Xin He

List of Publications by Year
in descending order

27 papers	7,614 citations	361296 20 h-index	501076 28 g-index
35 all docs	35 docs citations	35 times ranked	11423 citing authors

#	Article	IF	Citations
1	Annotating functional effects of non-coding variants in neuropsychiatric cell types by deep transfer learning. PLoS Computational Biology, 2022, 18, e1010011.	1.5	7
2	DECO: a framework for jointly analyzing de novo and rare case/control variants, and biological pathways. Briefings in Bioinformatics, 2021, 22, .	3.2	6
3	A functional genomics pipeline identifies pleiotropy and cross-tissue effects within obesity-associated GWAS loci. Nature Communications, 2021, 12, 5253.	5.8	19
4	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. Science Advances, 2020, 6, .	4.7	31
5	Allele-specific open chromatin in human iPSC neurons elucidates functional disease variants. Science, 2020, 369, 561-565.	6.0	77
6	Primo: integration of multiple GWAS and omics QTL summary statistics for elucidation of molecular mechanisms of trait-associated SNPs and detection of pleiotropy in complex traits. Genome Biology, 2020, 21, 236.	3.8	26
7	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. Nature Communications, 2020, 11, 2929.	5.8	10
8	Genetic analyses support the contribution of mRNA N6-methyladenosine (m6A) modification to human disease heritability. Nature Genetics, 2020, 52, 939-949.	9.4	113
9	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
10	Mendelian randomization accounting for correlated and uncorrelated pleiotropic effects using genome-wide summary statistics. Nature Genetics, 2020, 52, 740-747.	9.4	298
11	A comparative study of the genetic components of three subcategories of autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1720-1731.	4.1	22
12	Detailed modeling of positive selection improves detection of cancer driver genes. Nature Communications, 2019, 10, 3399.	5.8	49
13	Jump-seq: Genome-Wide Capture and Amplification of 5-Hydroxymethylcytosine Sites. Journal of the American Chemical Society, 2019, 141, 8694-8697.	6.6	26
14	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. Molecular Metabolism, 2019, 22, 96-109.	3.0	102
15	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	9.4	235
16	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. American Journal of Human Genetics, 2018, 102, 1031-1047.	2.6	26
17	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. Cell Reports, 2018, 24, 2029-2041.	2.9	64
18	Evolution of transcript modification by N⁶-methyladenosine in primates. Genome Research, 2017, 27, 385-392.	2.4	49

#	Article	IF	Citations
19	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. Molecular Psychiatry, 2017, 22, 1282-1290.	4.1	95
20	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
21	Genes with de novo mutations are shared by four neuropsychiatric disorders discovered from NPdenovo database. Molecular Psychiatry, 2016, 21, 290-297.	4.1	167
22	De novo ChIP-seq analysis. Genome Biology, 2015, 16, 205.	3.8	10
23	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	3.8	1,219
24	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	2.6	111
25	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
26	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825
27	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	1.5	253