

Guohua Wang

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

4,743
citations

236925

25
h-index

161849

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g-index

68
all docs

68
docs citations

68
times ranked

5998
citing authors

#	ARTICLE	IF	CITATIONS
1	A survey on computational methods in discovering protein inhibitors of SARS-CoV-2. Briefings in Bioinformatics, 2022, 23, .	6.5	15
2	Drug-target interaction predication via multi-channel graph neural networks. Briefings in Bioinformatics, 2022, 23, .	6.5	38
3	Detection of transcription factors binding to methylated DNA by deep recurrent neural network. Briefings in Bioinformatics, 2022, 23, .	6.5	14
4	dPromoter-XGBoost: Detecting promoters and strength by combining multiple descriptors and feature selection using XGBoost. Methods, 2022, 204, 215-222.	3.8	13
5	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
6	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
7	Supervised graph co-contrastive learning for drug-target interaction prediction. Bioinformatics, 2022, 38, 2847-2854.	4.1	26
8	scESI: evolutionary sparse imputation for single-cell transcriptomes from nearest neighbor cells. Briefings in Bioinformatics, 2022, 23, .	6.5	4
9	Decoding the molecular regulation mechanism of plant architecture in woody plants. New Phytologist, 2022, 235, 8-10.	7.3	0
10	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
11	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
12	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
13	Effects of DNA Methylation on TFs in Human Embryonic Stem Cells. Frontiers in Genetics, 2021, 12, 639461.	2.3	15
14	AlignGraph2: similar genome-assisted reassembly pipeline for PacBio long reads. Briefings in Bioinformatics, 2021, 22, .	6.5	3
15	Identifying Plant Pentatricopeptide Repeat Proteins Using a Variable Selection Method. Frontiers in Plant Science, 2021, 12, 506681.	3.6	21
16	The stacking strategy-based hybrid framework for identifying non-coding RNAs. Briefings in Bioinformatics, 2021, 22, .	6.5	28
17	Evaluating disease similarity based on gene network reconstruction and representation. Bioinformatics, 2021, 37, 3579-3587.	4.1	15
18	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. ELife, 2021, 10, .	6.0	15

#	ARTICLE	IF	CITATIONS
19	A deep learning approach for filtering structural variants in short read sequencing data. Briefings in Bioinformatics, 2021, 22, .	6.5	32
20	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
21	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
22	Identification of Prognostic Biomarkers for Bladder Cancer Based on DNA Methylation Profile. Frontiers in Cell and Developmental Biology, 2021, 9, 817086.	3.7	8
23	SLDMS: A Tool for Calculating the Overlapping Regions of Sequences. Frontiers in Plant Science, 2021, 12, 813036.	3.6	0
24	Gene regulatory networks controlling vertebrate retinal regeneration. Science, 2020, 370, .	12.6	248
25	BYASE: a Python library for estimating gene and isoform level allele-specific expression. Bioinformatics, 2020, 36, 4955-4956.	4.1	4
26	Evaluating individual genome similarity with a topic model. Bioinformatics, 2020, 36, 4757-4764.	4.1	1
27	Identification of methylation states of DNA regions for Illumina methylation BeadChip. BMC Genomics, 2020, 21, 672.	2.8	12
28	ECFS-DEA: an ensemble classifier-based feature selection for differential expression analysis on expression profiles. BMC Bioinformatics, 2020, 21, 43.	2.6	66
29	AFS-DEA: An automatic feature selection platform for differential expression analysis. , 2020, , .		0
30	Continuous culture of urine-derived bladder cancer cells for precision medicine. Protein and Cell, 2019, 10, 902-907.	11.0	23
31	MeDReaders: a database for transcription factors that bind to methylated DNA. Nucleic Acids Research, 2018, 46, D146-D151.	14.5	94
32	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	2.8	46
33	Methods of MicroRNA Promoter Prediction and Transcription Factor Mediated Regulatory Network. BioMed Research International, 2017, 2017, 1-8.	1.9	50
34	Assessing the model transferability for prediction of transcription factor binding sites based on chromatin accessibility. BMC Bioinformatics, 2017, 18, 355.	2.6	22
35	Similarity computation strategies in the microRNA-disease network: a survey. Briefings in Functional Genomics, 2016, 15, elv024.	2.7	172
36	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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37	Transcription factors as readers and effectors of DNA methylation. <i>Nature Reviews Genetics</i> , 2016, 17, 551-565.	16.3	482
38	ARQiv-HTS, a versatile whole-organism screening platform enabling in vivo drug discovery at high-throughput rates. <i>Nature Protocols</i> , 2016, 11, 2432-2453.	12.0	50
39	Bioinformatics Methods and Biological Interpretation for Next-Generation Sequencing Data. <i>BioMed Research International</i> , 2015, 2015, 1-2.	1.9	7
40	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. <i>BioMed Research International</i> , 2015, 2015, 1-7.	1.9	13
41	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. <i>BMC Genomics</i> , 2015, 16, 49.	2.8	132
42	Pro-Permeability Factors After Dexamethasone Implant in Retinal Vein Occlusion; the Ozurdex for Retinal Vein Occlusion (ORVO) Study. <i>American Journal of Ophthalmology</i> , 2015, 160, 313-321.e19.	3.3	35
43	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. <i>Bioinformatics</i> , 2015, 31, 2475-2481.	4.1	136
44	Identification of regulatory regions of bidirectional genes in cervical cancer. <i>BMC Medical Genomics</i> , 2013, 6, S5.	1.5	16
45	Potential roles of microRNAs in regulating long intergenic noncoding RNAs. <i>BMC Medical Genomics</i> , 2013, 6, S7.	1.5	71
46	Predicting human microRNA-disease associations based on support vector machine. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 8, 282.	0.1	208
47	BinMemPredict: a Web Server and Software for Predicting Membrane Protein Types. <i>Current Proteomics</i> , 2013, 10, 2-9.	0.3	59
48	SIDD: A Semantically Integrated Database towards a Global View of Human Disease. <i>PLoS ONE</i> , 2013, 8, e75504.	2.5	46
49	Chromatin structure characteristics of pre-miRNA genomic sequences. <i>BMC Genomics</i> , 2011, 12, 329.	2.8	13
50	Prioritization of disease microRNAs through a human phenome-microRNAome network. <i>BMC Systems Biology</i> , 2010, 4, S2.	3.0	335
51	Signal Transducers and Activators of Transcription-1 (STAT1) Regulates microRNA Transcription in Interferon β -Stimulated HeLa Cells. <i>PLoS ONE</i> , 2010, 5, e11794.	2.5	61
52	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
53	Predicting human microRNA-disease associations based on support vector machine. , 2010, , .		16
54	An approach for prioritizing disease-related microRNAs based on genomic data integration. , 2010, , .		20

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55	RNA Polymerase II Binding Patterns Reveal Genomic Regions Involved in MicroRNA Gene Regulation. PLoS ONE, 2010, 5, e13798.	2.5	49
56	miR2Disease: a manually curated database for microRNA deregulation in human disease. Nucleic Acids Research, 2009, 37, D98-D104.	14.5	1,255
57	Estradiol-regulated microRNAs control estradiol response in breast cancer cells. Nucleic Acids Research, 2009, 37, 4850-4861.	14.5	310
58	xIP-seq Platform: An Integrative Framework for High-Throughput Sequencing Data Analysis. , 2009, , .		2
59	Identification of transcription factor and microRNA binding sites in responsible to fetal alcohol syndrome. BMC Genomics, 2008, 9, S19.	2.8	24
60	Transcription factor and microRNA regulation in androgen-dependent and -independent prostate cancer cells. BMC Genomics, 2008, 9, S22.	2.8	108
61	AKT Alters Genome-Wide Estrogen Receptor $\hat{\pm}$ Binding and Impacts Estrogen Signaling in Breast Cancer. Molecular and Cellular Biology, 2008, 28, 7487-7503.	2.3	87
62	Ensemble classification based signature discovery for cancer diagnosis in RNA expression profiles across different platforms. Briefings in Bioinformatics, 0, , .	6.5	1