Andrew D Bretherick

List of Publications by Year
in descending order

16	2,252	949033 11	1051228 16
papers	citations	h-index	g-index

27	27	27	5787
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomeâ€Wide Association Study of NAFLD Using Electronic Health Records. Hepatology Communications, 2022, 6, 297-308.	2.0	33
2	Genomeâ€wide analysis identifies gallstoneâ€susceptibility loci including genes regulating gastrointestinal motility. Hepatology, 2022, 75, 1081-1094.	3.6	12
3	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
4	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
5	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. International Journal of Epidemiology, 2021, 50, 1482-1497.	0.9	14
6	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
7	Identification of epigenome-wide DNA methylation differences between carriers of APOE Îµ4 and APOE Îµ2 alleles. Genome Medicine, 2021, 13, 1.	3.6	76
8	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
9	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. EBioMedicine, 2021, 74, 103730.	2.7	5
10	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
11	Epigenomeâ€wide analyses identify DNA methylation signatures of dementia risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12078.	1.2	8
12	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. Clinical Epigenetics, 2020, 12, 95.	1.8	6
13	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. PLoS Genetics, 2020, 16, e1008785.	1.5	29
14	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	5.8	37
15	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	2.8	170
16	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	1.5	17