

Guoliang Li

List of Publications by Year in descending order

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89
papers

9,785
citations

61857

43
h-index

49773

87
g-index

98
all docs

98
docs citations

98
times ranked

15621
citing authors

#	ARTICLE	IF	CITATIONS
1	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
2	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010, 20, 320-331.	2.4	930
3	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015, 163, 1611-1627.	13.5	881
4	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
5	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
6	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013, 504, 306-310.	13.7	405
7	Telomerase directly regulates NF- κ B-dependent transcription. <i>Nature Cell Biology</i> , 2012, 14, 1270-1281.	4.6	309
8	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
9	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
10	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010, 11, R22.	13.9	255
11	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
12	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
13	Cellular reprogramming by the conjoint action of ER α , FOXA1, and GATA3 to a ligand-inducible growth state. <i>Molecular Systems Biology</i> , 2011, 7, 526.	3.2	169
14	A Common Deletion in the APOBEC3 Genes and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2013, 105, 573-579.	3.0	141
15	Integrative model of genomic factors for determining binding site selection by estrogen receptor α . <i>Molecular Systems Biology</i> , 2010, 6, 456.	3.2	139
16	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	4.7	137
17	TNF α signals through specialized factories where responsive coding and miRNA genes are transcribed. <i>EMBO Journal</i> , 2012, 31, 4404-4414.	3.5	122
18	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	9.4	112

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19	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015, 12, 272-285.	2.9	112
20	3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data. <i>Journal of Computational Biology</i> , 2013, 20, 831-846.	0.8	110
21	Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways. <i>Plant Physiology</i> , 2016, 171, 2041-2054.	2.3	109
22	Identification of a Functional Genetic Variant at 16q12.1 for Breast Cancer Risk: Results from the Asia Breast Cancer Consortium. <i>PLoS Genetics</i> , 2010, 6, e1001002.	1.5	107
23	Common Variation in Vitamin D Pathway Genes Predicts Circulating 25-Hydroxyvitamin D Levels among African Americans. <i>PLoS ONE</i> , 2011, 6, e28623.	1.1	103
24	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	2.9	102
25	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
26	Distinct distribution and prognostic significance of molecular subtypes of breast cancer in Chinese women: a population-based cohort study. <i>BMC Cancer</i> , 2011, 11, 292.	1.1	93
27	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632.	5.8	93
28	Evaluation of Breast Cancer Susceptibility Loci in Chinese Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2357-2365.	1.1	92
29	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, 4991-4999.	1.4	92
30	Genetic and Clinical Predictors for Breast Cancer Risk Assessment and Stratification Among Chinese Women. <i>Journal of the National Cancer Institute</i> , 2010, 102, 972-981.	3.0	90
31	<i>NODULES WITH ACTIVATED DEFENSE 1</i> is required for maintenance of rhizobial endosymbiosis in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2016, 212, 176-191.	3.5	90
32	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. <i>Cell Host and Microbe</i> , 2017, 22, 561-573.e4.	5.1	89
33	APOBEC3 deletion polymorphism is associated with breast cancer risk among women of European ancestry. <i>Carcinogenesis</i> , 2013, 34, 2240-2243.	1.3	85
34	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012, 58, 289-299.	1.9	83
35	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
36	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	75

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37	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
38	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011, 21, 665-675.	2.4	74
39	Evaluation of 11 Breast Cancer Susceptibility Loci in African-American Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 2761-2764.	1.1	73
40	Replication and Functional Genomic Analyses of the Breast Cancer Susceptibility Locus at 6q25.1 Generalize Its Importance in Women of Chinese, Japanese, and European Ancestry. <i>Cancer Research</i> , 2011, 71, 1344-1355.	0.4	71
41	A genome-wide association study of breast cancer in women of African ancestry. <i>Human Genetics</i> , 2013, 132, 39-48.	1.8	70
42	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
43	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
44	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019, 20, 47.	1.2	51
45	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	3.8	48
46	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
47	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <i>Genome Biology</i> , 2012, 13, R82.	13.9	45
48	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
49	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
50	Silver nanoparticles impair zebrafish skeletal and cardiac myofibrillogenesis and sarcomere formation. <i>Aquatic Toxicology</i> , 2018, 200, 102-113.	1.9	34
51	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.	1.0	30
52	Imidazole facilitates electron transfer from organic reductants. <i>Bioelectrochemistry</i> , 2004, 64, 7-13.	2.4	27
53	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	6.5	27
54	Oxidation of 4-Methylcatechol: Implications for the Oxidation of Catecholamines. <i>Biochemistry</i> , 2007, 46, 6978-6983.	1.2	24

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55	Association of genetic variants for colorectal cancer differs by subtypes of polyps in the colorectum. <i>Carcinogenesis</i> , 2012, 33, 2417-2423.	1.3	23
56	Interaction of cigarette smoking and carcinogen-metabolizing polymorphisms in the risk of colorectal polyps. <i>Carcinogenesis</i> , 2013, 34, 779-786.	1.3	23
57	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021, 230, 1772-1786.	3.5	23
58	Chromatin Interaction Analysis with Updated ChIA-PET Tool (V3). <i>Genes</i> , 2019, 10, 554.	1.0	22
59	Profiling plant histone modification at single-cell resolution using snCUT&Tag. <i>Plant Biotechnology Journal</i> , 2022, 20, 420-422.	4.1	22
60	ASSEMB: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2022, 50, D60-D71.	6.5	20
61	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
62	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
63	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 2218-2221.	1.2	18
64	Urinary polyphenols, glutathione S-transferases copy number variation, and breast cancer risk: Results from the Shanghai women's health study. <i>Molecular Carcinogenesis</i> , 2012, 51, 379-388.	1.3	17
65	Identification of MyoD-Responsive Transcripts Reveals a Novel Long Non-coding RNA (lncRNA-AK143003) that Negatively Regulates Myoblast Differentiation. <i>Scientific Reports</i> , 2017, 7, 2828.	1.6	17
66	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.	2.2	15
67	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
68	The landscape of promoter-centred RNA-DNA interactions in rice. <i>Nature Plants</i> , 2022, 8, 157-170.	4.7	15
69	A Study of Prostaglandin Pathway Genes and Interactions with Current Nonsteroidal Anti-inflammatory Drug Use in Colorectal Adenoma. <i>Cancer Prevention Research</i> , 2012, 5, 855-863.	0.7	14
70	Using gene-environment interaction analyses to clarify the role of well-done meat and heterocyclic amine exposure in the etiology of colorectal polyps. <i>American Journal of Clinical Nutrition</i> , 2012, 96, 1119-1128.	2.2	14
71	Calcium/magnesium intake ratio, but not magnesium intake, interacts with genetic polymorphism in relation to colorectal neoplasia in a two-phase study. <i>Molecular Carcinogenesis</i> , 2016, 55, 1449-1457.	1.3	14
72	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.	1.1	13

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73	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, ChIP-Seq and ChIA-PET data. BMC Genomics, 2019, 20, 296.	1.2	12
74	Genome-Wide Association Study Identifies Possible Genetic Risk Factors for Colorectal Adenomas. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1219-1226.	1.1	11
75	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. PLoS ONE, 2011, 6, e26054.	1.1	11
76	Association of a single nucleotide polymorphism at 6q25.1,rs2046210, with endometrial cancer risk among Chinese women. Chinese Journal of Cancer, 2011, 30, 138-143.	4.9	10
77	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	1.1	9
78	Calcium Intake and Ion Transporter Genetic Polymorphisms Interact in Human Colorectal Neoplasia Risk in a 2-Phase Study. Journal of Nutrition, 2014, 144, 1734-1741.	1.3	9
79	Analyzing the Fitch Method for Reconstructing Ancestral States on Ultrametric Phylogenetic Trees. Bulletin of Mathematical Biology, 2010, 72, 1760-1782.	0.9	8
80	In silico identification of enhancers on the basis of a combination of transcription factor binding motif occurrences. Scientific Reports, 2016, 6, 32476.	1.6	8
81	Genetic variation in SLC7A2 interacts with calcium and magnesium intakes in modulating the risk of colorectal polyps. Journal of Nutritional Biochemistry, 2017, 47, 35-40.	1.9	8
82	Decoding the plant genome: From epigenome to 3D organization. Journal of Genetics and Genomics, 2020, 47, 425-435.	1.7	8
83	Active Learning for Causal Bayesian Network Structure with Non-symmetrical Entropy. Lecture Notes in Computer Science, 2009, , 290-301.	1.0	8
84	Statistical Models for Detecting Differential Chromatin Interactions Mediated by a Protein. PLoS ONE, 2014, 9, e97560.	1.1	7
85	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. BMC Bioinformatics, 2020, 21, 451.	1.2	5
86	Emergence of 3D genomics. Chinese Science Bulletin, 2014, 59, 1165-1172.	0.4	5
87	Two new bag generators with multi-instance learning for image retrieval. , 2008, , .		1
88	Robust visual tracking via deep discriminative model. , 2017, , .		1
89	Identifying Causal Effects from Data for the Clinical Ventilation Process Modelling. , 2008, , .		0