Yadong Wang

List of Publications by Citations

117 papers	2,834 citations	20 h-index	52 g-index
141 ext. papers	3,975 ext. citations	5.5 avg, IF	5.54 L-index

#	Paper	IF	Citations
117	miR2Disease: a manually curated database for microRNA deregulation in human disease. *Nucleic Acids Research*, **2009**, 37, D98-104	20.1	1041
116	Review of Drug Repositioning Approaches and Resources. *International Journal of Biological Sciences*, **2018**, 14, 1232-1244	11.2	246
115	Identifying and removing haplotypic duplication in primary genome assemblies. *Bioinformatics*, **2020**, 36, 2896-2898	7.2	222
114	Predicting human microRNA-disease associations based on support vector machine. *International Journal of Data Mining and Bioinformatics*, **2013**, 8, 282-93	0.5	160
113	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. *Nucleic Acids Research*, **2015**, 43, D193-6	20.1	104
112	SemFunSim: a new method for measuring disease similarity by integrating semantic and gene functional association. *PLoS ONE*, **2014**, 9, e99415	3.7	83
111	MeDReaders: a database for transcription factors that bind to methylated DNA. *Nucleic Acids Research*, **2018**, 46, D146-D151	20.1	64
110	Low-rank and sparse decomposition based shape model and probabilistic atlas for automatic pathological organ segmentation. *Medical Image Analysis*, **2017**, 38, 30-49	15.4	46
109	Shape-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, 817-26	3.9	43
108	Extending gene ontology with gene association networks. *Bioinformatics*, **2016**, 32, 1185-94	7.2	37
107	Identifying term relations cross different gene ontology categories. *BMC Bioinformatics*, **2017**, 18, 573	3.6	36
106	TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChIP-Seq data. *BioMed Research International*, **2014**, 2014, 317642	3	35
105	Long-read-based human genomic structural variation detection with cuteSV. *Genome Biology*, **2020**, 21, 189	18.3	35
104	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. *Nature Communications*, **2021**, 12, 266	17.4	33
103	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. *BMC Bioinformatics*, **2015**, 16, 44	3.6	30
102	Predicting disease-related genes using integrated biomedical networks. *BMC Genomics*, **2017**, 18, 1043	4.5	29
101	Integrate GWAS, eQTL, and mQTL Data to Identify Alzheimer's Disease-Related Genes. *Frontiers in Genetics*, **2019**, 10, 1021	4.5	27

100	A gradient-boosting approach for filtering de novo mutations in parent-offspring trios. *Bioinformatics*, **2014**, 30, 1830-6	7.2	24
99	Comparison among dimensionality reduction techniques based on Random Projection for cancer classification. *Computational Biology and Chemistry*, **2016**, 65, 165-172	3.6	23
98	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. *BMC Genomics*, **2016**, 17 Suppl 5, 530	4.5	20
97	A framework for analyzing DNA methylation data from Illumina Infinium HumanMethylation450 BeadChip. *BMC Bioinformatics*, **2018**, 19, 115	3.6	18
96	Prediction for High Risk Clinical Symptoms of Epilepsy Based on Deep Learning Algorithm. *IEEE Access*, **2018**, 6, 77596-77605	3.5	18
95	An approach for prioritizing disease-related microRNAs based on genomic data integration **2010**,		17
94	deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. *Genome Biology*, **2019**, 20, 274	18.3	17
93	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. *Human Genetics*, **2017**, 136, 1279-1289	6.3	15
92	DisSetSim: an online system for calculating similarity between disease sets. *Journal of Biomedical Semantics*, **2017**, 8, 28	2.2	14
91	A generalized topological entropy for analyzing the complexity of DNA sequences. *PLoS ONE*, **2014**, 9, e88519	3.7	14
90	Improving alignment accuracy on homopolymer regions for semiconductor-based sequencing technologies. *BMC Genomics*, **2016**, 17 Suppl 7, 521	4.5	13
89	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. *BioMed Research International*, **2016**, 2016, 4130861	3	13
88	PERGA: a paired-end read guided de novo assembler for extending contigs using SVM and look ahead approach. *PLoS ONE*, **2014**, 9, e114253	3.7	12
87	Predicting circRNA-Disease Associations Based on circRNA Expression Similarity and Functional Similarity. *Frontiers in Genetics*, **2019**, 10, 832	4.5	11
86	TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain. *Bioinformatics*, **2019**, 35, i200-i207	7.2	11
85	Predicting human microRNA-disease associations based on support vector machine **2010**,		11
84	Extracting a biologically latent space of lung cancer epigenetics with variational autoencoders. *BMC Bioinformatics*, **2019**, 20, 568	3.6	11
83	FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. *Methods*, **2020**, 173, 83-93	4.6	11

82	Analyzing large-scale samples confirms the association between the rs1051730 polymorphism and lung cancer susceptibility. *Scientific Reports*, **2015**, 5, 15642	4.9	10
81	Weighted Network-Based Inference of Human MicroRNA-Disease Associations **2010**,		10
80	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. *Frontiers in Genetics*, **2019**, 10, 1309	4.5	9
79	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. *BMC Bioinformatics*, **2017**, 18, 270	3.6	9
78	A deep learning approach for filtering structural variants in short read sequencing data. *Briefings in Bioinformatics*, **2021**, 22,	13.4	9
77	CDL4CDRP: A Collaborative Deep Learning Approach for Clinical Decision and Risk Prediction. *Processes*, **2019**, 7, 265	2.9	8
76	Joint detection of copy number variations in parent-offspring trios. *Bioinformatics*, **2016**, 32, 1130-7	7.2	8
75	Statistical Approaches for the Construction and Interpretation of Human Protein-Protein Interaction Network. *BioMed Research International*, **2016**, 2016, 5313050	3	8
74	ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. *BMC Bioinformatics*, **2019**, 20, 573	3.6	8
73	Exploring DNA Methylation Data of Lung Cancer Samples with Variational Autoencoders **2018**,		8
72	Hidden Markov induced Dynamic Bayesian Network for recovering time evolving gene regulatory networks. *Scientific Reports*, **2015**, 5, 17841	4.9	7
71	Identifying Liver Cancer-Related Enhancer SNPs by Integrating GWAS and Histone Modification ChIP-seq Data. *BioMed Research International*, **2016**, 2016, 2395341	3	7
70	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. *BMC Bioinformatics*, **2019**, 20, 574	3.6	7
69	ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization **2018**,		7
68	Identifying Protein Biomarkers in Blood for Alzheimer's Disease. *Frontiers in Cell and Developmental Biology*, **2020**, 8, 472	5.7	6
67	FNSemSim: An improved disease similarity method based on network fusion **2017**,		6
66	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	1	6
65	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. *BioMed Research International*, **2015**, 2015, 757530	3	6

64	The minimum feature subset selection problem. *Journal of Computer Science and Technology*, **1997**, 12, 145-153	1.7	6
63	Identifying Alzheimerâs Disease-related miRNA Based on Semi-clustering. *Current Gene Therapy*, **2019**, 19, 216-223	4.3	6
62	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	5.8	6
61	Pan-Cancer Classification Based on Self-Normalizing Neural Networks and Feature Selection. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 766	5.8	6
60	DeepDNA: a hybrid convolutional and recurrent neural network for compressing human mitochondrial genomes **2018**,		6
59	Integrated entropy-based approach for analyzing exons and introns in DNA sequences. *BMC Bioinformatics*, **2019**, 20, 283	3.6	5
58	An Approximate Bufferless Network-on-Chip. *IEEE Access*, **2019**, 7, 141516-141532	3.5	5
57	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. *Current Bioinformatics*, **2020**, 15, 574-580	4.7	5
56	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. *Bioinformatics* , **2021**, 37, 2209-2211	7.2	5
55	LncDisAP: a computation model for LncRNA-disease association prediction based on multiple biological datasets. *BMC Bioinformatics*, **2019**, 20, 582	3.6	5
54	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. *BMC Bioinformatics*, **2021**, 22, 403	3.6	5
53	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. *Briefings in Bioinformatics*, **2021**,	13.4	5
52	3D surface voxel tracing corrector for accurate bone segmentation. *International Journal of Computer Assisted Radiology and Surgery*, **2018**, 13, 1549-1563	3.9	4
51	Privacy-Preserving Data Mining Based on Sample Selection and Singular Value Decomposition **2011** ,		4
50	Back propagation based on selective attention for fast convergence of training neural network		4
49	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. *Protein and Peptide Letters*, **2020**, 27, 295-302	1.9	4
48	Measuring phenotype semantic similarity using Human Phenotype Ontology **2016**,		4
47	A network-based pathway-expanding approach for pathway analysis. *BMC Bioinformatics*, **2016**, 17, 536	3.6	4

46	rMETL: sensitive mobile element insertion detection with long read realignment. *Bioinformatics*, **2019**, 35, 3484-3486	7.2	4
45	An automated quality control pipeline for eQTL analysis with RNA-seq data **2019**,		4
44	A network-based pathway-extending approach using DNA methylation and gene expression data to identify altered pathways. *Scientific Reports*, **2019**, 9, 11853	4.9	3
43	Segmentation of the hip joint in CT volumes using adaptive thresholding classification and normal direction correction **2013**, 36, 1059-1072		3
42	Reconstruct gene regulatory network using slice pattern model. *BMC Genomics*, **2009**, 10 Suppl 1, S2	4.5	3
41	Human mitochondrial genome compression using machine learning techniques. *Human Genomics*, **2019**, 13, 49	6.8	3
40	deSPI: efficient classification of metagenomics reads with lightweight de Bruijn graph-based reference indexing **2018**,		3
39	An online tool for measuring and visualizing phenotype similarities using HPO. *BMC Genomics*, **2018** , 19, 571	4.5	3
38	Prognostic prediction of carcinoma by a differential-regulatory-network-embedded deep neural network. *Computational Biology and Chemistry*, **2020**, 88, 107317	3.6	2
37	Finding disagreement pathway signatures and constructing an ensemble model for cancer classification. *Scientific Reports*, **2017**, 7, 10044	4.9	2
36	Automatic centerline detection of small three-dimensional vessel structures. *Journal of Electronic Imaging*, **2014**, 23, 013007	0.7	2
35	PmDNE: Prediction of miRNA-Disease Association Based on Network Embedding and Network Similarity Analysis. *BioMed Research International*, **2020**, 2020, 6248686	3	2
34	Prediction performance of twelve tumor mutation burden panels in melanoma and non-small cell lung cancer.. *Critical Reviews in Oncology/Hematology*, **2021**, 169, 103573	7	2
33	MGMIN: A Normalization Method for Correcting Probe Design Bias in Illumina Infinium HumanMethylation450 BeadChips. *Frontiers in Genetics*, **2020**, 11, 538492	4.5	2
32	ScGSLC: An unsupervised graph similarity learning framework for single-cell RNA-seq data clustering. *Computational Biology and Chemistry*, **2021**, 90, 107415	3.6	2
31	Identification of Parkinsonâs Disease-Causing Genes via Omics Data. *Frontiers in Genetics*, **2021**, 12, 712164	4.5	2
30	Evaluating individual genome similarity with a topic model. *Bioinformatics*, **2020**, 36, 4757-4764	7.2	1
29	A Pipeline for Reconstructing Somatic Copy Number Alternationâs Subclonal Population-Based Next-Generation Sequencing Data. *Frontiers in Genetics*, **2019**, 10, 1374	4.5	1

28	Contents, Construction Methods, Data Resources, and Functions Comparative Analysis of Bacteria Databases. *International Journal of Biological Sciences*, **2020**, 16, 838-848	11.2	1
27	PGsim: A Comprehensive and Highly Customizable Personal Genome Simulator. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 28	5.8	1
26	Modelling non-stationary gene regulatory process with hidden Markov Dynamic Bayesian Network **2012**,		1
25	Factor graph-aggregated heterogeneous network embedding for disease-gene association prediction. *BMC Bioinformatics*, **2021**, 22, 165	3.6	1
24	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. *Frontiers in Genetics*, **2021**, 12, 658352	4.5	1
23	IBI: Identification of Biomarker Genes in Individual Tumor Samples. *Frontiers in Genetics*, **2019**, 10, 1236	4.5	1
22	Identifying Candidate Diseases-related Metabolites Based on Disease Similarity **2018**,		1
21	Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks **2018**,		1
20	Fast variation-aware read alignment with deBGA-VARA **2018**,		1
19	Analysis for Early Seizure Detection System Based on Deep Learning Algorithm **2018**,		1
18	Explore potential disease related metabolites based on latent factor model.. *BMC Genomics*, **2022**, 23, 269	4.5	1
17	Differentially Expressed Mutant Genes Reveal Potential Prognostic Markers For Lung Adenocarcinoma **2021**,		1
16	DRBin: Metagenomic binning based on deep representation learning.. *Journal of Genetics and Genomics*, **2021**,	4	1
15	An improved advanced fragment analysis-based classification and risk stratification of pediatric acute lymphoblastic leukemia. *Cancer Cell International*, **2019**, 19, 110	6.4	0
14	Prediction of the disease causal genes based on heterogeneous network and multi-feature combination method.. *Computational Biology and Chemistry*, **2022**, 97, 107639	3.6	0
13	A Bipartite Network Module-Based Project to Predict Pathogen-Host Association. *Frontiers in Genetics*, **2019**, 10, 1357	4.5	0
12	IIMLP: integrated information-entropy-based method for LncRNA prediction. *BMC Bioinformatics*, **2021**, 22, 243	3.6	0
11	Pan-Cancer Metastasis Prediction Based on Graph Deep Learning Method. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 675978	5.7	0

10	PanSVR: Pan-Genome Augmented Short Read Realignment for Sensitive Detection of Structural Variations. *Frontiers in Genetics*, **2021**, 12, 731515	4.5	0
9	rMFilter: acceleration of long read-based structure variation calling by chimeric read filtering. *Bioinformatics*, **2017**, 33, 2750-2752	7.2	
8	Joint detection of germline and somatic copy number events in matched tumor-normal sample pairs. *Bioinformatics*, **2019**, 35, 4955-4961	7.2	
7	M2PP: a novel computational model for predicting drug-targeted pathogenic proteins.. *BMC Bioinformatics*, **2022**, 23, 7	3.6	
6	Filtering de novo indels in parent-offspring trios. *BMC Bioinformatics*, **2020**, 21, 547	3.6	
5	Short Read Alignment Based on Maximal Approximate Match Seeds. *Frontiers in Molecular Biosciences*, **2020**, 7, 572934	5.6	
4	Fast and Accurate Classification of Meta-Genomics Long Reads With deSAMBA. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 643645	5.7	
3	Optimizing gene set annotations combining GO structure and gene expression data. *BMC Systems Biology*, **2018**, 12, 133	3.5	
2	Fast and SNP-aware short read alignment with SALT. *BMC Bioinformatics*, **2021**, 22, 172	3.6	
1	OTUCD: Unsupervised GCN based metagenomics non-overlapping community detection.. *Computational Biology and Chemistry*, **2022**, 98, 107670	3.6	