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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	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
2	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	7.9	30
3	How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular Autism, 2021, 12, 66.	4.9	20
4	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. Molecular Autism, 2021, 12, 65.	4.9	22
5	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
6	Age dependent association of inbreeding with risk for schizophrenia in Egypt. Schizophrenia Research, 2020, 216, 450-459.	2.0	1
7	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
8	Maternal Effects as Causes of Risk for Obsessive-Compulsive Disorder. Biological Psychiatry, 2020, 87, 1045-1051.	1.3	18
9	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	6.4	91
10	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
11	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
12	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
13	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
14	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
15	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
16	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	21.4	64
17	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
18	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	12.8	316

#	Article	IF	Citations
19	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	1,219
20	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
21	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	6.2	819
22	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	21.4	977
23	Rare deleterious mutations of the gene EFR3A in autism spectrum disorders. Molecular Autism, 2014, 5, 31.	4.9	27
24	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
25	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	28.9	825
26	Refining genetically inferred relationships using treelet covariance smoothing. Annals of Applied Statistics, 2013, 7, 669-690.	1.1	9
27	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	4.9	357
28	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
29	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
30	Pleiotropy and principal components of heritability combine to increase power for association analysis. Genetic Epidemiology, 2008, 32, 9-19.	1.3	123
31	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