

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	TarPmiR: a new approach for microRNA target site prediction. <i>Bioinformatics</i> , 2016, 32, 2768-2775.	4.1	144
2	H3K4me2 reliably defines transcription factor binding regions in different cells. <i>Genomics</i> , 2014, 103, 222-228.	2.9	85
3	Interpretation of deep learning in genomics and epigenomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	67
4	Transcriptional regulation in eukaryotic ribosomal protein genes. <i>Genomics</i> , 2007, 90, 421-423.	2.9	49
5	Transcriptional regulation of co-expressed microRNA target genes. <i>Genomics</i> , 2011, 98, 445-452.	2.9	43
6	PETModule: a motif module based approach for enhancer target gene prediction. <i>Scientific Reports</i> , 2016, 6, 30043.	3.3	35
7	EPIP: a novel approach for condition-specific enhancer-promoter interaction prediction. <i>Bioinformatics</i> , 2019, 35, 3877-3883.	4.1	33
8	MOPAT: a graph-based method to predict recurrent cis-regulatory modules from known motifs. <i>Nucleic Acids Research</i> , 2008, 36, 4488-4497.	14.5	29
9	Thousands of Cis-Regulatory Sequence Combinations Are Shared by Arabidopsis and Poplar. <i>Plant Physiology</i> , 2012, 158, 145-155.	4.8	29
10	Systematic identification of conserved motif modules in the human genome. <i>BMC Genomics</i> , 2010, 11, 567.	2.8	28
11	Prognostic cancer gene signatures share common regulatory motifs. <i>Scientific Reports</i> , 2017, 7, 4750.	3.3	27
12	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
13	Systematic Prediction of cis-Regulatory Elements in the <i>Chlamydomonas reinhardtii</i> Genome Using Comparative Genomics. <i>Plant Physiology</i> , 2012, 160, 613-623.	4.8	25
14	Integrative analyses shed new light on human ribosomal protein gene regulation. <i>Scientific Reports</i> , 2016, 6, 28619.	3.3	25
15	Systematic discovery of cofactor motifs from ChIP-seq data by SIOMICS. <i>Methods</i> , 2015, 79-80, 47-51.	3.8	23
16	MBBC: an efficient approach for metagenomic binning based on clustering. <i>BMC Bioinformatics</i> , 2015, 16, 36.	2.6	23
17	Computational annotation of miRNA transcription start sites. <i>Briefings in Bioinformatics</i> , 2021, 22, 380-392.	6.5	23
18	MicroRNA modules prefer to bind weak and unconventional target sites. <i>Bioinformatics</i> , 2015, 31, 1366-1374.	4.1	21

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19	BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631.	4.1	18
20	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
21	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
22	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
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	CHIPMODULE: SYSTEMATIC DISCOVERY OF TRANSCRIPTION FACTORS AND THEIR COFACTORS FROM CHIP-SEQ DATA. , 2012, , .		10
25	CCmiR: a computational approach for competitive and cooperative microRNA binding prediction. <i>Bioinformatics</i> , 2018, 34, 198-206.	4.1	10
26	mixtureS: a novel tool for bacterial strain genome reconstruction from reads. <i>Bioinformatics</i> , 2021, 37, 575-577.	4.1	10
27	ChIPModule: systematic discovery of transcription factors and their cofactors from ChIP-seq data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 320-31.	0.7	8
28	Mining patterns in disease classification forests. <i>Journal of Biomedical Informatics</i> , 2010, 43, 820-827.	4.3	7
29	When old metagenomic data meet newly sequenced genomes, a case study. <i>PLoS ONE</i> , 2018, 13, e0198773.	2.5	7
30	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
31	A systematic evaluation of the computational tools for lncRNA identification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
32	A deep learning method for miRNA/isomiR target detection. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
33	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
34	Position-wise binding preference is important for miRNA target site prediction. <i>Bioinformatics</i> , 2020, 36, 3680-3686.	4.1	6
35	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
36	Computational analyses of bacterial strains from shotgun reads. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5

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37	A new measurement of sequence conservation. BMC Genomics, 2009, 10, 623.	2.8	4
38	An efficient algorithm to identify coordinately activated transcription factors. Genomics, 2010, 95, 143-150.	2.9	4
39	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. Statistics in Biosciences, 2012, 4, 157-176.	1.2	4
40	Urinary bladder hypertrophy characteristic of male ROMK Bartter TM s mice does not occur in female mice. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2018, 314, R334-R341.	1.8	4
41	Improving miRNA Target Prediction Using CLASH Data. Methods in Molecular Biology, 2019, 1970, 75-83.	0.9	4
42	Application of Deep Learning Models to MicroRNA Transcription Start Site Identification. , 2019, , .		4
43	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
44	PreDREM: a database of predicted DNA regulatory motifs from 349 human cell and tissue samples. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	3
45	An intriguing characteristic of enhancer-promoter interactions. BMC Genomics, 2021, 22, 163.	2.8	3
46	A systematic study of motif pairs that may facilitate enhancer TM promoter interactions. Journal of Integrative Bioinformatics, 2022, 19, .	1.5	2
47	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
48	Computational discovery of feature patterns in nucleosomal DNA sequences. Genomics, 2014, 104, 87-95.	2.9	1
49	Discover the semantic structure of human reference epigenome by differential latent dirichlet allocation. , 2017, , .		1
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	Whole genome identification of target genes of transcription factors. , 2010, , .		0
52	Hierarchical order of gene expression levels. , 2010, , .		0
53	FlexSLIM. , 2018, , .		0