

Guoliang Li

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88
papers

6,289
citations

33
h-index

79
g-index

101
ext. papers

7,922
ext. citations

12.4
avg, IF

5.26
L-index

#	Paper	IF	Citations
88	Diurnal RNAPII-tethered chromatin interactions are associated with rhythmic gene expression in rice.. <i>Genome Biology</i> , 2022 , 23, 7	18.3	0
87	RAB2A promotes cervical cancer progression as revealed by comprehensive analysis of HPV integration and proteome in longitudinal cervical samples.. <i>Clinical and Translational Medicine</i> , 2022 , 12, e767	5.7	
86	Profiling Plant Histone Modification at Single-cell Resolution Using snCUT&Tag.. <i>Plant Biotechnology Journal</i> , 2021 ,	11.6	2
85	CoolBox: a flexible toolkit for visual analysis of genomics data. <i>BMC Bioinformatics</i> , 2021 , 22, 489	3.6	1
84	Effects of parental environmental copper stress on offspring development: DNA methylation modification and responses of differentially methylated region-related genes in transcriptional expression. <i>Journal of Hazardous Materials</i> , 2021 , 424, 127600	12.8	0
83	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021 , 230, 1772-1786	9.8	7
82	Rapid and Low-Input Profiling of Histone Marks in Plants Using Nucleus CUT&Tag. <i>Frontiers in Plant Science</i> , 2021 , 12, 634679	6.2	3
81	Asymmetric epigenome maps of subgenomes reveal imbalanced transcription and distinct evolutionary trends in Brassica napus. <i>Molecular Plant</i> , 2021 , 14, 604-619	14.4	10
80	L2MXception: an improved Xception network for classification of peach diseases. <i>Plant Methods</i> , 2021 , 17, 36	5.8	3
79	TAD boundary and strength prediction by integrating sequence and epigenetic profile information. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
78	RUNX1-mediated alphaherpesvirus-host trans-species chromatin interaction promotes viral transcription. <i>Science Advances</i> , 2021 , 7,	14.3	6
77	Structural Variations of the 3D Genome Architecture in Cervical Cancer Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 706375	5.7	2
76	RiceLncPedia: a comprehensive database of rice long non-coding RNAs. <i>Plant Biotechnology Journal</i> , 2021 , 19, 1492-1494	11.6	4
75	Technologies for Capturing 3D Genome Architecture in Plants. <i>Trends in Plant Science</i> , 2021 , 26, 196-197	13.1	3
74	SurVirus: a repeat-aware virus integration caller. <i>Nucleic Acids Research</i> , 2021 , 49, e33	20.1	5
73	ASMcdb: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
72	RiceENCODE: A comprehensive epigenomic database as a rice Encyclopedia of DNA Elements. <i>Molecular Plant</i> , 2021 , 14, 1604-1606	14.4	2

71	HIVID2: an accurate tool to detect virus integrations in the host genome. <i>Bioinformatics</i> , 2021 ,	7.2	2
70	Robust capturing chromosome conformation using the DLO Hi-C 2.0 method. <i>Journal of Genetics and Genomics</i> , 2020 , 47, 655-658	4	0
69	Advances in technologies for 3D genomics research. <i>Science China Life Sciences</i> , 2020 , 63, 811-824	8.5	9
68	Integrative analysis of reference epigenomes in 20 rice varieties. <i>Nature Communications</i> , 2020 , 11, 26581	7.4	25
67	3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. <i>Genome Biology</i> , 2020 , 21, 143	18.3	28
66	HPV-CCDC106 integration alters local chromosome architecture and hijacks an enhancer by three-dimensional genome structure remodeling in cervical cancer. <i>Journal of Genetics and Genomics</i> , 2020 , 47, 437-450	4	21
65	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020 , 39, e103949	13	23
64	The DLO Hi-C Tool for Digestion-Ligation-Only Hi-C Chromosome Conformation Capture Data Analysis. <i>Genes</i> , 2020 , 11,	4.2	6
63	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <i>BMC Bioinformatics</i> , 2020 , 21, 451	3.6	2
62	Mapping long-range contacts between risk loci and target genes in human diseases with Capture Hi-C. <i>Clinical and Translational Medicine</i> , 2020 , 10, e183	5.7	1
61	Unraveling the 3D Genome Architecture in Plants: Present and Future. <i>Molecular Plant</i> , 2020 , 13, 1676-1693	17.4	17
60	Decoding the plant genome: From epigenome to 3D organization. <i>Journal of Genetics and Genomics</i> , 2020 , 47, 425-435	4	3
59	Copper stress induces zebrafish central neural system myelin defects via WNT/NOTCH-hoxb5b signaling and pou3f1/fam168a/fam168b DNA methylation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194612	6	7
58	ChIAMM: A Mixture Model for Statistical Analysis of Long-Range Chromatin Interactions From ChIA-PET Experiments. <i>Frontiers in Genetics</i> , 2020 , 11, 616160	4.5	1
57	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Molecular Ecology Resources</i> , 2020 , 20, 268-282	8.4	18
56	Common responses of fish embryos to metals: an integrated analysis of transcriptomes and methylomes in zebrafish embryos under the stress of copper ions or silver nanoparticles. <i>Metallomics</i> , 2019 , 11, 1452-1464	4.5	7
55	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019 , 20, 47	3.6	16
54	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, CHIP-Seq and ChIA-PET data. <i>BMC Genomics</i> , 2019 , 20, 296	4.5	5

53	The effects of Arabidopsis genome duplication on the chromatin organization and transcriptional regulation. <i>Nucleic Acids Research</i> , 2019 , 47, 7857-7869	20.1	29
52	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019 , 10, 2632	17.4	61
51	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019 , 10, 3640	17.4	39
50	Chromatin Interaction Analysis with Updated ChIA-PET Tool (V3). <i>Genes</i> , 2019 , 10,	4.2	8
49	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019 , 29, 223-235	9.7	24
48	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019 , 51, 138-150	36.3	99
47	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019 , 51, 224-229	36.3	266
46	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018 , 4, 90-97	11.5	82
45	Silver nanoparticles impair zebrafish skeletal and cardiac myofibrillogenesis and sarcomere formation. <i>Aquatic Toxicology</i> , 2018 , 200, 102-113	5.1	21
44	Digestion-ligation-only Hi-C is an efficient and cost-effective method for chromosome conformation capture. <i>Nature Genetics</i> , 2018 , 50, 754-763	36.3	45
43	A Large-Scale, Exome-Wide Association Study of Han Chinese Women Identifies Three Novel Loci Predisposing to Breast Cancer. <i>Cancer Research</i> , 2018 , 78, 3087-3097	10.1	17
42	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. <i>Nature Protocols</i> , 2017 , 12, 899-915	18.8	58
41	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. <i>Cell Host and Microbe</i> , 2017 , 22, 561-573.e4	23.4	60
40	Cooperation between the H3K27me3 Chromatin Mark and Non-CG Methylation in Epigenetic Regulation. <i>Plant Physiology</i> , 2016 , 172, 1131-1141	6.6	28
39	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. <i>Scientific Reports</i> , 2016 , 6, 36572	4.9	16
38	In silico identification of enhancers on the basis of a combination of transcription factor binding motif occurrences. <i>Scientific Reports</i> , 2016 , 6, 32476	4.9	7
37	Feedback Regulation of ABA Signaling and Biosynthesis by a bZIP Transcription Factor Targets Drought-Resistance-Related Genes. <i>Plant Physiology</i> , 2016 , 171, 2810-25	6.6	136
36	Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways. <i>Plant Physiology</i> , 2016 , 171, 2041-54	6.6	70

35	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015 , 16, 264	18.3	38
34	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015 , 163, 1611-27	56.2	585
33	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015 , 12, 272-85	10.6	84
32	The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2015 , 5, 17662	4.9	181
31	Cross-enhancement of ANGPTL4 transcription by HIF1 alpha and PPAR beta/delta is the result of the conformational proximity of two response elements. <i>Genome Biology</i> , 2014 , 15, R63	18.3	40
30	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <i>BMC Genomics</i> , 2014 , 15 Suppl 12, S11	4.5	55
29	Direct evidence for pitavastatin induced chromatin structure change in the KLF4 gene in endothelial cells. <i>PLoS ONE</i> , 2014 , 9, e96005	3.7	24
28	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014 , 42, 3028-43	20.1	22
27	Emergence of 3D genomics. <i>Chinese Science Bulletin</i> , 2014 , 59, 1165-1172	2.9	4
26	Statistical models for detecting differential chromatin interactions mediated by a protein. <i>PLoS ONE</i> , 2014 , 9, e97560	3.7	6
25	3D chromosome modeling with semi-definite programming and Hi-C data. <i>Journal of Computational Biology</i> , 2013 , 20, 831-46	1.7	86
24	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. <i>Cell</i> , 2013 , 155, 1507-20	56.2	255
23	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013 , 504, 306-310	50.4	313
22	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013 , 45, 852-9	36.3	94
21	Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2013 , 317-332	0.9	16
20	TNF β signals through specialized factories where responsive coding and miRNA genes are transcribed. <i>EMBO Journal</i> , 2012 , 31, 4404-14	13	93
19	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012 , 58, 289-99	4.6	69
18	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <i>Genome Biology</i> , 2012 , 13, R82	18.3	41

17	Large-scale functional organization of long-range chromatin interaction networks. <i>Cell Reports</i> , 2012 , 2, 1207-19	10.6	84
16	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
15	Long span DNA paired-end-tag (DNA-PET) sequencing strategy for the interrogation of genomic structural mutations and fusion-point-guided reconstruction of amplicons. <i>PLoS ONE</i> , 2012 , 7, e46152	3.7	11
14	Genetic variation of ESR1 and its co-activator PPARGC1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. <i>Breast Cancer Research</i> , 2011 , 13, R10	8.3	12
13	Cellular reprogramming by the conjoint action of ER β , FOXA1, and GATA3 to a ligand-inducible growth state. <i>Molecular Systems Biology</i> , 2011 , 7, 526	12.2	151
12	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011 , 43, 630-8	36.3	503
11	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 2218-21	4.7	15
10	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011 , 21, 665-75	9.7	68
9	Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. <i>Human Molecular Genetics</i> , 2011 , 20, 4991-9	5.6	79
8	Greedy selection of species for ancestral state reconstruction on phylogenies: elimination is better than insertion. <i>PLoS ONE</i> , 2010 , 5, e8985	3.7	7
7	Integrative model of genomic factors for determining binding site selection by estrogen receptor- α . <i>Molecular Systems Biology</i> , 2010 , 6, 456	12.2	126
6	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010 , 20, 320-31	9.7	772
5	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010 , 11, R22	18.3	199
4	Analyzing the fitch method for reconstructing ancestral states on ultrametric phylogenetic trees. <i>Bulletin of Mathematical Biology</i> , 2010 , 72, 1760-82	2.1	7
3	More taxa are not necessarily better for the reconstruction of ancestral character states. <i>Systematic Biology</i> , 2008 , 57, 647-53	8.4	45
2	DLO Hi-C Tool for Digestion-Ligation-Only Hi-C Chromosome Conformation Capture Data Analysis		1
1	CoolBox: A flexible toolkit for visual analysis of genomics data		1