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List of Publications by Year
in descending order

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34 papers	3,204 citations	430874 18 h-index	377865 34 g-index
51 all docs	51 docs citations	51 times ranked	7497 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
3	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	21.4	129
4	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	21.4	124
5	Picomolar concentrations of oligomeric alpha-synuclein sensitizes TLR4 to play an initiating role in Parkinsonâ€™s disease pathogenesis. Acta Neuropathologica, 2019, 137, 103-120.	7.7	103
6	Genomics implicates adaptive and innate immunity in Alzheimer's and Parkinson's diseases. Annals of Clinical and Translational Neurology, 2016, 3, 924-933.	3.7	84
7	Moving beyond neurons: the role of cell type-specific gene regulation in Parkinsonâ€™s disease heritability. Npj Parkinson's Disease, 2019, 5, 6.	5.3	83
8	Ancestry-agnostic estimation of DNA sample contamination from sequence reads. Genome Research, 2020, 30, 185-194.	5.5	51
9	Long- and short-term outcomes in renal allografts with deceased donors: A large recipient and donor genome-wide association study. American Journal of Transplantation, 2018, 18, 1370-1379.	4.7	47
10	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
11	Neuronal intranuclear inclusion disease is genetically heterogeneous. Annals of Clinical and Translational Neurology, 2020, 7, 1716-1725.	3.7	38
12	A genome-wide association study of suicide severity scores in bipolar disorder. Journal of Psychiatric Research, 2015, 65, 23-29.	3.1	36
13	Ten simple rules for conducting a mendelian randomization study. PLoS Computational Biology, 2021, 17, e1009238.	3.2	33
14	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
15	A Bayesian Method to Incorporate Hundreds of Functional Characteristics with Association Evidence to Improve Variant Prioritization. PLoS ONE, 2014, 9, e98122.	2.5	29
16	Exploring various polygenic risk scores for skin cancer in the phenomes of the Michigan genomics initiative and the UK Biobank with a visual catalog: PRSWeb. PLoS Genetics, 2019, 15, e1008202.	3.5	28
17	Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body diseases. Acta Neuropathologica, 2021, 142, 449-474.	7.7	27
18	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041.	12.8	22

#	Article	IF	Citations
19	Allele-Skewed DNA Modification in the Brain: Relevance to a Schizophrenia GWAS. American Journal of Human Genetics, 2016, 98, 956-962.	6.2	20
20	Itâ€™s All in the Brain: A Review of Available Functional Genomic Annotations. Biological Psychiatry, 2017, 81, 478-483.	1.3	14
21	The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. American Journal of Transplantation, 2019, 19, 2262-2273.	4.7	13
22	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
23	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	2.9	11
24	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. Communications Biology, 2022, 5, .	4.4	11
25	Protein kinase cAMP-dependent regulatory type II beta (PRKAR2B) gene variants in antipsychotic-induced weight gain. Human Psychopharmacology, 2014, 29, 330-335.	1.5	10
26	Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814.	1.3	9
27	Relative impact of indels versus SNPs on complex disease. Genetic Epidemiology, 2019, 43, 112-117.	1.3	9
28	Human-lineage-specific genomic elements are associated with neurodegenerative disease and APOE transcript usage. Nature Communications, 2021, 12, 2076.	12.8	9
29	Informing disease modelling with brain-relevant functional genomic annotations. Brain, 2019, 142, 3694-3712.	7.6	8
30	Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. Scientific Reports, 2015, 5, 13373.	3.3	7
31	GWAS of Hematuria. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 672-683.	4.5	7
32	Genetic determinants of low vitamin B12 levels in Alzheimer's disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2019, 11, 430-434.	2.4	3
33	One scientist coupleâ€™s five suggestions to solve the â€˜two body problemâ€™. Nature, 2021, , .	27.8	1
34	Teaching at the university level is not a hassle. Nature, 2019, 574, 285-285.	27.8	0