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List of Publications by Year
in descending order

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	Genome-wide gene-air pollution interaction analysis of lung function in 300,000 individuals. Environment International, 2022, 159, 107041.	4.8	8
2	COVID-19 and climatic factors: A global analysis. Environmental Research, 2021, 193, 110355.	3.7	93
3	Social inequality and the syndemic of chronic disease and COVID-19: county-level analysis in the USA. Journal of Epidemiology and Community Health, 2021, 75, 496-500.	2.0	76
4	Genetically Predicted Glucose-Dependent Insulinotropic Polypeptide (GIP) Levels and Cardiovascular Disease Risk Are Driven by Distinct Causal Variants in the GIPR Region. Diabetes, 2021, 70, 2706-2719.	0.3	12
5	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
6	The Y Chromosome: A Complex Locus for Genetic Analyses of Complex Human Traits. Genes, 2020, 11, 1273.	1.0	12
7	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	15.2	384
8	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
9	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
10	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
11	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
12	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
13	Using Y-Chromosomal Haplogroups in Genetic Association Studies and Suggested Implications. Genes, 2018, 9, 45.	1.0	4
14	Associations of Y chromosomal haplogroups with cardiometabolic risk factors and subclinical vascular measures in males during childhood and adolescence. Atherosclerosis, 2018, 274, 94-103.	0.4	19
15	Mitochondrial DNA Haplogroups and Breast Cancer Risk Factors in the Avon Longitudinal Study of Parents and Children (ALSPAC). Genes, 2018, 9, 395.	1.0	9
16	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
17	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	9.4	257
18	Listen to accused Turkish scientists. Nature, 2017, 543, 491-491.	13.7	2

#	Article	IF	Citations
19	Y Chromosome, Mitochondrial DNA and Childhood Behavioural Traits. Scientific Reports, 2017, 7, 11655.	1.6	4
20	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
21	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. Bioinformatics, 2017, 33, 79-86.	1.8	4
22	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. Bioinformatics, 2017, 33, 272-279.	1.8	822
23	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. Annals of Human Genetics, 2016, 80, 187-196.	0.3	41
24	Proxy Molecular Diagnosis from Whole-Exome Sequencing Reveals Papillon-Lefevre Syndrome Caused by a Missense Mutation in CTSC. PLoS ONE, 2015, 10, e0121351.	1.1	4
25	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. BioMed Research International, 2015, 2015, 1-16.	0.9	7
26	Nonsense Mutation in Coiled-Coil Domain Containing 151 Gene (CCDC151) Causes Primary Ciliary Dyskinesia. Human Mutation, 2014, 35, 1446-1448.	1.1	33