Guoliang Li

List of Publications by Year
in descending order

91 papers	8,900 citations	76326 40 h-index	46799 89 g-index
101 all docs	101 docs citations	101 times ranked	13574 citing authors

#	Article	IF	Citations
1	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
2	Dynamic changes in the human methylome during differentiation. Genome Research, 2010, 20, 320-331.	5.5	930
3	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. Cell, 2015, 163, 1611-1627.	28.9	881
4	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	21.4	567
5	Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense. Nature Genetics, 2019, 51, 224-229.	21.4	468
6	Chromatin connectivity maps reveal dynamic promoter–enhancer long-range associations. Nature, 2013, 504, 306-310.	27.8	405
7	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. Cell, 2013, 155, 1507-1520.	28.9	299
8	The genome sequence of Sea-Island cotton (Gossypium barbadense) provides insights into the allopolyploidization and development of superior spinnable fibres. Scientific Reports, 2016, 5, 17662.	3.3	294
9	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	9.6	255
10	Feedback Regulation of ABA Signaling and Biosynthesis by a bZIP Transcription Factor Targets Drought-Resistance-Related Genes. Plant Physiology, 2016, 171, 2810-2825.	4.8	245
11	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. Nature Genetics, 2019, 51, 138-150.	21.4	177
12	Cellular reprogramming by the conjoint action of ERα, FOXA1, and GATA3 to a ligand-inducible growth state. Molecular Systems Biology, 2011, 7, 526.	7.2	169
13	Integrative model of genomic factors for determining binding site selection by estrogen receptor-α. Molecular Systems Biology, 2010, 6, 456.	7.2	139
14	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. Nature Plants, 2018, 4, 90-97.	9.3	137
15	TNFα signals through specialized factories where responsive coding and miRNA genes are transcribed. EMBO Journal, 2012, 31, 4404-4414.	7.8	122
16	DNase I–hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	21.4	112
17	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285.	6.4	112
18	3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data. Journal of Computational Biology, 2013, 20, 831-846.	1.6	110

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19	Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways. Plant Physiology, 2016, 171, 2041-2054.	4.8	109
20	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	6.4	102
21	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. Nature Protocols, 2017, 12, 899-915.	12.0	99
22	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. Nature Communications, 2019, 10, 2632.	12.8	93
23	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.	2.9	92
24	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. Cell Host and Microbe, 2017, 22, 561-573.e4.	11.0	89
25	Integrative analysis of reference epigenomes in 20 rice varieties. Nature Communications, 2020, 11, 2658.	12.8	86
26	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	3.8	83
27	Digestion-ligation-only Hi-C is an efficient and cost-effective method for chromosome conformation capture. Nature Genetics, 2018, 50, 754-763.	21.4	78
28	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. BMC Genomics, 2014, 15, S11.	2.8	75
29	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. Nature Communications, 2019, 10, 3640.	12.8	75
30	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	5.5	74
31	3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. Genome Biology, 2020, 21, 143.	8.8	60
32	Cross-enhancement of ANGPTL4 transcription by HIF1 alpha and PPAR beta/delta is the result of the conformational proximity of two response elements. Genome Biology, 2014, 15, R63.	9.6	58
33	The effects of Arabidopsis genome duplication on the chromatin organization and transcriptional regulation. Nucleic Acids Research, 2019, 47, 7857-7869.	14.5	55
34	More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States. Systematic Biology, 2008, 57, 647-653.	5.6	53
35	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. BMC Bioinformatics, 2019, 20, 47.	2.6	51
36	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, *Chilo suppressalis*. Molecular Ecology Resources, 2020, 20, 268-282.	4.8	51

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37	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. Genome Biology, 2015, 16, 264.	8.8	48
38	Unraveling the 3D Genome Architecture in Plants: Present and Future. Molecular Plant, 2020, 13, 1676-1693.	8.3	48
39	HPV-CCDC106 integration alters local chromosome architecture and hijacks an enhancer by three-dimensional genome structure remodeling in cervical cancer. Journal of Genetics and Genomics, 2020, 47, 437-450.	3.9	48
40	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. Genome Research, 2019, 29, 223-235.	5.5	46
41	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. Genome Biology, 2012, 13, R82.	9.6	45
42	Asymmetric epigenome maps of subgenomes reveal imbalanced transcription and distinct evolutionary trends in Brassica napus. Molecular Plant, 2021, 14, 604-619.	8.3	43
43	Cooperation between the H3K27me3 chromatin marker and non-CG methylation in epigenetic regulation. Plant Physiology, 2016, 172, pp.01238.2016.	4.8	39
44	Direct Evidence for Pitavastatin Induced Chromatin Structure Change in the KLF4 Gene in Endothelial Cells. PLoS ONE, 2014, 9, e96005.	2.5	37
45	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. EMBO Journal, 2020, 39, e103949.	7.8	37
46	Silver nanoparticles impair zebrafish skeletal and cardiac myofibrillogenesis and sarcomere formation. Aquatic Toxicology, 2018, 200, 102-113.	4.0	34
47	Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data. Lecture Notes in Computer Science, 2013, , 317-332.	1.3	30
48	Dissecting the chromatin interactome of microRNA genes. Nucleic Acids Research, 2014, 42, 3028-3043.	14.5	27
49	Plant 3D genomics: the exploration and application of chromatin organization. New Phytologist, 2021, 230, 1772-1786.	7.3	23
50	Chromatin Interaction Analysis with Updated ChIA-PET Tool (V3). Genes, 2019, 10, 554.	2.4	22
51	Profiling plant histone modification at single‐cell resolution using snCUT&Tag. Plant Biotechnology Journal, 2022, 20, 420-422.	8.3	22
52	Structural Variations of the 3D Genome Architecture in Cervical Cancer Development. Frontiers in Cell and Developmental Biology, 2021, 9, 706375.	3.7	21
53	Copper stress induces zebrafish central neural system myelin defects via WNT/NOTCH-hoxb5b signaling and pou3f1/fam168a/fam168b DNA methylation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194612.	1.9	20
54	ASMdb: a comprehensive database for allele-specific DNA methylation in diverse organisms. Nucleic Acids Research, 2022, 50, D60-D71.	14.5	20

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55	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. Scientific Reports, 2016, 6, 36572.	3.3	19
56	A Large-Scale, Exome-Wide Association Study of Han Chinese Women Identifies Three Novel Loci Predisposing to Breast Cancer. Cancer Research, 2018, 78, 3087-3097.	0.9	19
57	CoolBox: a flexible toolkit for visual analysis of genomics data. BMC Bioinformatics, 2021, 22, 489.	2.6	19
58	Chromatin interaction networks and higher order architectures of eukaryotic genomes. Journal of Cellular Biochemistry, 2011, 112, 2218-2221.	2.6	18
59	Rapid and Low-Input Profiling of Histone Marks in Plants Using Nucleus CUT&Tag. Frontiers in Plant Science, 2021, 12, 634679.	3.6	17
60	RiceENCODE: A comprehensive epigenomic database as a rice Encyclopedia of DNA Elements. Molecular Plant, 2021, 14, 1604-1606.	8.3	17
61	L2MXception: an improved Xception network for classification of peach diseases. Plant Methods, 2021, 17, 36.	4.3	16
62	RiceLncPedia: a comprehensive database of rice long nonâ€coding RNAs. Plant Biotechnology Journal, 2021, 19, 1492-1494.	8.3	16
63	Genetic variation of ESR1 and its co-activator PPARGC1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. Breast Cancer Research, 2011, 13, R10.	5.0	15
64	The DLO Hi-C Tool for Digestion-Ligation-Only Hi-C Chromosome Conformation Capture Data Analysis. Genes, 2020, 11, 289.	2.4	15
65	SurVirus: a repeat-aware virus integration caller. Nucleic Acids Research, 2021, 49, e33-e33.	14.5	15
66	The landscape of promoter-centred RNAâ€"DNA interactions in rice. Nature Plants, 2022, 8, 157-170.	9.3	15
67	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.	2.5	13
68	Advances in technologies for 3D genomics research. Science China Life Sciences, 2020, 63, 811-824.	4.9	13
69	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, ChIP-Seq and ChIA-PET data. BMC Genomics, 2019, 20, 296.	2.8	12
70	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. Metallomics, 2019, 11, 1452-1464.	2.4	11
71	TAD boundary and strength prediction by integrating sequence and epigenetic profile information. Briefings in Bioinformatics, 2021, 22, .	6.5	11
72	RUNX1-mediated alphaherpesvirus-host trans-species chromatin interaction promotes viral transcription. Science Advances, 2021, 7, .	10.3	11

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73	Effects of parental environmental copper stress on offspring development: DNA methylation modification and responses of differentially methylated region-related genes in transcriptional expression. Journal of Hazardous Materials, 2022, 424, 127600.	12.4	10
74	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	2.5	9
75	Diurnal RNAPII-tethered chromatin interactions are associated with rhythmic gene expression in rice. Genome Biology, 2022, 23, 7.	8.8	9
76	Analyzing the Fitch Method for Reconstructing Ancestral States on Ultrametric Phylogenetic Trees. Bulletin of Mathematical Biology, 2010, 72, 1760-1782.	1.9	8
77	In silico identification of enhancers on the basis of a combination of transcription factor binding motif occurrences. Scientific Reports, 2016, 6, 32476.	3.3	8
78	Decoding the plant genome: From epigenome to 3D organization. Journal of Genetics and Genomics, 2020, 47, 425-435.	3.9	8
79	Technologies for Capturing 3D Genome Architecture in Plants. Trends in Plant Science, 2021, 26, 196-197.	8.8	8
80	Statistical Models for Detecting Differential Chromatin Interactions Mediated by a Protein. PLoS ONE, 2014, 9, e97560.	2.5	7
81	Deep Learning-Based Segmentation of Peach Diseases Using Convolutional Neural Network. Frontiers in Plant Science, 2022, 13, .	3.6	7
82	Mapping long€range contacts between risk loci and target genes in human diseases with Capture Hi€C. Clinical and Translational Medicine, 2020, 10, e183.	4.0	6
83	Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. BMC Genomics, 2019, 20, 322.	2.8	5
84	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. BMC Bioinformatics, 2020, 21, 451.	2.6	5
85	Emergence of 3D genomics. Chinese Science Bulletin, 2014, 59, 1165-1172.	0.7	5
86	Robust capturing chromosome conformation using the DLO Hi-C 2.0 method. Journal of Genetics and Genomics, 2020, 47, 655-658.	3.9	4
87	HIVID2: an accurate tool to detect virus integrations in the host genome. Bioinformatics, 2021, 37, 1821-1827.	4.1	4
88	ChIAMM: A Mixture Model for Statistical Analysis of Long-Range Chromatin Interactions From ChIA-PET Experiments. Frontiers in Genetics, 2020, 11, 616160.	2.3	3
89	RAB2A promotes cervical cancer progression as revealed by comprehensive analysis of HPV integration and proteome in longitudinal cervical samples. Clinical and Translational Medicine, 2022, 12, e767.	4.0	2
90	Chromosomal Translocations Detection in Cancer Cells Using Chromosomal Conformation Capture Data. Genes, 2022, 13, 1170.	2.4	2

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91	Reconstruction of Three-Dimensional Structures of Chromatin and Its Biological Implications. Scientia Sinica Vitae, 2014, 44, 794-802.	0.3	1