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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
2	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. BMJ Open, 2021, 11, e044474.	1.9	49
3	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
4	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	2.5	6
5	Enhancers in disease: molecular basis and emerging treatment strategies. Trends in Molecular Medicine, 2021, 27, 1060-1073.	6.7	84
6	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
7	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. Journal of Women's Health, 2021, 30, 1686-1692.	3.3	20
8	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. SSM - Population Health, 2021, 15, 100878.	2.7	53
9	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
10	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. European Journal of Human Genetics, 2020, 28, 253-263.	2.8	29
11	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	11.9	327
12	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. Nature Communications, 2020, 11, 4930.	12.8	20
13	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	1.3	14
14	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	2.6	38
15	Systematic Prioritization of Candidate Genes in Disease Loci Identifies TRAFD1 as a Master Regulator of IFNÎ <sup>3</sup> Signaling in Celiac Disease. Frontiers in Genetics, 2020, 11, 562434.	2.3	20
16	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
17	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	2.9	23
18	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. Human Genetics, 2019, 138, 375-388.	3.8	6

#	Article	IF	CITATIONS
19	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. Genome Biology, 2019, 20, 235.	8.8	26
20	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
21	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature Genetics, 2018, 50, 1524-1532.	21.4	97
22	A SNP panel for identification of DNA and RNA specimens. BMC Genomics, 2018, 19, 90.	2.8	47
23	Genome-wide identification of directed gene networks using large-scale population genomics data. Nature Communications, 2018, 9, 3097.	12.8	18
24	The genetic architecture of molecular traits. Current Opinion in Systems Biology, 2017, 1, 25-31.	2.6	6