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	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2022, 14, 7.	3.0	42
2	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	5.8	19
3	Leveraging Gene-Level Prediction as Informative Covariate in Hypothesis Weighting Improves Power for Rare Variant Association Studies. Genes, 2022, 13, 381.	1.0	0
4	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
5	Evaluating breast cancer predisposition genes in women of African ancestry. Genetics in Medicine, 2022, 24, 1468-1475.	1.1	2
6	A Bayesian framework to integrate multi-level genome-scale data for Autism risk gene prioritization. BMC Bioinformatics, 2022, 23, 146.	1.2	0
7	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
8	Integration of multidimensional splicing data and GWAS summary statistics for risk gene discovery. PLoS Genetics, 2022, 18, e1009814.	1.5	1
9	Blunted PTH response to vitamin D insufficiency/deficiency and colorectal neoplasia risk. Clinical Nutrition, 2021, 40, 3305-3313.	2.3	3
10	Improved Prognostic Stratification Using Circulating Tumor Cell Clusters in Patients with Metastatic Castration-Resistant Prostate Cancer. Cancers, 2021, 13, 268.	1.7	16
11	Incorporating European GWAS findings improve polygenic risk prediction accuracy of breast cancer among East Asians. Genetic Epidemiology, 2021, 45, 471-484.	0.6	7
12	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
13	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	5.8	29
14	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
15	Race disparities in genetic alterations within Wilms tumor specimens. Journal of Pediatric Surgery, 2021, 56, 1135-1141.	0.8	4
16	Whole-exome sequencing identifies somatic mutations and intratumor heterogeneity in inflammatory breast cancer. Npj Breast Cancer, 2021, 7, 72.	2.3	15
17	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
18	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

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19	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
20	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
21	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
22	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	28
23	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
24	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
25	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
26	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
27	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
28	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
29	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
30	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
31	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
32	A big-data approach to understanding metabolic rate and response to obesity in laboratory mice. ELife, 2020, 9, .	2.8	54
33	Incidental Pulmonary Metastases Revealing Subcentimeter Papillary Thyroid Carcinoma. AACE Clinical Case Reports, 2020, 6, e273-e278.	0.4	0
34	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
35	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
36	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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37	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
38	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
39	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. , 2020, 16, e1007522.		0
40	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
41	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. Reproductive Sciences, 2019, 26, 496-502.	1.1	13
42	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
43	Insight into the Etiology of Undifferentiated Soft Tissue Sarcomas from a Novel Mouse Model. Molecular Cancer Research, 2019, 17, 1024-1035.	1.5	8
44	Methods for the Analysis and Interpretation for Rare Variants Associated with Complex Traits. Current Protocols in Human Genetics, 2019, 101, e83.	3.5	11
45	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
46	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
47	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
48	De novopattern discovery enables robust assessment of functional consequences of non-coding variants. Bioinformatics, 2019, 35, 1453-1460.	1.8	15
49	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
50	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
51	Molecular and epidemiologic characterization of Wilms tumor from Baghdad, Iraq. World Journal of Pediatrics, 2018, 14, 585-593.	0.8	8
52	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
53	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
54	Cancer driver gene discovery through an integrative genomics approach in a non-parametric Bayesian framework. Bioinformatics, 2017, 33, 483-490.	1.8	22

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55	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
56	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
57	Leveraging blood serotonin as an endophenotype to identify de novo and rare variants involved in autism. Molecular Autism, 2017, 8, 14.	2.6	50
58	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
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	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
61	The impact of genotype calling errors on family-based studies. Scientific Reports, 2016, 6, 28323.	1.6	12
62	A computational method for genotype calling in family-based sequencing data. BMC Bioinformatics, 2016, 17, 37.	1.2	8
63	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. Human Molecular Genetics, 2016, 25, 3361-3371.	1.4	40
64	Joint detection of copy number variations in parent-offspring trios. Bioinformatics, 2016, 32, 1130-1137.	1.8	18
65	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
66	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	0.6	97
67	RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. Bioinformatics, 2016, 32, 1423-1426.	1.8	366
68	Genetic and chromosomal alterations in K enyan W ilms T umor. Genes Chromosomes and Cancer, 2015, 54, 702-715.	1.5	22
69	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	1.5	3
70	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	1.8	14
71	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
72	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

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73	A Bayesian framework for de novo mutation calling in parents-offspring trios. Bioinformatics, 2015, 31, 1375-1381.	1.8	87
74	A gradient-boosting approach for filtering de novo mutations in parentâ€“offspring trios. Bioinformatics, 2014, 30, 1830-1836.	1.8	33
75	Improved Variant Calling Accuracy by Merging Replicates in Whole-Exome Sequencing Studies. BioMed Research International, 2014, 2014, 1-7.	0.9	12
76	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
77	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
78	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
79	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
80	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
81	Identifying Rare Variants Associated with Complex Traits via Sequencing. Current Protocols in Human Genetics, 2013, 78, Unit 1.26.	3.5	29
82	Genotype calling and haplotyping in parent-offspring trios. Genome Research, 2013, 23, 142-151.	2.4	46
83	QPLOT: A Quality Assessment Tool for Next Generation Sequencing Data. BioMed Research International, 2013, 2013, 1-4.	0.9	17
84	A Likelihood-Based Framework for Variant Calling and De Novo Mutation Detection in Families. PLoS Genetics, 2012, 8, e1002944.	1.5	71
85	Discovery of Rare Variants via Sequencing: Implications for the Design of Complex Trait Association Studies. PLoS Genetics, 2009, 5, e1000481.	1.5	123
86	Deviations from Hardy-Weinberg Equilibrium in Parental and Unaffected Sibling Genotype Data. Human Heredity, 2009, 67, 104-115.	0.4	20
87	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
88	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