

Guoliang Li

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

8,900
citations

76196

40
h-index

46693

89
g-index

101
all docs

101
docs citations

101
times ranked

13574
citing authors

#	ARTICLE	IF	CITATIONS
1	ASSEMB: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2022, 50, D60-D71.	6.5	20
2	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> , 2022, 424, 127600.	6.5	10
3	Diurnal RNAPII-tethered chromatin interactions are associated with rhythmic gene expression in rice. <i>Genome Biology</i> , 2022, 23, 7.	3.8	9
4	Profiling plant histone modification at single-cell resolution using snCUT&Tag. <i>Plant Biotechnology Journal</i> , 2022, 20, 420-422.	4.1	22
5	The landscape of promoter-centred RNA-DNA interactions in rice. <i>Nature Plants</i> , 2022, 8, 157-170.	4.7	15
6	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.	1.7	2
7	Deep Learning-Based Segmentation of Peach Diseases Using Convolutional Neural Network. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
8	Chromosomal Translocations Detection in Cancer Cells Using Chromosomal Conformation Capture Data. <i>Genes</i> , 2022, 13, 1170.	1.0	2
9	Technologies for Capturing 3D Genome Architecture in Plants. <i>Trends in Plant Science</i> , 2021, 26, 196-197.	4.3	8
10	SurVirus: a repeat-aware virus integration caller. <i>Nucleic Acids Research</i> , 2021, 49, e33-e33.	6.5	15
11	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021, 230, 1772-1786.	3.5	23
12	Rapid and Low-Input Profiling of Histone Marks in Plants Using Nucleus CUT&Tag. <i>Frontiers in Plant Science</i> , 2021, 12, 634679.	1.7	17
13	Asymmetric epigenome maps of subgenomes reveal imbalanced transcription and distinct evolutionary trends in <i>Brassica napus</i> . <i>Molecular Plant</i> , 2021, 14, 604-619.	3.9	43
14	L2MXception: an improved Xception network for classification of peach diseases. <i>Plant Methods</i> , 2021, 17, 36.	1.9	16
15	TAD boundary and strength prediction by integrating sequence and epigenetic profile information. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
16	RUNX1-mediated alphaherpesvirus-host trans-species chromatin interaction promotes viral transcription. <i>Science Advances</i> , 2021, 7, .	4.7	11
17	Structural Variations of the 3D Genome Architecture in Cervical Cancer Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 706375.	1.8	21
18	RiceLncPedia: a comprehensive database of rice long non-coding RNAs. <i>Plant Biotechnology Journal</i> , 2021, 19, 1492-1494.	4.1	16

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19	RiceENCODE: A comprehensive epigenomic database as a rice Encyclopedia of DNA Elements. <i>Molecular Plant</i> , 2021, 14, 1604-1606.	3.9	17
20	HIVID2: an accurate tool to detect virus integrations in the host genome. <i>Bioinformatics</i> , 2021, 37, 1821-1827.	1.8	4
21	CoolBox: a flexible toolkit for visual analysis of genomics data. <i>BMC Bioinformatics</i> , 2021, 22, 489.	1.2	19
22	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.	2.2	51
23	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <i>BMC Bioinformatics</i> , 2020, 21, 451.	1.2	5
24	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.	1.7	6
25	Unraveling the 3D Genome Architecture in Plants: Present and Future. <i>Molecular Plant</i> , 2020, 13, 1676-1693.	3.9	48
26	Decoding the plant genome: From epigenome to 3D organization. <i>Journal of Genetics and Genomics</i> , 2020, 47, 425-435.	1.7	8
27	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.	0.9	20
28	ChiAMM: A Mixture Model for Statistical Analysis of Long-Range Chromatin Interactions From ChIA-PET Experiments. <i>Frontiers in Genetics</i> , 2020, 11, 616160.	1.1	3
29	Robust capturing chromosome conformation using the DLO Hi-C 2.0 method. <i>Journal of Genetics and Genomics</i> , 2020, 47, 655-658.	1.7	4
30	Advances in technologies for 3D genomics research. <i>Science China Life Sciences</i> , 2020, 63, 811-824.	2.3	13
31	Integrative analysis of reference epigenomes in 20 rice varieties. <i>Nature Communications</i> , 2020, 11, 2658.	5.8	86
32	3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. <i>Genome Biology</i> , 2020, 21, 143.	3.8	60
33	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.	1.7	48
34	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020, 39, e103949.	3.5	37
35	The DLO Hi-C Tool for Digestion-Ligation-Only Hi-C Chromosome Conformation Capture Data Analysis. <i>Genes</i> , 2020, 11, 289.	1.0	15
36	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019, 10, 3640.	5.8	75

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37	Chromatin Interaction Analysis with Updated ChIA-PET Tool (V3). <i>Genes</i> , 2019, 10, 554.	1.0	22
38	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.	1.0	11
39	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019, 20, 47.	1.2	51
40	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, CHIP-Seq and ChIA-PET data. <i>BMC Genomics</i> , 2019, 20, 296.	1.2	12
41	The effects of Arabidopsis genome duplication on the chromatin organization and transcriptional regulation. <i>Nucleic Acids Research</i> , 2019, 47, 7857-7869.	6.5	55
42	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632.	5.8	93
43	Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. <i>BMC Genomics</i> , 2019, 20, 322.	1.2	5
44	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019, 29, 223-235.	2.4	46
45	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019, 51, 138-150.	9.4	177
46	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.	9.4	468
47	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	4.7	137
48	Silver nanoparticles impair zebrafish skeletal and cardiac myofibrillogenesis and sarcomere formation. <i>Aquatic Toxicology</i> , 2018, 200, 102-113.	1.9	34
49	Digestion-ligation-only Hi-C is an efficient and cost-effective method for chromosome conformation capture. <i>Nature Genetics</i> , 2018, 50, 754-763.	9.4	78
50	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.	0.4	19
51	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. <i>Nature Protocols</i> , 2017, 12, 899-915.	5.5	99
52	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. <i>Cell Host and Microbe</i> , 2017, 22, 561-573.e4.	5.1	89
53	Feedback Regulation of ABA Signaling and Biosynthesis by a bZIP Transcription Factor Targets Drought-Resistance-Related Genes. <i>Plant Physiology</i> , 2016, 171, 2810-2825.	2.3	245
54	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> , 2016, 5, 17662.	1.6	294

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55	Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways. <i>Plant Physiology</i> , 2016, 171, 2041-2054.	2.3	109
56	Cooperation between the H3K27me3 chromatin marker and non-CG methylation in epigenetic regulation. <i>Plant Physiology</i> , 2016, 172, pp.01238.2016.	2.3	39
57	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. <i>Scientific Reports</i> , 2016, 6, 36572.	1.6	19
58	In silico identification of enhancers on the basis of a combination of transcription factor binding motif occurrences. <i>Scientific Reports</i> , 2016, 6, 32476.	1.6	8
59	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	3.8	48
60	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015, 163, 1611-1627.	13.5	881
61	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015, 12, 272-285.	2.9	112
62	Direct Evidence for Pitavastatin Induced Chromatin Structure Change in the KLF4 Gene in Endothelial Cells. <i>PLoS ONE</i> , 2014, 9, e96005.	1.1	37
63	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	6.5	27
64	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.	13.9	58
65	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	75
66	Reconstruction of Three-Dimensional Structures of Chromatin and Its Biological Implications. <i>Scientia Sinica Vitae</i> , 2014, 44, 794-802.	0.1	1
67	Emergence of 3D genomics. <i>Chinese Science Bulletin</i> , 2014, 59, 1165-1172.	0.4	5
68	Statistical Models for Detecting Differential Chromatin Interactions Mediated by a Protein. <i>PLoS ONE</i> , 2014, 9, e97560.	1.1	7
69	3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data. <i>Journal of Computational Biology</i> , 2013, 20, 831-846.	0.8	110
70	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
71	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013, 504, 306-310.	13.7	405
72	DNase hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	9.4	112

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73	Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data. Lecture Notes in Computer Science, 2013, , 317-332.	1.0	30
74	TNF α signals through specialized factories where responsive coding and miRNA genes are transcribed. EMBO Journal, 2012, 31, 4404-4414.	3.5	122
75	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	1.9	83
76	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. Genome Biology, 2012, 13, R82.	13.9	45
77	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	2.9	102
78	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
79	Long Span DNA Paired-End-Tag (DNA-PET) Sequencing Strategy for the Interrogation of Genomic Structural Mutations and Fusion-Point-Guided Reconstruction of Amplicons. PLoS ONE, 2012, 7, e46152.	1.1	13
80	Genetic variation of ESR1 and its co-activator PPAR γ 1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. Breast Cancer Research, 2011, 13, R10.	2.2	15
81	Cellular reprogramming by the conjoint action of ER α , FOXA1, and GATA3 to a ligand-inducible growth state. Molecular Systems Biology, 2011, 7, 526.	3.2	169
82	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	9.4	567
83	Chromatin interaction networks and higher order architectures of eukaryotic genomes. Journal of Cellular Biochemistry, 2011, 112, 2218-2221.	1.2	18
84	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	2.4	74
85	Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. Human Molecular Genetics, 2011, 20, 4991-4999.	1.4	92
86	Analyzing the Fitch Method for Reconstructing Ancestral States on Ultrametric Phylogenetic Trees. Bulletin of Mathematical Biology, 2010, 72, 1760-1782.	0.9	8
87	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	1.1	9
88	Integrative model of genomic factors for determining binding site selection by estrogen receptor α . Molecular Systems Biology, 2010, 6, 456.	3.2	139
89	Dynamic changes in the human methylome during differentiation. Genome Research, 2010, 20, 320-331.	2.4	930
90	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	13.9	255

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91	More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States. <i>Systematic Biology</i> , 2008, 57, 647-653.	2.7	53