Mulin Jun Li

List of Publications by Year
in descending order

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57 papers	3,152 citations	218592 26 h-index	182361 51 g-index
64 all docs	64 docs citations	64 times ranked	7872 citing authors

#	Article	IF	Citations
1	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	9.4	1,112
2	GWASdb: a database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2012, 40, D1047-D1054.	6.5	204
3	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
4	webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. Nucleic Acids Research, 2022, 50, D1123-D1130.	6.5	160
5	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
6	QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes. Nucleic Acids Research, 2020, 48, D983-D991.	6.5	82
7	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
8	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic Acids Research, 2018, 46, W114-W120.	6.5	69
9	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
10	Long noncoding RNA LINC00305 promotes inflammation by activating the AHRR-NF-Î°B pathway in human monocytes. Scientific Reports, 2017, 7, 46204.	1.6	53
11	A fast and accurate SNP detection algorithm for next-generation sequencing data. Nature Communications, 2012, 3, 1258.	5.8	51
12	Serine metabolism antagonizes antiviral innate immunity by preventing ATP6V0d2-mediated YAP lysosomal degradation. Cell Metabolism, 2021, 33, 971-987.e6.	7.2	51
13	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
14	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
15	Targeting Super-Enhancer-Driven Oncogenic Transcription by CDK7 Inhibition in Anaplastic Thyroid Carcinoma. Thyroid, 2019, 29, 809-823.	2.4	42
16	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
17	Predicting regulatory variants with composite statistic. Bioinformatics, 2016, 32, 2729-2736.	1.8	40
18	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	6.5	39

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19	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
20	dbPSHP: a database of recent positive selection across human populations. Nucleic Acids Research, 2014, 42, D910-D916.	6.5	36
21	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
22	CHIMGEN: a Chinese imaging genetics cohort to enhance cross-ethnic and cross-geographic brain research. Molecular Psychiatry, 2020, 25, 517-529.	4.1	35
23	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
24	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	3.8	33
25	Activation of P-TEFb by cAMP-PKA signaling in autosomal dominant polycystic kidney disease. Science Advances, 2019, 5, eaaw3593.	4.7	33
26	Genetic variant representation, annotation and prioritization in the post-GWAS era. Cell Research, 2012, 22, 1505-1508.	5.7	31
27	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
28	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
29	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
30	DDGni: Dynamic delay gene-network inference from high-temporal data using gapped local alignment. Bioinformatics, 2014, 30, 377-383.	1.8	24
31	Global urbanicity is associated with brain and behaviour in young people. Nature Human Behaviour, 2022, 6, 279-293.	6.2	24
32	FastPval: a fast and memory efficient program to calculate very low P-values from empirical distribution. Bioinformatics, 2010, 26, 2897-2899.	1.8	21
33	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. Epigenetics, 2011, 6, 1505-1512.	1.3	19
34	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. Nucleic Acids Research, 2015, 43, W264-W269.	6.5	19
35	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
36	Hippocampal transcriptome-wide association study and neurobiological pathway analysis for Alzheimerâ€™s disease. PLoS Genetics, 2021, 17, e1009363.	1.5	18

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37	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
38	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
39	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. Genome Research, 2020, 30, 1789-1801.	2.4	14
40	JMJD6 modulates DNA damage response through downregulating H4K16ac independently of its enzymatic activity. Cell Death and Differentiation, 2020, 27, 1052-1066.	5.0	13
41	epiCOLOC: Integrating Large-Scale and Context-Dependent Epigenomics Features for Comprehensive Colocalization Analysis. Frontiers in Genetics, 2020, 11, 53.	1.1	13
42	Inducible CRISPRa screen identifies putative enhancers. Journal of Genetics and Genomics, 2021, 48, 917-927.	1.7	13
43	Current trend of annotating single nucleotide variation in humans â€“ A case study on SNVrap. Methods, 2015, 79-80, 32-40.	1.9	12
44	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
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	A powerful approach reveals numerous expression quantitative trait haplotypes in multiple tissues. Bioinformatics, 2018, 34, 3145-3150.	1.8	9
47	Diversity spectrum analysis identifies mutation-specific effects of cancer driver genes. Communications Biology, 2020, 3, 6.	2.0	9
48	vSampler: fast and annotation-based matched variant sampling tool. Bioinformatics, 2021, 37, 1915-1917.	1.8	8
49	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
50	The support of genetic evidence for cardiovascular risk induced by antineoplastic drugs. Science Advances, 2020, 6, .	4.7	7
51	Interrogating cell type-specific cooperation of transcriptional regulators in 3D chromatin. IScience, 2021, 24, 103468.	1.9	6
52	Methods and resources to access mutation-dependent effects on cancer drug treatment. Briefings in Bioinformatics, 2020, 21, 1886-1903.	3.2	5
53	Effects of lysine 2-hydroxyisobutyrylation on bacterial FabI activity and resistance to triclosan. Biochimie, 2021, 182, 197-205.	1.3	5
54	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

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55	A conditional gene-based association framework integrating isoform-level eQTL data reveals new susceptibility genes for schizophrenia. ELife, 2022, 11, .	2.8	5
56	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
57	Editorial: Deciphering Non-Coding Regulatory Variants: Computational and Functional Validation. Frontiers in Bioengineering and Biotechnology, 2021, 9, 769614.	2.0	2