Bingshan Li

List of Publications by Year
in descending order

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88	5,366	172386	98753
papers	citations	29 h-index	67 g-index

96	96	96	12664
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Methods for Detecting Associations with Rare Variants for Common Diseases: Application to Analysis of Sequence Data. American Journal of Human Genetics, 2008, 83, 311-321.	2.6	1,382
2	RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. Bioinformatics, 2016, 32, 1423-1426.	1.8	366
3	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
4	Transcriptome Analysis of Psoriasis in a Large Caseâ€“Control Sample: RNA-Seq Provides Insights into Disease Mechanisms. Journal of Investigative Dermatology, 2014, 134, 1828-1838.	0.3	318
5	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. Nature Genetics, 2014, 46, 533-542.	9.4	212
6	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
7	Longitudinally collected CTCs and CTC-clusters and clinical outcomes of metastatic breast cancer. Breast Cancer Research and Treatment, 2017, 161, 83-94.	1.1	156
8	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	9.4	135
9	Prospective assessment of the prognostic value of circulating tumor cells and their clusters in patients with advanced-stage breast cancer. Breast Cancer Research and Treatment, 2015, 154, 563-571.	1.1	124
10	Discovery of Rare Variants via Sequencing: Implications for the Design of Complex Trait Association Studies. PLoS Genetics, 2009, 5, e1000481.	1.5	123
11	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. Nature Neuroscience, 2019, 22, 691-699.	7.1	118
12	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. Gastroenterology, 2019, 156, 1455-1466.	0.6	111
13	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	0.6	97
14	Effects of Cancer Stage and Treatment Differences on Racial Disparities in Survival From Colon Cancer: A United States Population-Based Study. Gastroenterology, 2016, 150, 1135-1146.	0.6	92
15	A Bayesian framework for de novo mutation calling in parents-offspring trios. Bioinformatics, 2015, 31, 1375-1381.	1.8	87
16	Evaluating the Utility of Polygenic Risk Scores in Identifying High-Risk Individuals for Eight Common Cancers. JNCI Cancer Spectrum, 2020, 4, pkaa021.	1.4	75
17	A Comprehensive cis-eQTL Analysis Revealed Target Genes in Breast Cancer Susceptibility Loci Identified in Genome-wide Association Studies. American Journal of Human Genetics, 2018, 102, 890-903.	2.6	72
18	A Likelihood-Based Framework for Variant Calling and De Novo Mutation Detection in Families. PLoS Genetics, 2012, 8, e1002944.	1.5	71

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19	Cell-free circulating mitochondrial DNA content and risk of hepatocellular carcinoma in patients with chronic HBV infection. Scientific Reports, 2016, 6, 23992.	1.6	66
20	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
21	A big-data approach to understanding metabolic rate and response to obesity in laboratory mice. ELife, 2020, 9, .	2.8	54
22	Rare and common variants in extracellular matrix gene Fibrillin 2 (FBN2) are associated with macular degeneration. Human Molecular Genetics, 2014, 23, 5827-5837.	1.4	52
23	Leveraging blood serotonin as an endophenotype to identify de novo and rare variants involved in autism. Molecular Autism, 2017, 8, 14.	2.6	50
24	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.4	49
25	Genotype calling and haplotyping in parent-offspring trios. Genome Research, 2013, 23, 142-151.	2.4	46
26	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
27	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2022, 14, 7.	3.0	42
28	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. Human Molecular Genetics, 2016, 25, 3361-3371.	1.4	40
29	Association of clinical outcomes in metastatic breast cancer patients with circulating tumour cell and circulating cell-free DNA. European Journal of Cancer, 2019, 106, 133-143.	1.3	35
30	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€‰951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	3.0	35
31	A gradient-boosting approach for filtering de novo mutations in parentâ€“offspring trios. Bioinformatics, 2014, 30, 1830-1836.	1.8	33
32	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. Nature Medicine, 2020, 26, 98-109.	15.2	32
33	Prognostic value of HER2 status on circulating tumor cells in advanced-stage breast cancer patients with HER2-negative tumors. Breast Cancer Research and Treatment, 2020, 181, 679-689.	1.1	30
34	Identifying Rare Variants Associated with Complex Traits via Sequencing. Current Protocols in Human Genetics, 2013, 78, Unit 1.26.	3.5	29
35	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	5.8	29
36	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	28

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37	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	1.1	25
38	Rare Coding Variants and Breast Cancer Risk: Evaluation of Susceptibility Loci Identified in Genome-Wide Association Studies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 622-628.	1.1	24
39	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. Scientific Reports, 2017, 7, 3847.	1.6	23
40	Genetic and chromosomal alterations in K enyan W ilms T umor. Genes Chromosomes and Cancer, 2015, 54, 702-715.	1.5	22
41	Cancer driver gene discovery through an integrative genomics approach in a non-parametric Bayesian framework. Bioinformatics, 2017, 33, 483-490.	1.8	22
42	Multiâ€regional sequencing reveals intratumor heterogeneity and positive selection of somatic mtDNA mutations in hepatocellular carcinoma and colorectal cancer. International Journal of Cancer, 2018, 143, 1143-1152.	2.3	21
43	Deviations from Hardy-Weinberg Equilibrium in Parental and Unaffected Sibling Genotype Data. Human Heredity, 2009, 67, 104-115.	0.4	20
44	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	5.8	19
45	Joint detection of copy number variations in parent-offspring trios. Bioinformatics, 2016, 32, 1130-1137.	1.8	18
46	QPLOT: A Quality Assessment Tool for Next Generation Sequencing Data. BioMed Research International, 2013, 2013, 1-4.	0.9	17
47	Improved Prognostic Stratification Using Circulating Tumor Cell Clusters in Patients with Metastatic Castration-Resistant Prostate Cancer. Cancers, 2021, 13, 268.	1.7	16
48	De novopattern discovery enables robust assessment of functional consequences of non-coding variants. Bioinformatics, 2019, 35, 1453-1460.	1.8	15
49	Ca:Mg Ratio, APOE Cytosine Modifications, and Cognitive Function: Results from a Randomized Trial. Journal of Alzheimer's Disease, 2020, 75, 85-98.	1.2	15
50	Whole-exome sequencing identifies somatic mutations and intratumor heterogeneity in inflammatory breast cancer. Npj Breast Cancer, 2021, 7, 72.	2.3	15
51	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	1.8	14
52	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. Genetics, 2015, 201, 1329-1339.	1.2	14
53	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. EBioMedicine, 2019, 48, 203-211.	2.7	14
54	Integration of circulating tumor cell and neutrophil-lymphocyte ratio to identify high-risk metastatic castration-resistant prostate cancer patients. BMC Cancer, 2021, 21, 655.	1.1	14

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55	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
56	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. Reproductive Sciences, 2019, 26, 496-502.	1.1	13
57	Improved Variant Calling Accuracy by Merging Replicates in Whole-Exome Sequencing Studies. BioMed Research International, 2014, 2014, 1-7.	0.9	12
58	The impact of genotype calling errors on family-based studies. Scientific Reports, 2016, 6, 28323.	1.6	12
59	Site-specific selection reveals selective constraints and functionality of tumor somatic mtDNA mutations. Journal of Experimental and Clinical Cancer Research, 2017, 36, 168.	3.5	12
60	Incorporating Polygenic Risk Scores and Nongenetic Risk Factors for Breast Cancer Risk Prediction Among Asian Women. JAMA Network Open, 2022, 5, e2149030.	2.8	12
61	Methods for the Analysis and Interpretation for Rare Variants Associated with Complex Traits. Current Protocols in Human Genetics, 2019, 101, e83.	3.5	11
62	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. Genome Biology, 2020, 21, 217.	3.8	11
63	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1421-1430.	2.2	10
64	Integrating Genome and Methylome Data to Identify Candidate DNA Methylation Biomarkers for Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2079-2087.	1.1	10
65	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
66	A computational method for genotype calling in family-based sequencing data. BMC Bioinformatics, 2016, 17, 37.	1.2	8
67	Molecular and epidemiologic characterization of Wilms tumor from Baghdad, Iraq. World Journal of Pediatrics, 2018, 14, 585-593.	0.8	8
68	Insight into the Etiology of Undifferentiated Soft Tissue Sarcomas from a Novel Mouse Model. Molecular Cancer Research, 2019, 17, 1024-1035.	1.5	8
69	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. PLoS Computational Biology, 2020, 16, e1007522.	1.5	8
70	Incorporating European GWAS findings improve polygenic risk prediction accuracy of breast cancer among East Asians. Genetic Epidemiology, 2021, 45, 471-484.	0.6	7
71	Ignoring Intermarker Linkage Disequilibrium Induces False-Positive Evidence of Linkage for Consanguineous Pedigrees when Genotype Data Is Missing for Any Pedigree Member. Human Heredity, 2008, 65, 199-208.	0.4	6
72	Prospective and longitudinal evaluations of telomere length of circulating DNA as a risk predictor of hepatocellular carcinoma in HBV patients. Carcinogenesis, 2017, 38, 439-446.	1.3	6

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73	Race disparities in genetic alterations within Wilms tumor specimens. Journal of Pediatric Surgery, 2021, 56, 1135-1141.	0.8	4
74	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data fromâ€‰>â€‰2000 women of African-ancestry. Human Genetics, 2021, 140, 1449-1457.	1.8	4
75	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	1.5	3
76	Blunted PTH response to vitamin D insufficiency/deficiency and colorectal neoplasia risk. Clinical Nutrition, 2021, 40, 3305-3313.	2.3	3
77	A computational framework to unify orthogonal information in DNA methylation and copy number aberrations in cell-free DNA for early cancer detection. Briefings in Bioinformatics, 2022, 23, .	3.2	3
78	Evaluating breast cancer predisposition genes in women of African ancestry. Genetics in Medicine, 2022, 24, 1468-1475.	1.1	2
79	Integration of multidimensional splicing data and GWAS summary statistics for risk gene discovery. PLoS Genetics, 2022, 18, e1009814.	1.5	1
80	Incidental Pulmonary Metastases Revealing Subcentimeter Papillary Thyroid Carcinoma. AACE Clinical Case Reports, 2020, 6, e273-e278.	0.4	0
81	Leveraging Gene-Level Prediction as Informative Covariate in Hypothesis Weighting Improves Power for Rare Variant Association Studies. Genes, 2022, 13, 381.	1.0	0
82	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
83	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
84	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
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86	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
87	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
88	A Bayesian framework to integrate multi-level genome-scale data for Autism risk gene prioritization. BMC Bioinformatics, 2022, 23, 146.	1.2	0