Feng Cui

List of Publications by Year
in descending order

25 papers	548 citations	687363 13 h-index	677142 22 g-index
28 all docs	28 docs citations	28 times ranked	818 citing authors

#	Article	IF	Citations
1	Functional binding dynamics relevant to the evolution of zoonotic spillovers in endemic and emergent *Betacoronavirus* strains. Journal of Biomolecular Structure and Dynamics, 2022, 40, 10978-10996.	3.5	7
2	Vaccine candidate designed against carcinoembryonic antigen-related cell adhesion molecules using immunoinformatics tools. Journal of Biomolecular Structure and Dynamics, 2021, 39, 6084-6098.	3.5	8
3	Interpretable Structured Learning with Sparse Gated Sequence Encoder for Protein-Protein Interaction Prediction. , 2021, , .		0
4	Predicting Biomedical Interactions with Higher-Order Graph Convolutional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	4
5	Temporal gene regulation by p53 is associated with the rotational setting of its binding sites in nucleosomes. Cell Cycle, 2021, 20, 792-807.	2.6	2
6	Machine learning predicts nucleosome binding modes of transcription factors. BMC Bioinformatics, 2021, 22, 166.	2.6	3
7	Histopathological distinction of non-invasive and invasive bladder cancers using machine learning approaches. BMC Medical Informatics and Decision Making, 2020, 20, 162.	3.0	20
8	The nucleosome position-encoding WW/SS sequence pattern is depleted in mammalian genes relative to other eukaryotes. Nucleic Acids Research, 2019, 47, 7942-7954.	14.5	8
9	GNE: a deep learning framework for gene network inference by aggregating biological information. BMC Systems Biology, 2019, 13, 38.	3.0	35
10	BioVR: a platform for virtual reality assisted biological data integration and visualization. BMC Bioinformatics, 2019, 20, 78.	2.6	33
11	p53 binding sites in normal and cancer cells are characterized by distinct chromatin context. Cell Cycle, 2017, 16, 2073-2085.	2.6	27
12	Cell type-specific transcriptome profiling in mammalian brains. Frontiers in Bioscience - Landmark, 2016, 21, 973-985.	3.0	6
13	The proto-chromatosome: A fundamental subunit of chromatin?. Nucleus, 2016, 7, 382-387.	2.2	8
14	Novel nucleosomal particles containing core histones and linker DNA but no histone H1. Nucleic Acids Research, 2016, 44, 573-581.	14.5	20
15	Cross-species Transcriptomic Comparison of *In Vitro* and *In Vivo* Mammalian Neural Cells. Bioinformatics and Biology Insights, 2015, 9, BBI.S33124.	2.0	14
16	A Computational Pipeline for Cross-Species Analysis of RNA-seq Data Using R and Bioconductor. Bioinformatics and Biology Insights, 2015, 9, BBI.S30884.	2.0	15
17	Topological diversity of chromatin fibers: Interplay between nucleosome repeat length, DNA linking number and the level of transcription. AIMS Biophysics, 2015, 2, 613-629.	0.6	21
18	nuMap: A Web Platform for Accurate Prediction of Nucleosome Positioning. Genomics, Proteomics and Bioinformatics, 2014, 12, 249-253.	6.9	13

#	ARTICLE	IF	CITATIONS
19	Prediction of nucleosome rotational positioning in yeast and human genomes based on sequence-dependent DNA anisotropy. BMC Bioinformatics, 2014, 15, 313.	2.6	17
20	Rotational positioning of nucleosomes facilitates selective binding of p53 to response elements associated with cell cycle arrest. Nucleic Acids Research, 2014, 42, 836-847.	14.5	43
21	Transcriptional activation of yeast genes disrupts intragenic nucleosome phasing. Nucleic Acids Research, 2012, 40, 10753-10764.	14.5	36
22	Impact of Alu repeats on the evolution of human p53 binding sites. Biology Direct, 2011, 6, 2.	4.6	72
23	Structure-based Analysis of DNA Sequence Patterns Guiding Nucleosome Positioningin vitro. Journal of Biomolecular Structure and Dynamics, 2010, 27, 821-841.	3.5	68
24	Distinctive sequence patterns in metazoan and yeast nucleosomes: Implications for linker histone binding to AT-rich and methylated DNA. Nucleic Acids Research, 2009, 37, 2818-2829.	14.5	63
25	KNOWLEDGE-BASED VERSUS EXPERIMENTALLY ACQUIRED DISTANCE AND ANGLE CONSTRAINTS FOR NMR STRUCTURE REFINEMENT. Journal of Bioinformatics and Computational Biology, 2008, 06, 283-300.	0.8	3