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List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

4,352
citations

516215

16
h-index

500791

28
g-index

32
all docs

32
docs citations

32
times ranked

11108
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
2	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. <i>Bioinformatics</i> , 2017, 33, 272-279.	1.8	822
3	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
4	Using human genetics to understand the disease impacts of testosterone in men and women. <i>Nature Medicine</i> , 2020, 26, 252-258.	15.2	384
5	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
6	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
7	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
8	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
9	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.	2.6	106
10	COVID-19 and climatic factors: A global analysis. <i>Environmental Research</i> , 2021, 193, 110355.	3.7	93
11	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	4.1	83
12	Social inequality and the syndemic of chronic disease and COVID-19: county-level analysis in the USA. <i>Journal of Epidemiology and Community Health</i> , 2021, 75, 496-500.	2.0	76
13	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	0.7	69
14	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. <i>Annals of Human Genetics</i> , 2016, 80, 187-196.	0.3	41
15	Nonsense Mutation in Coiled-Coil Domain Containing 151 Gene (<i>CCDC151</i>) Causes Primary Ciliary Dyskinesia. <i>Human Mutation</i> , 2014, 35, 1446-1448.	1.1	33
16	Associations of Y chromosomal haplogroups with cardiometabolic risk factors and subclinical vascular measures in males during childhood and adolescence. <i>Atherosclerosis</i> , 2018, 274, 94-103.	0.4	19
17	The Y Chromosome: A Complex Locus for Genetic Analyses of Complex Human Traits. <i>Genes</i> , 2020, 11, 1273.	1.0	12
18	Genetically Predicted Glucose-Dependent Insulinotropic Polypeptide (GIP) Levels and Cardiovascular Disease Risk Are Driven by Distinct Causal Variants in the <i>GIPR</i> Region. <i>Diabetes</i> , 2021, 70, 2706-2719.	0.3	12

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19	Mitochondrial DNA Haplogroups and Breast Cancer Risk Factors in the Avon Longitudinal Study of Parents and Children (ALSPAC). <i>Genes</i> , 2018, 9, 395.	1.0	9
20	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. <i>Environment International</i> , 2022, 159, 107041.	4.8	8
21	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. <i>BioMed Research International</i> , 2015, 2015, 1-16.	0.9	7
22	Proxy Molecular Diagnosis from Whole-Exome Sequencing Reveals Papillon-Lefevre Syndrome Caused by a Missense Mutation in CTSC. <i>PLoS ONE</i> , 2015, 10, e0121351.	1.1	4
23	Y Chromosome, Mitochondrial DNA and Childhood Behavioural Traits. <i>Scientific Reports</i> , 2017, 7, 11655.	1.6	4
24	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. <i>Bioinformatics</i> , 2017, 33, 79-86.	1.8	4
25	Using Y-Chromosomal Haplogroups in Genetic Association Studies and Suggested Implications. <i>Genes</i> , 2018, 9, 45.	1.0	4
26	Listen to accused Turkish scientists. <i>Nature</i> , 2017, 543, 491-491.	13.7	2