Hebing Chen

List of Publications by Year
in descending order

20 papers	458 citations	1040056 9 h-index
23 all docs	23 docs citations	23 times ranked

940533
16 g-index

851 citing authors

#	Article	IF	Citations
1	Inferring transcription factor regulatory networks from single-cell ATAC-seq data based on graph neural networks. Nature Machine Intelligence, 2022, 4, 389-400.	16.0	13
2	Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. Advanced Science, 2022, 9, e2200818.	11.2	10
3	Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. Briefings in Bioinformatics, 2021, 22, .	6.5	5
4	Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	16
5	Synergistic alterations in the multilevel chromatin structure anchor dysregulated genes in small cell lung cancer. Computational and Structural Biotechnology Journal, 2021, 19, 5946-5959.	4.1	6
6	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. PLoS Computational Biology, 2020, 16, e1007287.	3.2	56
7	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
8	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
9	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
10	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
11	Genome-wide identification and analysis of A-to-I RNA editing events in the malignantly transformed cell lines from bronchial epithelial cell line induced by Î±-particles radiation. PLoS ONE, 2019, 14, e0213047.	2.5	3
12	Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. RNA Biology, 2019, 16, 1010-1021.	3.1	7
13	A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. Briefings in Bioinformatics, 2019, 20, 1524-1541.	6.5	48
14	CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. PeerJ, 2018, 6, e5951.	2.0	9
15	3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. Nucleic Acids Research, 2017, 45, D643-D649.	14.5	90
16	iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607.	2.5	2
17	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633.	3.3	24
18	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. Scientific Reports, 2015, 5, 8465.	3.3	41

#	ARTICLE	IF	CITATIONS
19	Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. PLoS ONE, 2012, 7, e41374.	2.5	119
20	ARDesigner: A web-based system for allosteric RNA design. Journal of Biotechnology, 2010, 150, 466-473.	3.8	9