Guohua Wang

List of Publications by Year
in descending order

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62

papers

4,743

citations

236925

25

h-index

161849

54

g-index

68

all docs

68

docs citations

68

times ranked

5998

citing authors

#	Article	IF	Citations
1	miR2Disease: a manually curated database for microRNA deregulation in human disease. Nucleic Acids Research, 2009, 37, D98-D104.	14.5	1,255
2	Transcription factors as readers and effectors of DNA methylation. Nature Reviews Genetics, 2016, 17, 551-565.	16.3	482
3	Prioritization of disease microRNAs through a human phenome-microRNAome network. BMC Systems Biology, 2010, 4, S2.	3.0	335
4	Estradiol-regulated microRNAs control estradiol response in breast cancer cells. Nucleic Acids Research, 2009, 37, 4850-4861.	14.5	310
5	Gene regulatory networks controlling vertebrate retinal regeneration. Science, 2020, 370, .	12.6	248
6	Predicting human microRNA-disease associations based on support vector machine. International Journal of Data Mining and Bioinformatics, 2013, 8, 282.	0.1	208
7	Similarity computation strategies in the microRNA-disease network: a survey. Briefings in Functional Genomics, 2016, 15, elv024.	2.7	172
8	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. Bioinformatics, 2015, 31, 2475-2481.	4.1	136
9	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. BMC Genomics, 2015, 16, 49.	2.8	132
10	Transcription factor and microRNA regulation in androgen-dependent and -independent prostate cancer cells. BMC Genomics, 2008, 9, S22.	2.8	108
11	MeDReaders: a database for transcription factors that bind to methylated DNA. Nucleic Acids Research, 2018, 46, D146-D151.	14.5	94
12	AKT Alters Genome-Wide Estrogen Receptor Î± Binding and Impacts Estrogen Signaling in Breast Cancer. Molecular and Cellular Biology, 2008, 28, 7487-7503.	2.3	87
13	Potential roles of microRNAs in regulating long intergenic noncoding RNAs. BMC Medical Genomics, 2013, 6, S7.	1.5	71
14	ECFS-DEA: an ensemble classifier-based feature selection for differential expression analysis on expression profiles. BMC Bioinformatics, 2020, 21, 43.	2.6	66
15	BP4RNAseq: a babysitter package for retrospective and newly generated RNA-seq data analyses using both alignment-based and alignment-free quantification method. Bioinformatics, 2021, 37, 1319-1321.	4.1	64
16	Signal Transducers and Activators of Transcription-1 (STAT1) Regulates microRNA Transcription in Interferon Î³-Stimulated HeLa Cells. PLoS ONE, 2010, 5, e11794.	2.5	61
17	BinMemPredict: a Web Server and Software for Predicting Membrane Protein Types. Current Proteomics, 2013, 10, 2-9.	0.3	59
18	Pro-permeability Factors in Diabetic Macular Edema; the Diabetic Macular Edema Treated With Ozurdex Trial. American Journal of Ophthalmology, 2016, 168, 13-23.	3.3	56

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19	ARQiv-HTS, a versatile whole-organism screening platform enabling in vivo drug discovery at high-throughput rates. Nature Protocols, 2016, 11, 2432-2453.	12.0	50
20	Methods of MicroRNA Promoter Prediction and Transcription Factor Mediated Regulatory Network. BioMed Research International, 2017, 2017, 1-8.	1.9	50
21	RNA Polymerase II Binding Patterns Reveal Genomic Regions Involved in MicroRNA Gene Regulation. PLoS ONE, 2010, 5, e13798.	2.5	49
22	SIDD: A Semantically Integrated Database towards a Global View of Human Disease. PLoS ONE, 2013, 8, e75504.	2.5	46
23	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	2.8	46
24	Drugâ€“target interaction predication via multi-channel graph neural networks. Briefings in Bioinformatics, 2022, 23, .	6.5	38
25	Pro-Permeability Factors After Dexamethasone Implant in Retinal Vein Occlusion; the Ozurdex for Retinal Vein Occlusion (ORVO) Study. American Journal of Ophthalmology, 2015, 160, 313-321.e19.	3.3	35
26	A deep learning approach for filtering structural variants in short read sequencing data. Briefings in Bioinformatics, 2021, 22, .	6.5	32
27	The stacking strategy-based hybrid framework for identifying non-coding RNAs. Briefings in Bioinformatics, 2021, 22, .	6.5	28
28	Supervised graph co-contrastive learning for drugâ€“target interaction prediction. Bioinformatics, 2022, 38, 2847-2854.	4.1	26
29	Identification of transcription factor and microRNA binding sites in responsible to fetal alcohol syndrome. BMC Genomics, 2008, 9, S19.	2.8	24
30	Continuous culture of urine-derived bladder cancer cells for precision medicine. Protein and Cell, 2019, 10, 902-907.	11.0	23
31	Assessing the model transferability for prediction of transcription factor binding sites based on chromatin accessibility. BMC Bioinformatics, 2017, 18, 355.	2.6	22
32	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. Nature Communications, 2021, 12, 795.	12.8	22
33	Identifying Plant Pentatricopeptide Repeat Proteins Using a Variable Selection Method. Frontiers in Plant Science, 2021, 12, 506681.	3.6	21
34	An approach for prioritizing disease-related microRNAs based on genomic data integration. , 2010, , .		20
35	Predicting human microRNA-disease associations based on support vector machine. , 2010, , .		16
36	Identification of regulatory regions of bidirectional genes in cervical cancer. BMC Medical Genomics, 2013, 6, S5.	1.5	16

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37	An interpretable deep learning workflow for discovering subvisual abnormalities in CT scans of COVID-19 inpatients and survivors. Nature Machine Intelligence, 2022, 4, 494-503.	16.0	16
38	Effects of DNA Methylation on TFs in Human Embryonic Stem Cells. Frontiers in Genetics, 2021, 12, 639461.	2.3	15
39	Evaluating disease similarity based on gene network reconstruction and representation. Bioinformatics, 2021, 37, 3579-3587.	4.1	15
40	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. ELife, 2021, 10, .	6.0	15
41	A survey on computational methods in discovering protein inhibitors of SARS-CoV-2. Briefings in Bioinformatics, 2022, 23, .	6.5	15
42	Detection of transcription factors binding to methylated DNA by deep recurrent neural network. Briefings in Bioinformatics, 2022, 23, .	6.5	14
43	Chromatin structure characteristics of pre-miRNA genomic sequences. BMC Genomics, 2011, 12, 329.	2.8	13
44	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. BioMed Research International, 2015, 2015, 1-7.	1.9	13
45	dPromoter-XGBoost: Detecting promoters and strength by combining multiple descriptors and feature selection using XGBoost. Methods, 2022, 204, 215-222.	3.8	13
46	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
47	Identification of methylation states of DNA regions for Illumina methylation BeadChip. BMC Genomics, 2020, 21, 672.	2.8	12
48	Identification of Diagnostic Markers for Breast Cancer Based on Differential Gene Expression and Pathway Network. Frontiers in Cell and Developmental Biology, 2021, 9, 811585.	3.7	12
49	i6mA-Vote: Cross-Species Identification of DNA N6-Methyladenine Sites in Plant Genomes Based on Ensemble Learning With Voting. Frontiers in Plant Science, 2022, 13, 845835.	3.6	11
50	ReRF-Pred: predicting amyloidogenic regions of proteins based on their pseudo amino acid composition and tripeptide composition. BMC Bioinformatics, 2021, 22, 545.	2.6	9
51	Identification of Prognostic Biomarkers for Bladder Cancer Based on DNA Methylation Profile. Frontiers in Cell and Developmental Biology, 2021, 9, 817086.	3.7	8
52	Bioinformatics Methods and Biological Interpretation for Next-Generation Sequencing Data. BioMed Research International, 2015, 2015, 1-2.	1.9	7
53	Polycomb proteins control floral determinacy by H3K27me3-mediated repression of pluripotency genes in <i>Arabidopsis thaliana</i>. Journal of Experimental Botany, 2022, 73, 2385-2402.	4.8	7
54	BYASE: a Python library for estimating gene and isoform level allele-specific expression. Bioinformatics, 2020, 36, 4955-4956.	4.1	4

#	ARTICLE	IF	CITATIONS
55	scESI: evolutionary sparse imputation for single-cell transcriptomes from nearest neighbor cells. Briefings in Bioinformatics, 2022, 23, .	6.5	4
56	AlignGraph2: similar genome-assisted reassembly pipeline for PacBio long reads. Briefings in Bioinformatics, 2021, 22, .	6.5	3
57	xIP-seq Platform: An Integrative Framework for High-Throughput Sequencing Data Analysis. , 2009, , .		2
58	Evaluating individual genome similarity with a topic model. Bioinformatics, 2020, 36, 4757-4764.	4.1	1
59	Ensemble classification based signature discovery for cancer diagnosis in RNA expression profiles across different platforms. Briefings in Bioinformatics, 0, , .	6.5	1
60	AFS-DEA: An automatic feature selection platform for differential expression analysis. , 2020, , .		0
61	SLDMS: A Tool for Calculating the Overlapping Regions of Sequences. Frontiers in Plant Science, 2021, 12, 813036.	3.6	0
62	Decoding the molecular regulation mechanism of plant architecture in woody plants. New Phytologist, 2022, 235, 8-10.	7.3	0