Yadong Wang

List of Publications by Year in descending order

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138	5,162	257101	123241
papers	citations	24 h-index	61 g-index

141	141	141	5697
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	miR2Disease: a manually curated database for microRNA deregulation in human disease. Nucleic Acids Research, 2009, 37, D98-D104.	6.5	1,255
2	Identifying and removing haplotypic duplication in primary genome assemblies. Bioinformatics, 2020, 36, 2896-2898.	1.8	1,221
3	Review of Drug Repositioning Approaches and Resources. International Journal of Biological Sciences, 2018, 14, 1232-1244.	2.6	429
4	Predicting human microRNA-disease associations based on support vector machine. International Journal of Data Mining and Bioinformatics, 2013, 8, 282.	0.1	208
5	Long-read-based human genomic structural variation detection with cuteSV. Genome Biology, 2020, 21, 189.	3.8	164
6	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	6.5	124
7	SemFunSim: A New Method for Measuring Disease Similarity by Integrating Semantic and Gene Functional Association. PLoS ONE, 2014, 9, e99415.	1.1	117
8	MeDReaders: a database for transcription factors that bind to methylated DNA. Nucleic Acids Research, 2018, 46, D146-D151.	6.5	94
9	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. Nature Communications, 2021, 12, 266.	5.8	87
10	Low-rank and sparse decomposition based shape model and probabilistic atlas for automatic pathological organ segmentation. Medical Image Analysis, 2017, 38, 30-49.	7.0	62
11	Shapeâ€“intensity prior level set combining probabilistic atlas and probability map constrains for automatic liver segmentation from abdominal CT images. International Journal of Computer Assisted Radiology and Surgery, 2016, 11, 817-826.	1.7	50
12	TF2LncRNA: Identifying Common Transcription Factors for a List of lncRNA Genes from ChIP-Seq Data. BioMed Research International, 2014, 2014, 1-5.	0.9	47
13	Comparison among dimensionality reduction techniques based on Random Projection for cancer classification. Computational Biology and Chemistry, 2016, 65, 165-172.	1.1	46
14	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	1.2	46
15	Identifying term relations cross different gene ontology categories. BMC Bioinformatics, 2017, 18, 573.	1.2	46
16	Extending gene ontology with gene association networks. Bioinformatics, 2016, 32, 1185-1194.	1.8	42
17	deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. Genome Biology, 2019, 20, 274.	3.8	41
18	Integrate GWAS, eQTL, and mQTL Data to Identify Alzheimerâ€™s Disease-Related Genes. Frontiers in Genetics, 2019, 10, 1021.	1.1	40

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19	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. BMC Bioinformatics, 2015, 16, 44.	1.2	39
20	A framework for analyzing DNA methylation data from Illumina Infinium HumanMethylation450 BeadChip. BMC Bioinformatics, 2018, 19, 115.	1.2	37
21	Prediction for High Risk Clinical Symptoms of Epilepsy Based on Deep Learning Algorithm. IEEE Access, 2018, 6, 77596-77605.	2.6	37
22	A gradient-boosting approach for filtering de novo mutations in parentâ€“offspring trios. Bioinformatics, 2014, 30, 1830-1836.	1.8	33
23	A deep learning approach for filtering structural variants in short read sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	32
24	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. Human Genetics, 2017, 136, 1279-1289.	1.8	27
25	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. BMC Bioinformatics, 2021, 22, 403.	1.2	27
26	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. BMC Genomics, 2016, 17, 530.	1.2	26
27	FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. Methods, 2020, 173, 83-93.	1.9	26
28	Improving alignment accuracy on homopolymer regions for semiconductor-based sequencing technologies. BMC Genomics, 2016, 17, 521.	1.2	24
29	TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain. Bioinformatics, 2019, 35, i200-i207.	1.8	23
30	Extracting a biologically latent space of lung cancer epigenetics with variational autoencoders. BMC Bioinformatics, 2019, 20, 568.	1.2	23
31	Disease Module Identification Based on Representation Learning of Complex Networks Integrated From GWAS, eQTL Summaries, and Human Interactome. Frontiers in Bioengineering and Biotechnology, 2020, 8, 418.	2.0	22
32	An approach for prioritizing disease-related microRNAs based on genomic data integration. , 2010, , .		20
33	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. Bioinformatics, 2021, 37, 2209-2211.	1.8	20
34	PERGA: A Paired-End Read Guided De Novo Assembler for Extending Contigs Using SVM and Look Ahead Approach. PLoS ONE, 2014, 9, e114253.	1.1	18
35	Joint detection of copy number variations in parent-offspring trios. Bioinformatics, 2016, 32, 1130-1137.	1.8	18
36	Analyzing large-scale samples confirms the association between the rs1051730 polymorphism and lung cancer susceptibility. Scientific Reports, 2015, 5, 15642.	1.6	17

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37	Identifying Liver Cancer-Related Enhancer SNPs by Integrating GWAS and Histone Modification ChIP-seq Data. BioMed Research International, 2016, 2016, 1-6.	0.9	17
38	DisSetSim: an online system for calculating similarity between disease sets. Journal of Biomedical Semantics, 2017, 8, 28.	0.9	17
39	Pan-Cancer Classification Based on Self-Normalizing Neural Networks and Feature Selection. Frontiers in Bioengineering and Biotechnology, 2020, 8, 766.	2.0	17
40	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. Frontiers in Genetics, 2019, 10, 1309.	1.1	17
41	The minimum feature subset selection problem. Journal of Computer Science and Technology, 1997, 12, 145-153.	0.9	16
42	Predicting human microRNA-disease associations based on support vector machine. , 2010, , .		16
43	A Generalized Topological Entropy for Analyzing the Complexity of DNA Sequences. PLoS ONE, 2014, 9, e88519.	1.1	16
44	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. BioMed Research International, 2016, 2016, 1-8.	0.9	16
45	Predicting circRNA-Disease Associations Based on circRNA Expression Similarity and Functional Similarity. Frontiers in Genetics, 2019, 10, 832.	1.1	16
46	Exploring DNA Methylation Data of Lung Cancer Samples with Variational Autoencoders. , 2018, , .		15
47	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. Briefings in Bioinformatics, 2022, 23, .	3.2	15
48	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. BioMed Research International, 2015, 2015, 1-7.	0.9	13
49	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. BMC Bioinformatics, 2019, 20, 573.	1.2	13
50	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
51	Hidden Markov induced Dynamic Bayesian Network for recovering time evolving gene regulatory networks. Scientific Reports, 2016, 5, 17841.	1.6	12
52	Statistical Approaches for the Construction and Interpretation of Human Protein-Protein Interaction Network. BioMed Research International, 2016, 2016, 1-7.	0.9	11
53	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. BMC Bioinformatics, 2017, 18, 270.	1.2	11
54	DeepDNA: a hybrid convolutional and recurrent neural network for compressing human mitochondrial genomes. , 2018, , .		11

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55	LncDisAP: a computation model for LncRNA-disease association prediction based on multiple biological datasets. BMC Bioinformatics, 2019, 20, 582.	1.2	11
56	ScGSLC: An unsupervised graph similarity learning framework for single-cell RNA-seq data clustering. Computational Biology and Chemistry, 2021, 90, 107415.	1.1	11
57	Integrated entropy-based approach for analyzing exons and introns in DNA sequences. BMC Bioinformatics, 2019, 20, 283.	1.2	10
58	CDL4CDRP: A Collaborative Deep Learning Approach for Clinical Decision and Risk Prediction. Processes, 2019, 7, 265.	1.3	10
59	rMETL: sensitive mobile element insertion detection with long read realignment. Bioinformatics, 2019, 35, 3484-3486.	1.8	10
60	Factor graph-aggregated heterogeneous network embedding for disease-gene association prediction. BMC Bioinformatics, 2021, 22, 165.	1.2	10
61	WDNfinder: A method for minimum driver node set detection and analysis in directed and weighted biological network. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750021.	0.3	9
62	An Approximate Bufferless Network-on-Chip. IEEE Access, 2019, 7, 141516-141532.	2.6	9
63	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. BMC Bioinformatics, 2019, 20, 574.	1.2	9
64	Privacy-Preserving Data Mining Based on Sample Selection and Singular Value Decomposition. , 2011, , .		8
65	FNSemSim: An improved disease similarity method based on network fusion. , 2017, , .		8
66	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization. , 2018, , .		8
67	An automated quality control pipeline for eQTL analysis with RNA-seq data. , 2019, , .		8
68	Prognostic prediction of carcinoma by a differential-regulatory-network-embedded deep neural network. Computational Biology and Chemistry, 2020, 88, 107317.	1.1	8
69	Identifying Alzheimerâ€™s Disease-related miRNA Based on Semi-clustering. Current Gene Therapy, 2019, 19, 216-223.	0.9	8
70	An online tool for measuring and visualizing phenotype similarities using HPO. BMC Genomics, 2018, 19, 571.	1.2	7
71	3D surface voxel tracing corrector for accurate bone segmentation. International Journal of Computer Assisted Radiology and Surgery, 2018, 13, 1549-1563.	1.7	7
72	Human mitochondrial genome compression using machine learning techniques. Human Genomics, 2019, 13, 49.	1.4	7

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73	Identifying Protein Biomarkers in Blood for Alzheimer's Disease. Frontiers in Cell and Developmental Biology, 2020, 8, 472.	1.8	7
74	Identification of Parkinsonâ€™s Disease-Causing Genes via Omics Data. Frontiers in Genetics, 2021, 12, 712164.	1.1	7
75	Reconstruct gene regulatory network using slice pattern model. BMC Genomics, 2009, 10, S2.	1.2	6
76	Measuring phenotype semantic similarity using Human Phenotype Ontology. , 2016, , .		6
77	interacCircos: an R package based on JavaScript libraries for the generation of interactive circos plots. Bioinformatics, 2021, 37, 3642-3644.	1.8	6
78	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. Protein and Peptide Letters, 2020, 27, 295-302.	0.4	6
79	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. Current Bioinformatics, 2020, 15, 574-580.	0.7	6
80	Back propagation based on selective attention for fast convergence of training neural network. , 0, , .		5
81	Automatic centerline detection of small three-dimensional vessel structures. Journal of Electronic Imaging, 2014, 23, 013007.	0.5	5
82	A network-based pathway-extending approach using DNA methylation and gene expression data to identify altered pathways. Scientific Reports, 2019, 9, 11853.	1.6	5
83	Pan-Cancer Metastasis Prediction Based on Graph Deep Learning Method. Frontiers in Cell and Developmental Biology, 2021, 9, 675978.	1.8	5
84	Explore potential disease related metabolites based on latent factor model. BMC Genomics, 2022, 23, 269.	1.2	5
85	Segmentation of the hip joint in CT volumes using adaptive thresholding classification and normal direction correction. Journal of the Chinese Institute of Engineers, Transactions of the Chinese Institute of Engineers,Series A/Chung-kuo Kung Ch'eng Hsuch K'an, 2013, 36, 1059-1072.	0.6	4
86	A network-based pathway-expanding approach for pathway analysis. BMC Bioinformatics, 2016, 17, 536.	1.2	4
87	Pysubsim-tree: A package for simulating tumor genomes according to tumor evolution history. , 2017, , .		4
88	Pre-SCNAClonal: Efficient GC bias correction for SCNA based tumor subclonal populations inferring. , 2017, , .		4
89	A Bipartite Network Module-Based Project to Predict Pathogenâ€“Host Association. Frontiers in Genetics, 2019, 10, 1357.	1.1	4
90	Finding disagreement pathway signatures and constructing an ensemble model for cancer classification. Scientific Reports, 2017, 7, 10044.	1.6	3

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91	Identifying Candidate Diseases-related Metabolites Based on Disease Similarity. , 2018, , .		3
92	deSPI: efficient classification of metagenomics reads with lightweight de Bruijn graph-based reference indexing. , 2018, , .		3
93	Y-SPCR: A new dimensionality reduction method for gene expression data classification. , 2019, , .		3
94	PGsim: A Comprehensive and Highly Customizable Personal Genome Simulator. Frontiers in Bioengineering and Biotechnology, 2020, 8, 28.	2.0	3
95	PmDNE: Prediction of miRNA-Disease Association Based on Network Embedding and Network Similarity Analysis. BioMed Research International, 2020, 2020, 1-9.	0.9	3
96	OTUCD: Unsupervised GCN based metagenomics non-overlapping community detection. Computational Biology and Chemistry, 2022, 98, 107670.	1.1	3
97	PERGA. , 2013, , .		2
98	DisSetSim: An online system for calculating similarity between disease sets. , 2016, , .		2
99	A bucket index correction based method for compression of genomic sequencing data. , 2017, , .		2
100	Analysis for Early Seizure Detection System Based on Deep Learning Algorithm. , 2018, , .		2
101	An improved advanced fragment analysis-based classification and risk stratification of pediatric acute lymphoblastic leukemia. Cancer Cell International, 2019, 19, 110.	1.8	2
102	IBI: Identification of Biomarker Genes in Individual Tumor Samples. Frontiers in Genetics, 2019, 10, 1236.	1.1	2
103	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. Frontiers in Genetics, 2021, 12, 658352.	1.1	2
104	PanSVR: Pan-Genome Augmented Short Read Realignment for Sensitive Detection of Structural Variations. Frontiers in Genetics, 2021, 12, 731515.	1.1	2
105	MGMIN: A Normalization Method for Correcting Probe Design Bias in Illumina Infinium HumanMethylation450 BeadChips. Frontiers in Genetics, 2020, 11, 538492.	1.1	2
106	GONET: A Deep Network to Annotate Proteins via Recurrent Convolution Networks. , 2020, , .		2
107	Prediction performance of twelve tumor mutation burden panels in melanoma and non-small cell lung cancer. Critical Reviews in Oncology/Hematology, 2022, 169, 103573.	2.0	2
108	Prediction of the Disease Causal Genes Based on Heterogeneous Network and Multi-Feature Combination Method. Computational Biology and Chemistry, 2022, 97, 107639.	1.1	2

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109	Differentially Expressed Mutant Genes Reveal Potential Prognostic Markers For Lung Adenocarcinoma. , 2021, , .		2
110	DRBin: Metagenomic binning based on deep representation learning. Journal of Genetics and Genomics, 2021, , .	1.7	2
111	Multi-Agent System Negotiation Based on Expanded Contract Net Protocol Research. , 0, , .		1
112	Empirical bayes model comparisons for differential methylation analysis. , 2011, , .		1
113	Modelling non-stationary gene regulatory process with hidden Markov Dynamic Bayesian Network. , 2012, , .		1
114	DMcompress: Dynamic Markov models for bacterial genome compression. , 2016, , .		1
115	Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks. , 2018, , .		1
116	Fast variation-aware read alignment with deBGA-VARA. , 2018, , .		1
117	Evaluating individual genome similarity with a topic model. Bioinformatics, 2020, 36, 4757-4764.	1.8	1
118	A Pipeline for Reconstructing Somatic Copy Number Alternationâ€™s Subclonal Population-Based Next-Generation Sequencing Data. Frontiers in Genetics, 2019, 10, 1374.	1.1	1
119	Contents, Construction Methods, Data Resources, and Functions Comparative Analysis of Bacteria Databases. International Journal of Biological Sciences, 2020, 16, 838-848.	2.6	1
120	Fast and Accurate Classification of Meta-Genomics Long Reads With deSAMBA. Frontiers in Cell and Developmental Biology, 2021, 9, 643645.	1.8	1
121	IIMLP: integrated information-entropy-based method for LncRNA prediction. BMC Bioinformatics, 2021, 22, 243.	1.2	1
122	Assessment of Machine Learning Methods for Classification in Single Cell ATAC-seq. , 2020, , .		1
123	M2PP: a novel computational model for predicting drug-targeted pathogenic proteins. BMC Bioinformatics, 2022, 23, 7.	1.2	1
124	PocaCNV: A Tool to Detect Copy Number Variants from Population-Scale Genome Sequencing Data. , 2021, , .		1
125	Research and design of cooperative engagement system based on multi-agent. , 0, , .		0
126	rMFilter: acceleration of long read-based structure variation calling by chimeric read filtering. Bioinformatics, 2017, 33, 2750-2752.	1.8	0

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127	rCANID: read Clustering and Assembly-based Novel Insertion Detection tool. , 2018, , .		0
128	Optimizing gene set annotations combining GO structure and gene expression data. BMC Systems Biology, 2018, 12, 133.	3.0	0
129	Predicting candidate disease-related lncRNAs based on network random walk. , 2018, , .		0
130	Joint detection of germline and somatic copy number events in matched tumorâ€“normal sample pairs. Bioinformatics, 2019, 35, 4955-4961.	1.8	0
131	A Bidirectional Fuzzy Index and Approximate Search Algorithm for Next Generation Sequencing. , 2019, , .		0
132	DNMFilter_Indel: Filtering de novo Indels in Parent-Offspring Trios. , 2019, , .		0
133	SALT: a fast, memory-efficient and SNP-aware short read alignment tool. , 2019, , .		0
134	An Approach for Prediction of Enhancers Based on the Bayesian Model. , 2019, , .		0
135	Short Read Alignment Based on Maximal Approximate Match Seeds. Frontiers in Molecular Biosciences, 2020, 7, 572934.	1.6	0
136	An integrated approach for copy number variation discovery in parentâ€“offspring trios. Briefings in Bioinformatics, 2021, 22, .	3.2	0
137	Fast and SNP-aware short read alignment with SALT. BMC Bioinformatics, 2021, 22, 172.	1.2	0
138	Filtering de novo indels in parent-offspring trios. BMC Bioinformatics, 2020, 21, 547.	1.2	0