

Guoliang Li

List of Publications by Year in descending order

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89

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61984

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docs citations

98

times ranked

15621

citing authors

#	ARTICLE	IF	CITATIONS
1	ASMDb: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2022, 50, D60-D71.	14.5	20
2	Profiling plant histone modification at single-cell resolution using snCUT&Tag. <i>Plant Biotechnology Journal</i> , 2022, 20, 420-422.	8.3	22
3	The landscape of promoter-centred RNA-DNA interactions in rice. <i>Nature Plants</i> , 2022, 8, 157-170.	9.3	15
4	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021, 230, 1772-1786.	7.3	23
5	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <i>BMC Bioinformatics</i> , 2020, 21, 451.	2.6	5
6	Decoding the plant genome: From epigenome to 3D organization. <i>Journal of Genetics and Genomics</i> , 2020, 47, 425-435.	3.9	8
7	The DLO Hi-C Tool for Digestion-Ligation-Only Hi-C Chromosome Conformation Capture Data Analysis. <i>Genes</i> , 2020, 11, 289.	2.4	15
8	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019, 10, 3640.	12.8	75
9	Chromatin Interaction Analysis with Updated ChIA-PET Tool (V3). <i>Genes</i> , 2019, 10, 554.	2.4	22
10	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019, 20, 47.	2.6	51
11	Hierarchical cooperation of transcription factors from integration analysis of DNA sequences, ChIP-Seq and ChIA-PET data. <i>BMC Genomics</i> , 2019, 20, 296.	2.8	12
12	The effects of Arabidopsis genome duplication on the chromatin organization and transcriptional regulation. <i>Nucleic Acids Research</i> , 2019, 47, 7857-7869.	14.5	55
13	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632.	12.8	93
14	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019, 29, 223-235.	5.5	46
15	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019, 51, 138-150.	21.4	177
16	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.	21.4	468
17	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018, 4, 90-97.	9.3	137
18	Silver nanoparticles impair zebrafish skeletal and cardiac myofibrillogenesis and sarcomere formation. <i>Aquatic Toxicology</i> , 2018, 200, 102-113.	4.0	34

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19	Digestion-ligation-only Hi-C is an efficient and cost-effective method for chromosome conformation capture. <i>Nature Genetics</i> , 2018, 50, 754-763.	21.4	78
20	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.	0.9	19
21	Genetic variation in SLC7A2 interacts with calcium and magnesium intakes in modulating the risk of colorectal polyps. <i>Journal of Nutritional Biochemistry</i> , 2017, 47, 35-40.	4.2	8
22	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.	3.3	17
23	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. <i>Nature Protocols</i> , 2017, 12, 899-915.	12.0	99
24	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. <i>Cell Host and Microbe</i> , 2017, 22, 561-573.e4.	11.0	89
25	Robust visual tracking via deep discriminative model. , 2017, , .		1
26	<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.	7.3	90
27	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.	2.7	14
28	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.	4.8	245
29	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.	3.3	294
30	Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways. <i>Plant Physiology</i> , 2016, 171, 2041-2054.	4.8	109
31	Cooperation between the H3K27me3 chromatin marker and non-CG methylation in epigenetic regulation. <i>Plant Physiology</i> , 2016, 172, pp.01238.2016.	4.8	39
32	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. <i>Scientific Reports</i> , 2016, 6, 36572.	3.3	19
33	In silico identification of enhancers on the basis of a combination of transcription factor binding motif occurrences. <i>Scientific Reports</i> , 2016, 6, 32476.	3.3	8
34	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	8.8	48
35	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015, 163, 1611-1627.	28.9	881
36	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015, 12, 272-285.	6.4	112

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37	Direct Evidence for Pitavastatin Induced Chromatin Structure Change in the KLF4 Gene in Endothelial Cells. PLoS ONE, 2014, 9, e96005.	2.5	37
38	Dissecting the chromatin interactome of microRNA genes. Nucleic Acids Research, 2014, 42, 3028-3043.	14.5	27
39	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.	2.9	9
40	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
41	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. BMC Genomics, 2014, 15, S11.	2.8	75
42	Emergence of 3D genomics. Chinese Science Bulletin, 2014, 59, 1165-1172.	0.7	5
43	Statistical Models for Detecting Differential Chromatin Interactions Mediated by a Protein. PLoS ONE, 2014, 9, e97560.	2.5	7
44	Interaction of cigarette smoking and carcinogen-metabolizing polymorphisms in the risk of colorectal polyps. Carcinogenesis, 2013, 34, 779-786.	2.8	23
45	3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data. Journal of Computational Biology, 2013, 20, 831-846.	1.6	110
46	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. Cell, 2013, 155, 1507-1520.	28.9	299
47	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. Nature, 2013, 504, 306-310.	27.8	405
48	A genome-wide association study of breast cancer in women of African ancestry. Human Genetics, 2013, 132, 39-48.	3.8	70
49	A Common Deletion in the APOBEC3 Genes and Breast Cancer Risk. Journal of the National Cancer Institute, 2013, 105, 573-579.	6.3	141
50	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	21.4	112
51	APOBEC3 deletion polymorphism is associated with breast cancer risk among women of European ancestry. Carcinogenesis, 2013, 34, 2240-2243.	2.8	85
52	Genome-Wide Association Study Identifies Possible Genetic Risk Factors for Colorectal Adenomas. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1219-1226.	2.5	11
53	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
54	A Study of Prostaglandin Pathway Genes and Interactions with Current Nonsteroidal Anti-inflammatory Drug Use in Colorectal Adenoma. Cancer Prevention Research, 2012, 5, 855-863.	1.5	14

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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.	2.8	23
56	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.	4.7	14
57	Telomerase directly regulates NF- κ B-dependent transcription. <i>Nature Cell Biology</i> , 2012, 14, 1270-1281.	10.3	309
58	TNF α signals through specialized factories where responsive coding and miRNA genes are transcribed. <i>EMBO Journal</i> , 2012, 31, 4404-4414.	7.8	122
59	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012, 58, 289-299.	3.8	83
60	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <i>Genome Biology</i> , 2012, 13, R82.	9.6	45
61	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	6.4	102
62	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	28.9	1,096
63	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.	2.5	13
64	Urinary polyphenols, glutathione <i>S</i> -transferases copy number variation, and breast cancer risk: Results from the Shanghai women's health study. <i>Molecular Carcinogenesis</i> , 2012, 51, 379-388.	2.7	17
65	Genetic variation of ESR1 and its co-activator PPAR γ C1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. <i>Breast Cancer Research</i> , 2011, 13, R10.	5.0	15
66	Common Variation in Vitamin D Pathway Genes Predicts Circulating 25-Hydroxyvitamin D Levels among African Americans. <i>PLoS ONE</i> , 2011, 6, e28623.	2.5	103
67	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.	7.2	169
68	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.	2.6	93
69	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	21.4	567
70	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 2218-2221.	2.6	18
71	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.	5.5	74
72	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.	0.9	71

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73	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
74	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. PLoS ONE, 2011, 6, e26054.	2.5	11
75	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
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	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	2.5	9
78	Integrative model of genomic factors for determining binding site selection by estrogen receptor α . Molecular Systems Biology, 2010, 6, 456.	7.2	139
79	Genetic and Clinical Predictors for Breast Cancer Risk Assessment and Stratification Among Chinese Women. Journal of the National Cancer Institute, 2010, 102, 972-981.	6.3	90
80	Identification of a Functional Genetic Variant at 16q12.1 for Breast Cancer Risk: Results from the Asia Breast Cancer Consortium. PLoS Genetics, 2010, 6, e1001002.	3.5	107
81	Evaluation of Breast Cancer Susceptibility Loci in Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2357-2365.	2.5	92
82	Dynamic changes in the human methylome during differentiation. Genome Research, 2010, 20, 320-331.	5.5	930
83	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	9.6	255
84	Evaluation of 11 Breast Cancer Susceptibility Loci in African-American Women. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2761-2764.	2.5	73
85	Active Learning for Causal Bayesian Network Structure with Non-symmetrical Entropy. Lecture Notes in Computer Science, 2009, , 290-301.	1.3	8
86	Two new bag generators with multi-instance learning for image retrieval. , 2008, , .		1
87	Identifying Causal Effects from Data for the Clinical Ventilation Process Modelling. , 2008, , .		0
88	Oxidation of 4-Methylcatechol:Â Implications for the Oxidation of Catecholamines. Biochemistry, 2007, 46, 6978-6983.	2.5	24
89	Imidazole facilitates electron transfer from organic reductants. Bioelectrochemistry, 2004, 64, 7-13.	4.6	27