Mulin Jun Li

List of Publications by Year
in descending order

57 papers	3,152 citations	218381 26 h-index	182168 51 g-index
64 all docs	64 docs citations	64 times ranked	7872 citing authors

#	Article	IF	Citations
1	VannoPortal: multiscale functional annotation of human genetic variants for interrogating molecular mechanism of traits and diseases. Nucleic Acids Research, 2022, 50, D1408-D1416.	6.5	31
2	webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. Nucleic Acids Research, 2022, 50, D1123-D1130.	6.5	160
3	Global urbanicity is associated with brain and behaviour in young people. Nature Human Behaviour, 2022, 6, 279-293.	6.2	24
4	Deviation from baseline mutation burden provides powerful and robust rare-variants association test for complex diseases. Nucleic Acids Research, 2022, 50, e34-e34.	6.5	3
5	A conditional gene-based association framework integrating isoform-level eQTL data reveals new susceptibility genes for schizophrenia. ELife, 2022, 11, .	2.8	5
6	Powerful and robust inference of complex phenotypes' causal genes with dependent expression quantitative loci by a median-based Mendelian randomization. American Journal of Human Genetics, 2022, 109, 838-856.	2.6	8
7	vSampler: fast and annotation-based matched variant sampling tool. Bioinformatics, 2021, 37, 1915-1917.	1.8	8
8	Hippocampal transcriptome-wide association study and neurobiological pathway analysis for Alzheimerâ€™s disease. PLoS Genetics, 2021, 17, e1009363.	1.5	18
9	Effects of lysine 2-hydroxyisobutyrylation on bacterial FabI activity and resistance to triclosan. Biochimie, 2021, 182, 197-205.	1.3	5
10	Serine metabolism antagonizes antiviral innate immunity by preventing ATP6V0d2-mediated YAP lysosomal degradation. Cell Metabolism, 2021, 33, 971-987.e6.	7.2	51
11	Coagulation factors and the incidence of COVID-19 severity: Mendelian randomization analyses and supporting evidence. Signal Transduction and Targeted Therapy, 2021, 6, 222.	7.1	15
12	Inducible CRISPRa screen identifies putative enhancers. Journal of Genetics and Genomics, 2021, 48, 917-927.	1.7	13
13	Editorial: Deciphering Non-Coding Regulatory Variants: Computational and Functional Validation. Frontiers in Bioengineering and Biotechnology, 2021, 9, 769614.	2.0	2
14	Interrogating cell type-specific cooperation of transcriptional regulators in 3D chromatin. IScience, 2021, 24, 103468.	1.9	6
15	Genome-wide association and functional interrogation identified a variant at 3p26.1 modulating ovarian cancer survival among Chinese women. Cell Discovery, 2021, 7, 121.	3.1	5
16	QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes. Nucleic Acids Research, 2020, 48, D983-D991.	6.5	82
17	JMJD6 modulates DNA damage response through downregulating H4K16ac independently of its enzymatic activity. Cell Death and Differentiation, 2020, 27, 1052-1066.	5.0	13
18	CHIMGEN: a Chinese imaging genetics cohort to enhance cross-ethnic and cross-geographic brain research. Molecular Psychiatry, 2020, 25, 517-529.	4.1	35

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19	Methods and resources to access mutation-dependent effects on cancer drug treatment. Briefings in Bioinformatics, 2020, 21, 1886-1903.	3.2	5
20	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. Genome Research, 2020, 30, 1789-1801.	2.4	14
21	The support of genetic evidence for cardiovascular risk induced by antineoplastic drugs. Science Advances, 2020, 6, .	4.7	7
22	HRP2â€“DPF3aâ€“BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription. Nucleic Acids Research, 2020, 48, 6563-6582.	6.5	25
23	Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction. Computational and Structural Biotechnology Journal, 2020, 18, 558-570.	1.9	37
24	epiCOLOC: Integrating Large-Scale and Context-Dependent Epigenomics Features for Comprehensive Colocalization Analysis. Frontiers in Genetics, 2020, 11, 53.	1.1	13
25	Diversity spectrum analysis identifies mutation-specific effects of cancer driver genes. Communications Biology, 2020, 3, 6.	2.0	9
26	WITER: a powerful method for estimation of cancer-driver genes using a weighted iterative regression modelling background mutation counts. Nucleic Acids Research, 2019, 47, e96-e96.	6.5	28
27	CAUSALdb: a database for disease/trait causal variants identified using summary statistics of genome-wide association studies. Nucleic Acids Research, 2019, 48, D807-D816.	6.5	34
28	regBase: whole genome base-wise aggregation and functional prediction for human non-coding regulatory variants. Nucleic Acids Research, 2019, 47, e134-e134.	6.5	41
29	Activation of P-TEFb by cAMP-PKA signaling in autosomal dominant polycystic kidney disease. Science Advances, 2019, 5, eaaw3593.	4.7	33
30	Targeting Super-Enhancer-Driven Oncogenic Transcription by CDK7 Inhibition in Anaplastic Thyroid Carcinoma. Thyroid, 2019, 29, 809-823.	2.4	42
31	Integrated transcriptomic and regulatory network analyses identify microRNA-200c as a novel repressor of human pluripotent stem cell-derived cardiomyocyte differentiation and maturation. Cardiovascular Research, 2018, 114, 894-906.	1.8	44
32	A powerful approach reveals numerous expression quantitative trait haplotypes in multiple tissues. Bioinformatics, 2018, 34, 3145-3150.	1.8	9
33	Neurobiological substrates underlying the effect of genomic risk for depression on the conversion of amnestic mild cognitive impairment. Brain, 2018, 141, 3457-3471.	3.7	18
34	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic Acids Research, 2018, 46, W114-W120.	6.5	69
35	Long noncoding RNA LINC00305 promotes inflammation by activating the AHRR-NF-ÎºB pathway in human monocytes. Scientific Reports, 2017, 7, 46204.	1.6	53
36	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	6.5	36

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37	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. Nucleic Acids Research, 2017, 45, W215-W221.	6.5	12
38	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	6.5	39
39	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	3.8	33
40	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
41	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	1.8	40
42	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	6.5	184
43	Rare SNP rs12731181 in the miR-590-3p Target Site of the Prostaglandin F _{2Î±} Receptor Gene Confers Risk for Essential Hypertension in the Han Chinese Population. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1687-1695.	1.1	15
44	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. Nucleic Acids Research, 2015, 43, W264-W269.	6.5	19
45	wKGGSeq: A Comprehensive Strategy-Based and Disease-Targeted Online Framework to Facilitate Exome Sequencing Studies of Inherited Disorders. Human Mutation, 2015, 36, 496-503.	1.1	10
46	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	9.4	1,112
47	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. Briefings in Bioinformatics, 2015, 16, 393-412.	3.2	58
48	Current trend of annotating single nucleotide variation in humans â€“ A case study on SNVrap. Methods, 2015, 79-80, 32-40.	1.9	12
49	dbPSHP: a database of recent positive selection across human populations. Nucleic Acids Research, 2014, 42, D910-D916.	6.5	36
50	DDGni: Dynamic delay gene-network inference from high-temporal data using gapped local alignment. Bioinformatics, 2014, 30, 377-383.	1.8	24
51	GWAS3D: detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. Nucleic Acids Research, 2013, 41, W150-W158.	6.5	101
52	Genetic variant representation, annotation and prioritization in the post-GWAS era. Cell Research, 2012, 22, 1505-1508.	5.7	31
53	GWASdb: a database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2012, 40, D1047-D1054.	6.5	204
54	A fast and accurate SNP detection algorithm for next-generation sequencing data. Nature Communications, 2012, 3, 1258.	5.8	51

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55	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. Epigenetics, 2011, 6, 1505-1512.	1.3	19
56	ChIP-Array: combinatory analysis of ChIP-seq/chip and microarray gene expression data to discover direct/indirect targets of a transcription factor. Nucleic Acids Research, 2011, 39, W430-W436.	6.5	49
57	FastPval: a fast and memory efficient program to calculate very low P-values from empirical distribution. Bioinformatics, 2010, 26, 2897-2899.	1.8	21