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List of Publications by Year
in descending order

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Version: 2024-02-01

46 papers	24,247 citations	109321 35 h-index	243625 44 g-index
51 all docs	51 docs citations	51 times ranked	33592 citing authors

#	Article	IF	Citations
1	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
2	Mendelian imputation of parental genotypes improves estimates of direct genetic effects. Nature Genetics, 2022, 54, 897-905.	21.4	31
3	Deconstructing the sources of genotype-phenotype associations in humans. Science, 2019, 365, 1396-1400.	12.6	170
4	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	12.6	720
5	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	21.4	147
6	Selection against variants in the genome associated with educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E727-E732.	7.1	149
7	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
8	Reproductive fitness and genetic risk of psychiatric disorders in the general population. Nature Communications, 2017, 8, 15833.	12.8	30
9	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	2.2	89
10	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
11	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	12.8	52
12	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
13	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	5.3	59
14	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	21.4	283
15	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	21.4	214
16	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	21.4	663
17	Rare mutations associating with serum creatinine and chronic kidney disease. Human Molecular Genetics, 2014, 23, 6935-6943.	2.9	52
18	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	21.4	294

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19	Common and low-frequency variants associated with genome-wide recombination rate. Nature Genetics, 2014, 46, 11-16.	21.4	116
20	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
21	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
22	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	27.8	559
23	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	27.8	7,490
24	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
25	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	21.4	1,247
26	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	27.8	1,399
27	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
28	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
29	FURTHER EXPLORATIONS OF LIKELIHOOD THEORY FOR MONTE CARLO INTEGRATION. , 2007, , 563-592.		3
30	Abstract 2921: Genome-wide Association Reveals Sequence Variants on 4q25 that Affect the Risk of Atrial Fibrillation and Stroke. Circulation, 2007, 116, .	1.6	0
31	Abstract 2318: The Type 2 Diabetes Gene CDKAL1 Discovered by Genome-wide Association is Expressed in Beta Cells and Modulated by Glucose Concentration. Circulation, 2007, 116, .	1.6	1
32	Reply to â€œMany hypotheses but no replication for the association between PDE4D and strokeâ€• Nature Genetics, 2006, 38, 1092-1093.	21.4	20
33	Reply to â€œA call for accurate phenotype definition in the study of complex disordersâ€• Nature Genetics, 2004, 36, 3-4.	21.4	11
34	Recombination rate and reproductive success in humans. Nature Genetics, 2004, 36, 1203-1206.	21.4	176
35	A high-resolution recombination map of the human genome. Nature Genetics, 2002, 31, 241-247.	21.4	1,571
36	Allegro, a new computer program for multipoint linkage analysis. Nature Genetics, 2000, 25, 12-13.	21.4	737

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37	Inheritance of human longevity in Iceland. European Journal of Human Genetics, 2000, 8, 743-749.	2.8	230
38	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. Nature Genetics, 1997, 17, 84-87.	21.4	288
39	Diabetes, dependence, asymptotics, selection and significance. Nature Genetics, 1997, 17, 148-148.	21.4	8
40	The properties of the cross-match estimate and split sampling. Annals of Statistics, 1997, 25, .	2.6	3
41	Covariance Structure and Convergence Rate of the Gibbs Sampler with Various Scans. Journal of the Royal Statistical Society Series B: Methodological, 1995, 57, 157-169.	0.7	57
42	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	3.1	665
43	A gene defect that causes conduction system disease and dilated cardiomyopathy maps to chromosome 1p1â€“1q1. Nature Genetics, 1994, 7, 546-551.	21.4	187
44	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278.	3.1	262
45	Sequential imputation and multipoint linkage analysis. Genetic Epidemiology, 1993, 10, 483-488.	1.3	18
46	Efficient methods for computing linkage likelihoods of recessive diseases in inbred pedigrees. Genetic Epidemiology, 1991, 8, 81-103.	1.3	16