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List of Publications by Year
in descending order

31 papers	10,883 citations	331670 21 h-index	434195 31 g-index
37 all docs	37 docs citations	37 times ranked	15003 citing authors

#	Article	IF	Citations
1	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
2	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
3	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
4	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	1,219
5	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	21.4	977
6	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	28.9	825
7	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	6.2	819
8	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	4.9	357
9	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	12.8	316
10	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	21.4	235
11	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
12	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. Biological Psychiatry, 2015, 77, 775-784.	1.3	133
13	Pleiotropy and principal components of heritability combine to increase power for association analysis. Genetic Epidemiology, 2008, 32, 9-19.	1.3	123
14	On the Use of General Control Samples for Genome-wide Association Studies: Genetic Matching Highlights Causal Variants. American Journal of Human Genetics, 2008, 82, 453-463.	6.2	120
15	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. American Journal of Human Genetics, 2014, 94, 870-883.	6.2	116
16	A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohnâ€™s Disease and Human Gut Microbiome Composition. Gastroenterology, 2016, 151, 724-732.	1.3	109
17	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	6.4	91
18	Semisoft clustering of single-cell data. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 466-471.	7.1	71

#	Article	IF	Citations
19	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	21.4	64
20	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. Biological Psychiatry, 2018, 83, 589-597.	1.3	38
21	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	7.9	30
22	Rare deleterious mutations of the gene EFR3A in autism spectrum disorders. Molecular Autism, 2014, 5, 31.	4.9	27
23	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. Molecular Autism, 2021, 12, 65.	4.9	22
24	How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular Autism, 2021, 12, 66.	4.9	20
25	Maternal Effects as Causes of Risk for Obsessive-Compulsive Disorder. Biological Psychiatry, 2020, 87, 1045-1051.	1.3	18
26	Using ancestry matching to combine familyâ€based and unrelated samples for genomeâ€wide association studies. Statistics in Medicine, 2010, 29, 2932-2945.	1.6	15
27	Cohort profile: Epidemiology and Genetics of Obsessiveâ€“compulsive disorder and chronic tic disorders in Sweden (EGOS). Social Psychiatry and Psychiatric Epidemiology, 2020, 55, 1383-1393.	3.1	13
28	Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. Translational Psychiatry, 2021, 11, 171.	4.8	13
29	Refining genetically inferred relationships using treelet covariance smoothing. Annals of Applied Statistics, 2013, 7, 669-690.	1.1	9
30	Joint evaluation of serum C-Reactive Protein levels and polygenic risk scores as risk factors for schizophrenia. Psychiatry Research, 2018, 261, 148-153.	3.3	6
31	Age dependent association of inbreeding with risk for schizophrenia in Egypt. Schizophrenia Research, 2020, 216, 450-459.	2.0	1