

Bing Ren

List of Publications by Year in descending order

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66
papers

26,914
citations

81743

39
h-index

98622

67
g-index

75
all docs

75
docs citations

75
times ranked

35075
citing authors

#	ARTICLE	IF	CITATIONS
1	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063
2	N6-methyladenosine-dependent regulation of messenger RNA stability. <i>Nature</i> , 2014, 505, 117-120.	13.7	3,138
3	Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. <i>Nature Genetics</i> , 2007, 39, 311-318.	9.4	2,898
4	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , 2009, 459, 108-112.	13.7	2,225
5	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
6	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
7	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
8	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. <i>Cell</i> , 2012, 149, 1368-1380.	13.5	912
9	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. <i>Cell</i> , 2015, 162, 900-910.	13.5	846
10	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	13.7	779
11	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
12	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
13	Chromatin Domains: The Unit of Chromosome Organization. <i>Molecular Cell</i> , 2016, 62, 668-680.	4.5	653
14	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	13.7	605
15	Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. <i>Cell</i> , 2012, 148, 816-831.	13.5	478
16	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , 2012, 22, 246-258.	2.4	476
17	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. <i>Nature Genetics</i> , 2013, 45, 1198-1206.	9.4	431
18	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361

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19	The 3D Genome in Transcriptional Regulation and Pluripotency. <i>Cell Stem Cell</i> , 2014, 14, 762-775.	5.2	353
20	Genome-wide mapping and analysis of chromosome architecture. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 743-755.	16.1	324
21	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. <i>Molecular Cell</i> , 2014, 56, 286-297.	4.5	285
22	Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates. <i>Cell Stem Cell</i> , 2015, 16, 386-399.	5.2	222
23	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	13.7	215
24	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
25	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> , 2018, 173, 1796-1809.e17.	13.5	165
26	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 533-546.e7.	5.2	157
27	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	131
28	Nonlinear simulations of wave-induced motions of a freely floating body using WCSPH method. <i>Applied Ocean Research</i> , 2015, 50, 1-12.	1.8	121
29	A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. <i>Genome Research</i> , 2016, 26, 397-405.	2.4	111
30	Use of Chromatin Immunoprecipitation Assays in Genome-Wide Location Analysis of Mammalian Transcription Factors. <i>Methods in Enzymology</i> , 2003, 376, 304-315.	0.4	79
31	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1633-E1640.	3.3	78
32	HUGIn: Hi-C Unifying Genomic Interrogator. <i>Bioinformatics</i> , 2017, 33, 3793-3795.	1.8	69
33	Application of smoothed particle hydrodynamics for modeling the wave-moored floating breakwater interaction. <i>Applied Ocean Research</i> , 2017, 67, 277-290.	1.8	67
34	MPE-seq, a new method for the genome-wide analysis of chromatin structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3457-65.	3.3	66
35	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. <i>Cell Reports</i> , 2019, 29, 495-510.e6.	2.9	66
36	Hyper-Editing of Cell-Cycle Regulatory and Tumor Suppressor RNA Promotes Malignant Progenitor Propagation. <i>Cancer Cell</i> , 2019, 35, 81-94.e7.	7.7	64

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37	Human centromeric CENP-A chromatin is a homotypic, octameric nucleosome at all cell cycle points. <i>Journal of Cell Biology</i> , 2017, 216, 607-621.	2.3	53
38	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021, 39, 1000-1007.	9.4	53
39	Numerical modelling of regular wave slamming on subface of open-piled structures with the corrected SPH method. <i>Applied Ocean Research</i> , 2012, 34, 173-186.	1.8	48
40	Coordinated histone modifications and chromatin reorganization in a single cell revealed by FRET biosensors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11681-E11690.	3.3	48
41	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2051-2063.	0.8	39
42	Potential application of submerged horizontal plate as a wave energy breakwater: A 2D study using the WCSPH method. <i>Ocean Engineering</i> , 2019, 185, 27-46.	1.9	39
43	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. <i>Nature Communications</i> , 2021, 12, 6636.	5.8	31
44	A non-reflective spectral wave maker for SPH modeling of nonlinear wave motion. <i>Wave Motion</i> , 2018, 79, 112-128.	1.0	30
45	Transcriptional Enhancers: Bridging the Genome and Phenome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 17-26.	2.0	28
46	Numerical analysis of wave-induced current within the inhomogeneous coral reef using a refined SPH model. <i>Coastal Engineering</i> , 2020, 156, 103616.	1.7	28
47	Preventive Inhibition of Liver Tumorigenesis by Systemic Activation of Innate Immune Functions. <i>Cell Reports</i> , 2017, 21, 1870-1882.	2.9	22
48	The MUC5B-associated variant rs35705950 resides within an enhancer subject to lineage- and disease-dependent epigenetic remodeling. <i>JCI Insight</i> , 2021, 6, .	2.3	21
49	SPH Modeling of Wave Transformation over a Coral Reef with Seawall. <i>Journal of Waterway, Port, Coastal and Ocean Engineering</i> , 2019, 145, .	0.5	20
50	Using a genetic algorithm to improve oil spill prediction. <i>Marine Pollution Bulletin</i> , 2018, 135, 386-396.	2.3	19
51	The layout of submerged horizontal plate breakwater (SHPB) with respect to the tidal-level variation. <i>Coastal Engineering Journal</i> , 2018, 60, 280-298.	0.7	17
52	KDM1A maintains genome-wide homeostasis of transcriptional enhancers. <i>Genome Research</i> , 2021, 31, 186-197.	2.4	17
53	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. <i>ELife</i> , 2021, 10, .	2.8	15
54	A CRISPR Connection between Chromatin Topology and Genetic Disorders. <i>Cell</i> , 2015, 161, 955-957.	13.5	13

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55	Laboratory investigation of the hydroelastic effect on liquid sloshing in rectangular tanks. Journal of Hydrodynamics, 2014, 26, 751-761.	1.3	12
56	Closing the distance on obesity culprits. Nature, 2014, 507, 309-310.	13.7	11
57	Numerical Simulation of Hydrodynamic Characteristics on an Arc Crown Wall using Volume of Fluid Method Based on BFC. Journal of Hydrodynamics, 2011, 23, 767-776.	1.3	9
58	SPH Simulation of Wave Scattering by a Heaving Submerged Horizontal Plate. International Journal of Ocean and Coastal Engineering, 2018, 01, .	0.3	9
59	Experimental investigation of wave slamming on an open structure supported elastically. China Ocean Engineering, 2016, 30, 967-978.	0.6	6
60	Experimental study of nonlinear behaviors of a free-floating body in waves. China Ocean Engineering, 2016, 30, 421-430.	0.6	5
61	SPH evaluation of the hydrodynamic consequences induced by reef degradation. Wave Motion, 2020, 96, 102579.	1.0	4
62	Three-Dimensional Numerical Simulation of Wave Slamming on an Open Structure. Journal of Hydrodynamics, 2012, 24, 526-534.	1.3	3
63	Experimental investigation of regular wave propagation over an idealized reef model. Journal of Hydrodynamics, 2020, 32, 717-726.	1.3	3
64	Improved epicardial cardiac fibroblast generation from iPSCs. Journal of Molecular and Cellular Cardiology, 2022, 164, 58-68.	0.9	3
65	Laboratory study on the hydrodynamic and structural characteristic of violent sloshing in elastic tanks. Ships and Offshore Structures, 2015, , 1-12.	0.9	2
66	EXPERIMENTAL STUDY OF IRREGULAR WAVE IMPACT ON PILED WHARF WITH PERMEABLE SLOPE SHORE CONNECTING. , 2004, , .		0