Computers in Biology and Medicine, 2022, 146, 105569.	3.9	18
6	Editorial: Machine Learning-Based Methods for RNA Data Analysis. Frontiers in Genetics, 2022, 13, .	1.1	0
7	Computational drug repositioning using similarity constrained weight regularization matrix factorization: A case of <scp>COVID</scp>â€19. Journal of Cellular and Molecular Medicine, 2022, 26, 3772-3782.	1.6	10
8	Evaluating the performance of dropout imputation and clustering methods for single-cell RNA sequencing data. Computers in Biology and Medicine, 2022, 146, 105697.	3.9	9
9	Cancer susceptibility genes: update and systematic perspectives. Innovation(China), 2022, 3, 100277.	5.2	8
10	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	5.8	35
11	A Streamlined scRNA-Seq Data Analysis Framework Based on Improved Sparse Subspace Clustering. IEEE Access, 2021, 9, 9719-9727.	2.6	18
12	A Novel Hybrid Feature Selection and Ensemble Learning Framework for Unbalanced Cancer Data Diagnosis With Transcriptome and Functional Proteomic. IEEE Access, 2021, 9, 51659-51668.	2.6	6
13	Detecting TYMS Tandem Repeat Polymorphism by the PSSD Method Based on Next-generation Sequencing. Current Bioinformatics, 2021, 15, 1153-1159.	0.7	1
14	Prioritizing antiviral drugs against SARS-CoV-2 by integrating viral complete genome sequences and drug chemical structures. Scientific Reports, 2021, 11, 6248.	1.6	31
15	A Systematic Analysis on COVID-19 Patients in Inner Mongolia Based on Dynamic Monitoring. BioMed Research International, 2021, 2021, 1-8.	0.9	2
16	Genomic variation, origin tracing, and vaccine development of SARS-CoV-2: A systematic review. Innovation(China), 2021, 2, 100116.	5.2	39
17	Evaluating DNA Methylation, Gene Expression, Somatic Mutation, and Their Combinations in Inferring Tumor Tissue-of-Origin. Frontiers in Cell and Developmental Biology, 2021, 9, 619330.	1.8	80
18	Application of Circulating Tumor DNA as a Biomarker for Non-Small Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 725938.	1.3	20

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19	Identifying Breast Cancer-Related Genes Based on a Novel Computational Framework Involving KEGG Pathways and PPI Network Modularity. Frontiers in Genetics, 2021, 12, 596794.	1.1	17
20	Protective Role of a New Polysaccharide Extracted from Lonicera japonica Thunb in Mice with Ulcerative Colitis Induced by Dextran Sulphate Sodium. BioMed Research International, 2021, 2021, 1-9.	0.9	19
21	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. GeroScience, 2020, 42, 353-372.	2.1	50
22	Identifying Effective Antiviral Drugs Against SARS-CoV-2 by Drug Repositioning Through Virus-Drug Association Prediction. Frontiers in Genetics, 2020, 11, 577387.	1.1	20
23	Improved Human Age Prediction by Using Gene Expression Profiles From Multiple Tissues. Frontiers in Genetics, 2020, 11, 1025.	1.1	14
24	An Improved Anticancer Drug-Response Prediction Based on an Ensemble Method Integrating Matrix Completion and Ridge Regression. Molecular Therapy - Nucleic Acids, 2020, 21, 676-686.	2.3	71
25	Assessing the Impact of Data Preprocessing on Analyzing Next Generation Sequencing Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 817.	2.0	22
26	Probing antiviral drugs against SARS-CoV-2 through virus-drug association prediction based on the KATZ method. Genomics, 2020, 112, 4427-4434.	1.3	32
27	A Neural Network Framework for Predicting the Tissue-of-Origin of 15 Common Cancer Types Based on RNA-Seq Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 737.	2.0	39
28	A machine learning framework to trace tumor tissue-of-origin of 13 types of cancer based on DNA somatic mutation. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165916.	1.8	46
29	LRMCMDA: Predicting miRNA-Disease Association by Integrating Low-Rank Matrix Completion With miRNA and Disease Similarity Information. IEEE Access, 2020, 8, 80728-80738.	2.6	22
30	TOOme: A Novel Computational Framework to Infer Cancer Tissue-of-Origin by Integrating Both Gene Mutation and Expression. Frontiers in Bioengineering and Biotechnology, 2020, 8, 394.	2.0	63
31	Transcriptome analysis reveals the difference between â€œhealthyâ€•and â€œcommonâ€•aging and their connection with ageâ€related diseases. Aging Cell, 2020, 19, e13121.	3.0	22
32	Single-cell RNA-seq clustering: datasets, models, and algorithms. RNA Biology, 2020, 17, 765-783.	1.5	50
33	Prioritizing Human Microbe-Disease Associations Utilizing a Node-Information-Based Link Propagation Method. IEEE Access, 2020, 8, 31341-31349.	2.6	9
34	CMF-Impute: an accurate imputation tool for single-cell RNA-seq data. Bioinformatics, 2020, 36, 3139-3147.	1.8	78
35	IMDAILM: Inferring miRNA-Disease Association by Integrating lncRNA and miRNA Data. IEEE Access, 2020, 8, 16517-16527.	2.6	11
36	Editorial: Bioinformatics Analysis of Single Cell Sequencing Data and Applications in Precision Medicine. Frontiers in Genetics, 2020, 10, 1358.	1.1	11

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37	Indicator Regularized Non-Negative Matrix Factorization Method-Based Drug Repurposing for COVID-19. Frontiers in Immunology, 2020, 11, 603615.	2.2	45
38	T Cell Receptor Repertoire Sequencing. Methods in Molecular Biology, 2020, 2204, 3-12.	0.4	3
39	A Review on Cancer of Unknown Primary Origin: The Role of Molecular Biomarkers in the Identification of Unknown Primary Origin. Methods in Molecular Biology, 2020, 2204, 109-119.	0.4	6
40	MVSC: A Multi-variation Simulator of Cancer Genome. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 326-333.	0.6	2
41	Inferring Latent Disease-lncRNA Associations by Faster Matrix Completion on a Heterogeneous Network. Frontiers in Genetics, 2019, 10, 769.	1.1	14
42	A new resource allocation strategy based on the relationship between subproblems for MOEA/D. Information Sciences, 2019, 501, 337-362.	4.0	18
43	Revealing Drug-Target Interactions with Computational Models and Algorithms. Molecules, 2019, 24, 1714.	1.7	42
44	Comparison of multi-tissue aging between human and mouse. Scientific Reports, 2019, 9, 6220.	1.6	15
45	Prediction of Protein Subcellular Localization Based on Fusion of Multi-view Features. Molecules, 2019, 24, 919.	1.7	21
46	Improved Pre-miRNAs Identification Through Mutual Information of Pre-miRNA Sequences and Structures. Frontiers in Genetics, 2019, 10, 119.	1.1	28
47	FCMDAP: using miRNA family and cluster information to improve the prediction accuracy of disease related miRNAs. BMC Systems Biology, 2019, 13, 26.	3.0	14
48	Biological ingredient complement chemical ingredient in the assessment of the quality of TCM preparations. Scientific Reports, 2019, 9, 5853.	1.6	15
49	Identifying Potential miRNAs–Disease Associations With Probability Matrix Factorization. Frontiers in Genetics, 2019, 10, 1234.	1.1	30
50	Molecular Network-Based Drug Prediction in Thyroid Cancer. International Journal of Molecular Sciences, 2019, 20, 263.	1.8	16
51	Predicting Influenza Antigenicity by Matrix Completion With Antigen and Antiserum Similarity. Frontiers in Microbiology, 2018, 9, 2500.	1.5	16
52	Computational Tools for Investigating Pathogen, Pathogen-Host Interaction, and Infectious Disease. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 2018, 1-2.	0.7	0
53	Applications of Bioinformatics and Systems Biology in Precision Medicine and Immunooncology. BioMed Research International, 2018, 2018, 1-2.	0.9	7
54	A quantile regression forest based method to predict drug response and assess prediction reliability. PLoS ONE, 2018, 13, e0205155.	1.1	21

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55	A Hybrid Deep Learning Model for Predicting Protein Hydroxylation Sites. International Journal of Molecular Sciences, 2018, 19, 2817.	1.8	27
56	Immunomodulatory activity of a novel polysaccharide from Lonicera japonica in immunosuppressed mice induced by cyclophosphamide. PLoS ONE, 2018, 13, e0204152.	1.1	67
57	Improved DNA-Binding Protein Identification by Incorporating Evolutionary Information Into the Chou's PseAAC. IEEE Access, 2018, 6, 66545-66556.	2.6	47
58	BPLLDA: Predicting lncRNA-Disease Associations Based on Simple Paths With Limited Lengths in a Heterogeneous Network. Frontiers in Genetics, 2018, 9, 411.	1.1	52
59	DECtp: Calling Differential Gene Expression Between Cancer and Normal Samples by Integrating Tumor Purity Information. Frontiers in Genetics, 2018, 9, 321.	1.1	8
60	Molecular Network-Based Identification of Competing Endogenous RNAs in Thyroid Carcinoma. Genes, 2018, 9, 44.	1.0	23
61	Monitoring microsatellite instability (MSI) in circulating tumor DNA by next-generation DNA-seq.. Journal of Clinical Oncology, 2018, 36, 12025-12025.	0.8	9
62	Identification of human age-associated gene co-expressions in functional modules using liquid association. Oncotarget, 2018, 9, 1063-1074.	0.8	16
63	Predicting influenza antigenicity from Hemagglutintin sequence data based on a joint random forest method. Scientific Reports, 2017, 7, 1545.	1.6	40
64	Matrix completion with side information and its applications in predicting the antigenicity of influenza viruses. Bioinformatics, 2017, 33, 3195-3201.	1.8	33
65	Human Pancreatic β Cell lncRNAs Control Cell-Specific Regulatory Networks. Cell Metabolism, 2017, 25, 400-411.	7.2	195
66	Global network random walk for predicting potential human lncRNA-disease associations. Scientific Reports, 2017, 7, 12442.	1.6	89
67	Network-based collaborative filtering recommendation model for inferring novel disease-related miRNAs. RSC Advances, 2017, 7, 44961-44971.	1.7	10
68	Screening drug-target interactions with positive-unlabeled learning. Scientific Reports, 2017, 7, 8087.	1.6	35
69	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. IEEE Access, 2017, 5, 26582-26590.	2.6	153
70	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. BMC Genomics, 2017, 18, 987.	1.2	19
71	A Review on Recent Computational Methods for Predicting Noncoding RNAs. BioMed Research International, 2017, 2017, 1-14.	0.9	25
72	Computational Molecular Networks and Network Pharmacology. BioMed Research International, 2017, 2017, 1-1.	0.9	58

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73	Using molecular functional networks to manifest connections between obesity and obesity-related diseases. Oncotarget, 2017, 8, 85136-85149.	0.8	8
74	Integrated Analysis of Multiscale Large-Scale Biological Data for Investigating Human Disease 2016. BioMed Research International, 2016, 2016, 1-2.	0.9	2
75	An Alignment-Free Algorithm in Comparing the Similarity of Protein Sequences Based on Pseudo-Markov Transition Probabilities among Amino Acids. PLoS ONE, 2016, 11, e0167430.	1.1	6
76	Development of a novel immuno-PCR for detection of avian leukosis virus. Journal of Virological Methods, 2016, 236, 25-28.	1.0	5
77	A systematic study on drug-response associated genes using baseline gene expressions of the Cancer Cell Line Encyclopedia. Scientific Reports, 2016, 6, 22811.	1.6	54
78	Discover the network mechanisms underlying the connections between aging and age-related diseases. Scientific Reports, 2016, 6, 32566.	1.6	40
79	A Dynamic 3D Graphical Representation for RNA Structure Analysis and Its Application in Non-Coding RNA Classification. PLoS ONE, 2016, 11, e0152238.	1.1	4
80	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	1.6	180
81	Error-prone pcr-based mutagenesis strategy for rapidly generating high-yield influenza vaccine candidates. Virology, 2015, 482, 234-243.	1.1	17
82	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
83	Integrative random forest for gene regulatory network inference. Bioinformatics, 2015, 31, i197-i205.	1.8	152
84	ALV-J GP37 Molecular Analysis Reveals Novel Virus-Adapted Sites and Three Tyrosine-Based Env Species. PLoS ONE, 2015, 10, e0122887.	1.1	6
85	Sequence-Based Antigenic Change Prediction by a Sparse Learning Method Incorporating Co-Evolutionary Information. PLoS ONE, 2014, 9, e106660.	1.1	21
86	Baf250a orchestrates an epigenetic pathway to repress the Nkx2.5-directed contractile cardiomyocyte program in the sinoatrial node. Cell Research, 2014, 24, 1201-1213.	5.7	33
87	Using Sequence Data To Infer the Antigenicity of Influenza Virus. MBio, 2013, 4, .	1.8	85
88	Quartet-Net: A Quartet-Based Method to Reconstruct Phylogenetic Networks. Molecular Biology and Evolution, 2013, 30, 1206-1217.	3.5	24
89	Identifying Antigenicity-Associated Sites in Highly Pathogenic H5N1 Influenza Virus Hemagglutinin by Using Sparse Learning. Journal of Molecular Biology, 2012, 422, 145-155.	2.0	43
90	AntigenMap 3D: an online antigenic cartography resource. Bioinformatics, 2012, 28, 1292-1293.	1.8	44

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91	Run Probabilities of Seed-Like Patterns and Identifying Good Transition Seeds. Journal of Computational Biology, 2008, 15, 1295-1313.	0.8	16
92	RUN PROBABILITY OF HIGH-ORDER SEED PATTERNS AND ITS APPLICATIONS TO FINDING GOOD TRANSITION SEEDS. , 2007, , .		0
93	Evaluating the Microsatellite Instability of Colorectal Cancer Based on Multimodal Deep Learning Integrating Histopathological and Molecular Data. Frontiers in Oncology, 0, 12, .	1.3	3