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List of Publications by Year
in descending order

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50 papers	8,139 citations	186265 28 h-index	182427 51 g-index
62 all docs	62 docs citations	62 times ranked	15466 citing authors

#	Article	IF	Citations
1	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
2	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	12.6	851
3	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
4	Subcortical brain volume differences in participants with attention deficit hyperactivity disorder in children and adults: a cross-sectional mega-analysis. Lancet Psychiatry,the, 2017, 4, 310-319.	7.4	565
5	Improved Detection of Common Variants Associated with Schizophrenia by Leveraging Pleiotropy with Cardiovascular-Disease Risk Factors. American Journal of Human Genetics, 2013, 92, 197-209.	6.2	422
6	Exploring Comorbidity Within Mental Disorders Among a Danish National Population. JAMA Psychiatry, 2019, 76, 259.	11.0	374
7	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. Nature Genetics, 2017, 49, 152-156.	21.4	350
8	Genetic assessment of age-associated Alzheimer disease risk: Development and validation of a polygenic hazard score. PLoS Medicine, 2017, 14, e1002258.	8.4	311
9	Improved Detection of Common Variants Associated with Schizophrenia and Bipolar Disorder Using Pleiotropy-Informed Conditional False Discovery Rate. PLoS Genetics, 2013, 9, e1003455.	3.5	298
10	All SNPs Are Not Created Equal: Genome-Wide Association Studies Reveal a Consistent Pattern of Enrichment among Functionally Annotated SNPs. PLoS Genetics, 2013, 9, e1003449.	3.5	268
11	Association between Mental Disorders and Subsequent Medical Conditions. New England Journal of Medicine, 2020, 382, 1721-1731.	27.0	258
12	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
13	Genetic correlations of polygenic disease traits: from theory to practice. Nature Reviews Genetics, 2019, 20, 567-581.	16.3	236
14	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
15	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
16	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. Nature Neuroscience, 2019, 22, 353-361.	14.8	173
17	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
18	Genetic Markers of Human Evolution Are Enriched in Schizophrenia. Biological Psychiatry, 2016, 80, 284-292.	1.3	92

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19	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	28.9	75
20	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	11.0	54
21	New statistical approaches exploit the polygenic architecture of schizophreniaâ€"implications for the underlying neurobiology. Current Opinion in Neurobiology, 2016, 36, 89-98.	4.2	53
22	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	7.9	49
23	Covariate-modulated local false discovery rate for genome-wide association studies. Bioinformatics, 2014, 30, 2098-2104.	4.1	46
24	Shared common variants in prostate cancer and blood lipids. International Journal of Epidemiology, 2014, 43, 1205-1214.	1.9	45
25	Heritability of Biomarkers of Oxidized Lipoproteins. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1704-1711.	2.4	44
26	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	2.8	36
27	Modeling the 3D Geometry of the Cortical Surface with Genetic Ancestry. Current Biology, 2015, 25, 1988-1992.	3.9	34
28	Leveraging Genomic Annotations and Pleiotropic Enrichment for Improved Replication Rates in Schizophrenia GWAS. PLoS Genetics, 2016, 12, e1005803.	3.5	34
29	Williams syndrome-specific neuroanatomical profile and its associations with behavioral features. NeuroImage: Clinical, 2017, 15, 343-347.	2.7	33
30	Identification of shared genetic variants between schizophrenia and lung cancer. Scientific Reports, 2018, 8, 674.	3.3	33
31	Large-scale genomics unveil polygenic architecture of human cortical surface area. Nature Communications, 2015, 6, 7549.	12.8	30
32	Novel Loci Associated With Attention-Deficit/Hyperactivity Disorder Are Revealed by Leveraging Polygenic Overlap With Educational Attainment. Journal of the American Academy of Child and Adolescent Psychiatry, 2018, 57, 86-95.	0.5	30
33	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
34	Genetic risks and clinical rewards. Nature Genetics, 2018, 50, 1210-1211.	21.4	23
35	An Empirical Bayes Mixture Model for Effect Size Distributions in Genome-Wide Association Studies. PLoS Genetics, 2015, 11, e1005717.	3.5	22
36	Probing the Association between Early Evolutionary Markers and Schizophrenia. PLoS ONE, 2017, 12, e0169227.	2.5	17

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37	Spatial fine-mapping for gene-by-environment effects identifies risk hot spots for schizophrenia. Nature Communications, 2018, 9, 5296.	12.8	17
38	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	3.3	16
39	Leveraging genome characteristics to improve gene discovery for putamen subcortical brain structure. Scientific Reports, 2017, 7, 15736.	3.3	15
40	Conservation of Distinct Genetically-Mediated Human Cortical Pattern. PLoS Genetics, 2016, 12, e1006143.	3.5	15
41	A large population-based investigation into the genetics of susceptibility to gastrointestinal infections and the link between gastrointestinal infections and mental illness. Human Genetics, 2020, 139, 593-604.	3.8	14
42	Human Heart Rate. Journal of the American College of Cardiology, 2014, 63, 358-368.	2.8	11
43	A comprehensive map of genetic relationships among diagnostic categories based on 48.6 million relative pairs from the Danish genealogy. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
44	Modeling prior information of common genetic variants improves gene discovery for neuroticism. Human Molecular Genetics, 2017, 26, 4530-4539.	2.9	10
45	Enrichment of genetic markers of recent human evolution in educational and cognitive traits. Scientific Reports, 2018, 8, 12585.	3.3	9
46	Associations between patterns in comorbid diagnostic trajectories of individuals with schizophrenia and etiological factors. Nature Communications, 2021, 12, 6617.	12.8	9
47	Genetic factors underlying the bidirectional relationship between autoimmune and mental disorders â€“ Findings from a Danish population-based study. Brain, Behavior, and Immunity, 2021, 91, 10-23.	4.1	8
48	Williams Syndrome neuroanatomical score associates with GTF2IRD1 in large-scale magnetic resonance imaging cohorts: a proof of concept for multivariate endophenotypes. Translational Psychiatry, 2018, 8, 114.	4.8	6
49	A new common functional coding variant at the DDC gene change renal enzyme activity and modify renal dopamine function. Scientific Reports, 2019, 9, 5055.	3.3	6
50	Indirect paths from genetics to education. Nature Genetics, 2022, 54, 372-373.	21.4	5