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	Impact of Alu repeats on the evolution of human p53 binding sites. Biology Direct, 2011, 6, 2.	4.6	72
2	Structure-based Analysis of DNA Sequence Patterns Guiding Nucleosome Positioningin vitro. Journal of Biomolecular Structure and Dynamics, 2010, 27, 821-841.	3.5	68
3	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
4	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
5	Transcriptional activation of yeast genes disrupts intragenic nucleosome phasing. Nucleic Acids Research, 2012, 40, 10753-10764.	14.5	36
6	GNE: a deep learning framework for gene network inference by aggregating biological information. BMC Systems Biology, 2019, 13, 38.	3.0	35
7	BioVR: a platform for virtual reality assisted biological data integration and visualization. BMC Bioinformatics, 2019, 20, 78.	2.6	33
8	p53 binding sites in normal and cancer cells are characterized by distinct chromatin context. Cell Cycle, 2017, 16, 2073-2085.	2.6	27
9	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
10	Novel nucleosomal particles containing core histones and linker DNA but no histone H1. Nucleic Acids Research, 2016, 44, 573-581.	14.5	20
11	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
12	Prediction of nucleosome rotational positioning in yeast and human genomes based on sequence-dependent DNA anisotropy. BMC Bioinformatics, 2014, 15, 313.	2.6	17
13	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
14	Cross-species Transcriptomic Comparison of *In Vitro* and *In Vivo* Mammalian Neural Cells. Bioinformatics and Biology Insights, 2015, 9, BBI.S33124.	2.0	14
15	nuMap: A Web Platform for Accurate Prediction of Nucleosome Positioning. Genomics, Proteomics and Bioinformatics, 2014, 12, 249-253.	6.9	13
16	The proto-chromatosome: A fundamental subunit of chromatin?. Nucleus, 2016, 7, 382-387.	2.2	8
17	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
18	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

#	Article	IF	Citations
19	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
20	Cell type-specific transcriptome profiling in mammalian brains. Frontiers in Bioscience - Landmark, 2016, 21, 973-985.	3.0	6
21	Predicting Biomedical Interactions with Higher-Order Graph Convolutional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	4
22	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
23	Machine learning predicts nucleosome binding modes of transcription factors. BMC Bioinformatics, 2021, 22, 166.	2.6	3
24	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
25	Interpretable Structured Learning with Sparse Gated Sequence Encoder for Protein-Protein Interaction Prediction. , 2021, , .		0