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	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
2	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
3	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	3.8	1,219
4	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825
5	Mendelian randomization accounting for correlated and uncorrelated pleiotropic effects using genome-wide summary statistics. Nature Genetics, 2020, 52, 740-747.	9.4	298
6	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	1.5	253
7	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
8	Genes with de novo mutations are shared by four neuropsychiatric disorders discovered from NPdenovo database. Molecular Psychiatry, 2016, 21, 290-297.	4.1	167
9	Genetic analyses support the contribution of mRNA N6-methyladenosine (m6A) modification to human disease heritability. Nature Genetics, 2020, 52, 939-949.	9.4	113
10	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	2.6	111
11	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
12	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
13	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
14	Allele-specific open chromatin in human iPSC neurons elucidates functional disease variants. Science, 2020, 369, 561-565.	6.0	77
15	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. Cell Reports, 2018, 24, 2029-2041.	2.9	64
16	Evolution of transcript modification by N⁶-methyladenosine in primates. Genome Research, 2017, 27, 385-392.	2.4	49
17	Detailed modeling of positive selection improves detection of cancer driver genes. Nature Communications, 2019, 10, 3399.	5.8	49
18	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. Science Advances, 2020, 6, .	4.7	31

#	Article	IF	Citations
19	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
20	Jump-seq: Genome-Wide Capture and Amplification of 5-Hydroxymethylcytosine Sites. Journal of the American Chemical Society, 2019, 141, 8694-8697.	6.6	26
21	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
22	A comparative study of the genetic components of three subcategories of autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1720-1731.	4.1	22
23	A functional genomics pipeline identifies pleiotropy and cross-tissue effects within obesity-associated GWAS loci. Nature Communications, 2021, 12, 5253.	5.8	19
24	De novo ChIP-seq analysis. Genome Biology, 2015, 16, 205.	3.8	10
25	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. Nature Communications, 2020, 11, 2929.	5.8	10
26	Annotating functional effects of non-coding variants in neuropsychiatric cell types by deep transfer learning. PLoS Computational Biology, 2022, 18, e1010011.	1.5	7
27	DECO: a framework for jointly analyzing de novo and rare case/control variants, and biological pathways. Briefings in Bioinformatics, 2021, 22, .	3.2	6