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List of Publications by Year
in descending order

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64 papers	30,050 citations	76031 42 h-index	107981 68 g-index
77 all docs	77 docs citations	77 times ranked	42605 citing authors

#	Article	IF	Citations
1	Effects of copy number variations on brain structure and risk for psychiatric illness: Largeâ€scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	1.9	30
2	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
3	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
4	Identification of genetic overlap and novel risk loci for attention-deficit/hyperactivity disorder and bipolar disorder. Molecular Psychiatry, 2021, 26, 4055-4065.	4.1	31
5	A meta-analysis uncovers the first sequence variant conferring risk of Bellâ€™s palsy. Scientific Reports, 2021, 11, 4188.	1.6	8
6	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
7	Identification of genetic loci associated with nocturnal enuresis: a genome-wide association study. The Lancet Child and Adolescent Health, 2021, 5, 201-209.	2.7	27
8	Germline variants at SOHLH2 influence multiple myeloma risk. Blood Cancer Journal, 2021, 11, 76.	2.8	6
9	Analysis of Diffusion Tensor Imaging Data From the UK Biobank Confirms Dosage Effect of 15q11.2 Copy Number Variation on White Matter and Shows Association With Cognition. Biological Psychiatry, 2021, 90, 307-316.	0.7	11
10	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. Intelligence, 2021, 88, 101565.	1.6	2
11	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. Communications Biology, 2021, 4, 1148.	2.0	12
12	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. BMJ Open, 2021, 11, e049709.	0.8	7
13	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
14	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
15	Identification of Genetic Loci Shared Between Attention-Deficit/Hyperactivity Disorder, Intelligence, and Educational Attainment. Biological Psychiatry, 2020, 87, 1052-1062.	0.7	13
16	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. Translational Psychiatry, 2019, 9, 258.	2.4	75
17	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
18	Brain age prediction using deep learning uncovers associated sequence variants. Nature Communications, 2019, 10, 5409.	5.8	238

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19	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
20	Reciprocal White Matter Changes Associated With Copy Number Variation at 15q11.2 BP1-BP2: A Diffusion Tensor Imaging Study. Biological Psychiatry, 2019, 85, 563-572.	0.7	29
21	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
22	Rare and Common Variants Conferring Risk of Tooth Agenesis. Journal of Dental Research, 2018, 97, 515-522.	2.5	52
23	MAP1B mutations cause intellectual disability and extensive white matter deficit. Nature Communications, 2018, 9, 3456.	5.8	21
24	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
25	Reproductive fitness and genetic risk of psychiatric disorders in the general population. Nature Communications, 2017, 8, 15833.	5.8	30
26	Sequence variant at 4q25 near PITX2 associates with appendicitis. Scientific Reports, 2017, 7, 3119.	1.6	14
27	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	5.8	52
28	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. Nature Communications, 2016, 7, 10572.	5.8	60
29	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. Nature Neuroscience, 2015, 18, 953-955.	7.1	351
30	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
31	CNVs conferring risk of autism or schizophrenia affect cognition in controls. Nature, 2014, 505, 361-366.	13.7	588
32	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	13.7	236
33	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. Nature Genetics, 2013, 45, 1371-1374.	9.4	125
34	A common biological basis of obesity and nicotine addiction. Translational Psychiatry, 2013, 3, e308-e308.	2.4	51
35	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
36	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	13.7	1,880

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37	Discovery of common variants associated with low TSH levels and thyroid cancer risk. Nature Genetics, 2012, 44, 319-322.	9.4	208
38	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
39	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
40	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	9.4	275
41	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	1.4	114
42	Common genetic variants associated with open-angle glaucoma. Human Molecular Genetics, 2011, 20, 2464-2471.	1.4	152
43	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
44	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	13.7	559
45	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
46	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	9.4	181
47	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	9.4	357
48	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
49	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
50	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
51	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
52	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	9.4	1,247
53	New sequence variants associated with bone mineral density. Nature Genetics, 2009, 41, 15-17.	9.4	328
54	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	9.4	248

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55	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	9.4	434
56	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
57	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615
58	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	9.4	668
59	Multiple Genetic Loci for Bone Mineral Density and Fractures. New England Journal of Medicine, 2008, 358, 2355-2365.	13.9	582
60	The Association of a SNP Upstream of INSIG2 with Body Mass Index is Reproduced in Several but Not All Cohorts. PLoS Genetics, 2007, 3, e61.	1.5	134
61	Common Sequence Variants in the LOXL1 Gene Confer Susceptibility to Exfoliation Glaucoma. Science, 2007, 317, 1397-1400.	6.0	657
62	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	9.4	966
63	Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes. Nature Genetics, 2006, 38, 320-323.	9.4	2,005
64	Composition of the founding population of Iceland: Biological distance and morphological variation in early historic Atlantic Europe. American Journal of Physical Anthropology, 2004, 124, 257-274.	2.1	37