

Weiqiang Zhou

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	GLI transcriptional repression is inert prior to Hedgehog pathway activation. <i>Nature Communications</i> , 2022, 13, 808.	12.8	15
2	Genome-wide prediction of chromatin accessibility based on gene expression. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2021, 13, e1544.	3.9	5
3	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	6.9	18
4	Reprogramming Transcription Factors Oct4 and Sox2 Induce a BRD-Dependent Immunosuppressive Transcriptome in GBM-Propagating Cells. <i>Cancer Research</i> , 2021, 81, 2457-2469.	0.9	31
5	63438 Differential chromatin accessibility at dorsal root ganglia enhancers is associated with nerve injury. <i>Journal of Clinical and Translational Science</i> , 2021, 5, 5-5.	0.6	0
6	EGFR Activates a TAZ-Driven Oncogenic Program in Glioblastoma. <i>Cancer Research</i> , 2021, 81, 3580-3592.	0.9	12
7	Distinct Cytokine and Chemokine Dysregulation in Hospitalized Children With Acute Coronavirus Disease 2019 and Multisystem Inflammatory Syndrome With Similar Levels of Nasopharyngeal Severe Acute Respiratory Syndrome Coronavirus 2 Shedding. <i>Journal of Infectious Diseases</i> , 2021, 224, 606-615.	4.0	30
8	Global gene expression and chromatin accessibility of the peripheral nervous system in animal models of persistent pain. <i>Journal of Neuroinflammation</i> , 2021, 18, 185.	7.2	6
9	A biomarker-authenticated model of schizophrenia implicating NPTX2 loss of function. <i>Science Advances</i> , 2021, 7, eabf6935.	10.3	17
10	Altered 3D chromatin structure permits inversional recombination at the <i>IgH</i> locus. <i>Science Advances</i> , 2020, 6, eaaz8850.	10.3	13
11	Single-cell ATAC-seq signal extraction and enhancement with SCATE. <i>Genome Biology</i> , 2020, 21, 161.	8.8	34
12	GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. <i>ELife</i> , 2020, 9, .	6.0	29
13	Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. <i>Nucleic Acids Research</i> , 2019, 47, e121-e121.	14.5	24
14	Sex differences in gene regulation in the dorsal root ganglion after nerve injury. <i>BMC Genomics</i> , 2019, 20, 147.	2.8	53
15	Sequential Enhancer Sequestration Dysregulates Recombination Center Formation at the <i>IgH</i> Locus. <i>Molecular Cell</i> , 2018, 70, 21-33.e6.	9.7	35
16	Transcriptional outcomes and kinetic patterning of gene expression in response to NF- κ B activation. <i>PLoS Biology</i> , 2018, 16, e2006347.	5.6	37
17	Single-cell regulome data analysis by SCRAT. <i>Bioinformatics</i> , 2017, 33, 2930-2932.	4.1	47
18	Genome-wide prediction of DNase I hypersensitivity using gene expression. <i>Nature Communications</i> , 2017, 8, 1038.	12.8	34

#	ARTICLE	IF	CITATIONS
19	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. <i>Human Heredity</i> , 2016, 81, 88-105.	0.8	3
20	HOXB7 Is an ER \pm Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015, 5, 944-959.	9.4	72
21	Mining of proteinâ€“protein interfacial residues from massive protein sequential and spatial data. <i>Fuzzy Sets and Systems</i> , 2015, 258, 101-116.	2.7	5
22	Alpha shape and Delaunay triangulation in studies of protein-related interactions. <i>Briefings in Bioinformatics</i> , 2014, 15, 54-64.	6.5	30
23	Identification of DNA-Binding and Protein-Binding Proteins Using Enhanced Graph Wavelet Features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1017-1031.	3.0	3
24	Prediction of anti-EGFR drug resistance base on binding free energy and hydrogen bond analysis. , 2013, , .		5
25	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. <i>Current Bioinformatics</i> , 2013, 8, 3-8.	1.5	1
26	Personalized prediction of EGFR mutation-induced drug resistance in lung cancer. <i>Scientific Reports</i> , 2013, 3, 2855.	3.3	34
27	A Survey on Structural Analysis of Nucleosome Core Particles. <i>Current Bioinformatics</i> , 2013, 8, 112-132.	1.5	0
28	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. <i>Current Bioinformatics</i> , 2013, 8, 3-8.	1.5	3
29	The relationship between geometric patterns of hydrogen bonds and periodic dinucleotides in nucleosome structures. <i>Journal of Theoretical Biology</i> , 2012, 313, 136-141.	1.7	4
30	Analysis of surface structures of hydrogen bonding in proteinâ€“ligand interactions using the alpha shape model. <i>Chemical Physics Letters</i> , 2012, 545, 125-131.	2.6	22
31	Analysis of ligand binding sites using alpha shapes. , 2012, , .		0
32	Correlation between the flexibility and periodic dinucleotide patterns in yeast nucleosomal DNA sequences. <i>Journal of Theoretical Biology</i> , 2011, 284, 92-98.	1.7	6
33	Prediction of DNA-binding protein based on statistical and geometric features and support vector machines. <i>Proteome Science</i> , 2011, 9, S1.	1.7	17
34	Prediction of Protein-protein Interactions Using Alpha Shape Modeling. , 2011, , .		4
35	Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. <i>Chemical Physics Letters</i> , 2010, 489, 225-228.	2.6	14
36	A discriminatory function for prediction of proteinâ€“DNA interactions based on alpha shape modeling. <i>Bioinformatics</i> , 2010, 26, 2541-2548.	4.1	20

#	ARTICLE	IF	CITATIONS
37	Prediction of DNA-binding protein based on alpha shape modeling. , 2010, , .		1