

Haiyan Hu

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

939
citations

430874

18
h-index

526287

27
g-index

61
all docs

61
docs citations

61
times ranked

1274
citing authors

#	ARTICLE	IF	CITATIONS
1	A systematic study of motif pairs that may facilitate enhancer-promoter interactions. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.5	2
2	Computational analyses of bacterial strains from shotgun reads. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
3	A deep learning method for miRNA/isomiR target detection. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
4	A systematic evaluation of the computational tools for ligand-receptor-based cell-cell interaction inference. <i>Briefings in Functional Genomics</i> , 2022, 21, 339-356.	2.7	7
5	Computational annotation of miRNA transcription start sites. <i>Briefings in Bioinformatics</i> , 2021, 22, 380-392.	6.5	23
6	mixtureS: a novel tool for bacterial strain genome reconstruction from reads. <i>Bioinformatics</i> , 2021, 37, 575-577.	4.1	10
7	Interpretation of deep learning in genomics and epigenomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	67
8	An intriguing characteristic of enhancer-promoter interactions. <i>BMC Genomics</i> , 2021, 22, 163.	2.8	3
9	A two-stream convolutional neural network for microRNA transcription start site feature integration and identification. <i>Scientific Reports</i> , 2021, 11, 5625.	3.3	7
10	A systematic evaluation of the computational tools for lncRNA identification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
11	Shared distal regulatory regions may contribute to the coordinated expression of human ribosomal protein genes. <i>Genomics</i> , 2020, 112, 2886-2893.	2.9	5
12	Vannilic acid ameliorates hyperglycemia-induced oxidative stress and inflammation in streptozotocin-induced diabetic rats. <i>Journal of King Saud University - Science</i> , 2020, 32, 2905-2911.	3.5	12
13	Position-wise binding preference is important for miRNA target site prediction. <i>Bioinformatics</i> , 2020, 36, 3680-3686.	4.1	6
14	EPIP: a novel approach for condition-specific enhancer-promoter interaction prediction. <i>Bioinformatics</i> , 2019, 35, 3877-3883.	4.1	33
15	Improving miRNA Target Prediction Using CLASH Data. <i>Methods in Molecular Biology</i> , 2019, 1970, 75-83.	0.9	4
16	BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631.	4.1	18
17	Application of Deep Learning Models to MicroRNA Transcription Start Site Identification. , 2019, , .		4
18	CCmiR: a computational approach for competitive and cooperative microRNA binding prediction. <i>Bioinformatics</i> , 2018, 34, 198-206.	4.1	10

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19	Urinary bladder hypertrophy characteristic of male ROMK Bartter TM s mice does not occur in female mice. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2018, 314, R334-R341.	1.8	4
20	FlexSLiM. , 2018, , .		0
21	When old metagenomic data meet newly sequenced genomes, a case study. <i>PLoS ONE</i> , 2018, 13, e0198773.	2.5	7
22	Prognostic cancer gene signatures share common regulatory motifs. <i>Scientific Reports</i> , 2017, 7, 4750.	3.3	27
23	rRNAFilter: A Fast Approach for Ribosomal RNA Read Removal Without a Reference Database. <i>Journal of Computational Biology</i> , 2017, 24, 368-375.	1.6	11
24	Discover the semantic structure of human reference epigenome by differential latent dirichlet allocation. , 2017, , .		1
25	PETModule: a motif module based approach for enhancer target gene prediction. <i>Scientific Reports</i> , 2016, 6, 30043.	3.3	35
26	MBMC: An Effective Markov Chain Approach for Binning Metagenomic Reads from Environmental Shotgun Sequencing Projects. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 470-479.	2.0	12
27	Integrative analyses shed new light on human ribosomal protein gene regulation. <i>Scientific Reports</i> , 2016, 6, 28619.	3.3	25
28	TarPmiR: a new approach for microRNA target site prediction. <i>Bioinformatics</i> , 2016, 32, 2768-2775.	4.1	144
29	PreDREM: a database of predicted DNA regulatory motifs from 349 human cell and tissue samples. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	3
30	Systematic discovery of cofactor motifs from ChIP-seq data by SIOMICS. <i>Methods</i> , 2015, 79-80, 47-51.	3.8	23
31	MBBC: an efficient approach for metagenomic binning based on clustering. <i>BMC Bioinformatics</i> , 2015, 16, 36.	2.6	23
32	Comprehensive discovery of DNA motifs in 349 human cells and tissues reveals new features of motifs. <i>Nucleic Acids Research</i> , 2015, 43, 74-83.	14.5	13
33	MicroRNA modules prefer to bind weak and unconventional target sites. <i>Bioinformatics</i> , 2015, 31, 1366-1374.	4.1	21
34	SIOMICS: a novel approach for systematic identification of motifs in ChIP-seq data. <i>Nucleic Acids Research</i> , 2014, 42, e35-e35.	14.5	26
35	Computational discovery of feature patterns in nucleosomal DNA sequences. <i>Genomics</i> , 2014, 104, 87-95.	2.9	1
36	H3K4me2 reliably defines transcription factor binding regions in different cells. <i>Genomics</i> , 2014, 103, 222-228.	2.9	85

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37	CHIPModule: systematic discovery of transcription factors and their cofactors from ChIP-seq data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 320-31.	0.7	8
38	Thousands of Cis-Regulatory Sequence Combinations Are Shared by Arabidopsis and Poplar. Plant Physiology, 2012, 158, 145-155.	4.8	29
39	Motif analysis unveils the possible co-regulation of chloroplast genes and nuclear genes encoding chloroplast proteins. Plant Molecular Biology, 2012, 80, 177-187.	3.9	3
40	Systematic Prediction of cis-Regulatory Elements in the Chlamydomonas reinhardtii Genome Using Comparative Genomics. Plant Physiology, 2012, 160, 613-623.	4.8	25
41	CHIPMODULE: SYSTEMATIC DISCOVERY OF TRANSCRIPTION FACTORS AND THEIR COFACTORS FROM CHIP-SEQ DATA. , 2012, , .		10
42	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. Statistics in Biosciences, 2012, 4, 157-176.	1.2	4
43	Transcriptional regulation of co-expressed microRNA target genes. Genomics, 2011, 98, 445-452.	2.9	43
44	Systematic identification of conserved motif modules in the human genome. BMC Genomics, 2010, 11, 567.	2.8	28
45	Mining patterns in disease classification forests. Journal of Biomedical Informatics, 2010, 43, 820-827.	4.3	7
46	An efficient algorithm to identify coordinately activated transcription factors. Genomics, 2010, 95, 143-150.	2.9	4
47	Whole genome identification of target genes of transcription factors. , 2010, , .		0
48	Hierarchical order of gene expression levels. , 2010, , .		0
49	A new measurement of sequence conservation. BMC Genomics, 2009, 10, 623.	2.8	4
50	An Efficient Method to Identify Conditionally Activated Transcription Factors and their Corresponding Signal Transduction Pathway Segments. Bioinformatics and Biology Insights, 2009, 3, BBI.S3485.	2.0	0
51	MOPAT: a graph-based method to predict recurrent cis-regulatory modules from known motifs. Nucleic Acids Research, 2008, 36, 4488-4497.	14.5	29
52	Networking pathways unveils association between obesity and non-insulin dependent diabetes mellitus. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 255-66.	0.7	2
53	Transcriptional regulation in eukaryotic ribosomal protein genes. Genomics, 2007, 90, 421-423.	2.9	49