

Xiaoman Li

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

672
citations

759233

12
h-index

610901

24
g-index

27
all docs

27
docs citations

27
times ranked

1094
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	Transcription Factors STAT6 and KLF4 Implement Macrophage Polarization via the Dual Catalytic Powers of MCPiP. <i>Journal of Immunology</i> , 2015, 194, 6011-6023.	0.8	143
3	Interpretation of deep learning in genomics and epigenomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	67
4	SETDB2 Links Glucocorticoid to Lipid Metabolism through Insig2a Regulation. <i>Cell Metabolism</i> , 2016, 24, 474-484.	16.2	46
5	EPIP: a novel approach for condition-specific enhancer-promoter interaction prediction. <i>Bioinformatics</i> , 2019, 35, 3877-3883.	4.1	33
6	Prognostic cancer gene signatures share common regulatory motifs. <i>Scientific Reports</i> , 2017, 7, 4750.	3.3	27
7	Systematic discovery of cofactor motifs from ChIP-seq data by SIOMICS. <i>Methods</i> , 2015, 79-80, 47-51.	3.8	23
8	MBBC: an efficient approach for metagenomic binning based on clustering. <i>BMC Bioinformatics</i> , 2015, 16, 36.	2.6	23
9	MicroRNA modules prefer to bind weak and unconventional target sites. <i>Bioinformatics</i> , 2015, 31, 1366-1374.	4.1	21
10	Differential open chromatin profile and transcriptomic signature define depot-specific human subcutaneous preadipocytes: primary outcomes. <i>Clinical Epigenetics</i> , 2018, 10, 148.	4.1	20
11	BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631.	4.1	18
12	A mixture model-based discriminate analysis for identifying ordered transcription factor binding site pairs in gene promoters directly regulated by estrogen receptor- α . <i>Bioinformatics</i> , 2006, 22, 2210-2216.	4.1	14
13	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
14	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
15	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
16	mixtureS: a novel tool for bacterial strain genome reconstruction from reads. <i>Bioinformatics</i> , 2021, 37, 575-577.	4.1	10
17	When old metagenomic data meet newly sequenced genomes, a case study. <i>PLoS ONE</i> , 2018, 13, e0198773.	2.5	7
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Computational analyses of bacterial strains from shotgun reads. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
22	Improving miRNA Target Prediction Using CLASH Data. <i>Methods in Molecular Biology</i> , 2019, 1970, 75-83.	0.9	4
23	Application of Deep Learning Models to MicroRNA Transcription Start Site Identification. , 2019, , .		4
24	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
25	An intriguing characteristic of enhancer-promoter interactions. <i>BMC Genomics</i> , 2021, 22, 163.	2.8	3
26	A systematic study of motif pairs that may facilitate enhancer-promoter interactions. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.5	2