Archie Campbell

List of Publications by Year
in descending order

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161	13,548	36303	33894
papers	citations	51 h-index	99 g-index

203	203	203	22480
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
2	Genomic insights into the origin of farming in the ancient Near East. Nature, 2016, 536, 419-424.	27.8	733
3	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
4	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
5	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	6.2	439
6	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
7	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
8	Cohort Profile: Generation Scotland: Scottish Family Health Study (GS:SFHS). The study, its participants and their potential for genetic research on health and illness. International Journal of Epidemiology, 2013, 42, 689-700.	1.9	353
9	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
10	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112â€‰117). Molecular Psychiatry, 2017, 22, 1376-1384.	7.9	351
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	Mental health before and during the COVID-19 pandemic in two longitudinal UK population cohorts. British Journal of Psychiatry, 2021, 218, 334-343.	2.8	330
13	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
14	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
15	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.	21.4	257
16	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
17	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
18	Cardiac Troponin T and Troponin I in the General Population. Circulation, 2019, 139, 2754-2764.	1.6	200

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19	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
20	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
21	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
22	Molecular genetic contributions to socioeconomic status and intelligence. Intelligence, 2014, 44, 26-32.	3.0	156
23	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. BMJ Open, 2014, 4, e006141.	1.9	150
24	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	8.8	146
25	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
26	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	6.2	125
27	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
28	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
29	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.6	122
30	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
31	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	8.2	117
32	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
33	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
34	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
35	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. Genome Medicine, 2017, 9, 23.	8.2	110
36	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. Clinical Epigenetics, 2020, 12, 115.	4.1	109

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37	Effect of Smoking on Blood Pressure and Resting Heart Rate. Circulation: Cardiovascular Genetics, 2015, 8, 832-841.	5.1	105
38	Epidemiology and Heritability of Major Depressive Disorder, Stratified by Age of Onset, Sex, and Illness Course in Generation Scotland: Scottish Family Health Study (GS:SFHS). PLoS ONE, 2015, 10, e0142197.	2.5	101
39	Comparison between High-Sensitivity Cardiac Troponin T and Cardiac Troponin I in a Large General Population Cohort. Clinical Chemistry, 2018, 64, 1607-1616.	3.2	101
40	Acute COVID-19 severity and mental health morbidity trajectories in patient populations of six nations: an observational study. Lancet Public Health, The, 2022, 7, e406-e416.	10.0	99
41	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
42	Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 429-437.	2.4	93
43	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. Nature Communications, 2019, 10, 2373.	12.8	86
44	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
45	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
46	A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104.	3.5	83
47	Identification of epigenome-wide DNA methylation differences between carriers of APOE Îµ4 and APOE Îµ2 alleles. Genome Medicine, 2021, 13, 1.	8.2	76
48	Self-reported medication use validated through record linkage to national prescribing data. Journal of Clinical Epidemiology, 2018, 94, 132-142.	5.0	75
49	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. Diabetes, 2019, 68, 207-219.	0.6	72
50	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. PLoS Genetics, 2016, 12, e1005804.	3.5	72
51	Chronic pain, depression and cardiovascular disease linked through a shared genetic predisposition: Analysis of a family-based cohort and twin study. PLoS ONE, 2017, 12, e0170653.	2.5	71
52	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	6.1	67
53	Factors associated with sharing e-mail information and mental health survey participation in large population cohorts. International Journal of Epidemiology, 2020, 49, 410-421.	1.9	67
54	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64

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55	Exploring causality in the association between circulating 25-hydroxyvitamin D and colorectal cancer risk: a large Mendelian randomisation study. BMC Medicine, 2018, 16, 142.	5.5	62
56	Genetic and Environmental Risk for Chronic Pain and the Contribution of Risk Variants for Major Depressive Disorder: A Family-Based Mixed-Model Analysis. PLoS Medicine, 2016, 13, e1002090.	8.4	60
57	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. European Journal of Human Genetics, 2016, 24, 919-923.	2.8	54
58	Blunted medial prefrontal cortico-limbic reward-related effective connectivity and depression. Brain, 2020, 143, 1946-1956.	7.6	54
59	Heavier smoking may lead to a relative increase in waist circumference: evidence for a causal relationship from a Mendelian randomisation meta-analysis. The CARTA consortium: TableÂ1. BMJ Open, 2015, 5, e008808.	1.9	53
60	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. Brain, Behavior, and Immunity, 2021, 92, 39-48.	4.1	53
61	Pedigree and genotyping quality analyses of over 10,000 DNA samples from the Generation Scotland: Scottish Family Health Study. BMC Medical Genetics, 2013, 14, 38.	2.1	51
62	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
63	Recent genomic heritage in Scotland. BMC Genomics, 2015, 16, 437.	2.8	46
64	Stratification by Smoking Status Reveals an Association of CHRNA5-A3-B4 Genotype with Body Mass Index in Never Smokers. PLoS Genetics, 2014, 10, e1004799.	3.5	45
65	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. Pharmacogenomics Journal, 2020, 20, 329-341.	2.0	45
66	The Dementias Platform UK (DPUK) Data Portal. European Journal of Epidemiology, 2020, 35, 601-611.	5.7	45
67	Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.	12.8	43
68	Common Genetic Variants Explain the Majority of the Correlation Between Height and Intelligence: The Generation Scotland Study. Behavior Genetics, 2014, 44, 91-96.	2.1	41
69	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40
70	Assessing the genetic overlap between BMI and cognitive function. Molecular Psychiatry, 2016, 21, 1477-1482.	7.9	39
71	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
72	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. Clinical Epigenetics, 2020, 12, 113.	4.1	38

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73	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	12.8	37
74	Urinary peptides in heart failure: a link to molecular pathophysiology. European Journal of Heart Failure, 2021, 23, 1875-1887.	7.1	37
75	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	6.0	37
76	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
77	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
78	Genetic Stratification to Identify Risk Groups for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 57, 275-283.	2.6	33
79	Genetic comorbidity between major depression and cardioâ€metabolic traits, stratified by age at onset of major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 309-330.	1.7	33
80	Genomeâ€Wide Association Study of NAFLD Using Electronic Health Records. Hepatology Communications, 2022, 6, 297-308.	4.3	33
81	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. EBioMedicine, 2016, 14, 161-167.	6.1	32
82	A genome-wide association study finds genetic variants associated with neck or shoulder pain in UK Biobank. Human Molecular Genetics, 2020, 29, 1396-1404.	2.9	32
83	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
84	Novel Urinary Peptidomic Classifier Predicts Incident Heart Failure. Journal of the American Heart Association, 2017, 6, .	3.7	30
85	Sex Differences in Cardiac Troponin I and T and the Prediction of Cardiovascular Events in the General Population. Clinical Chemistry, 2021, 67, 1351-1360.	3.2	30
86	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
87	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	2.9	27
88	Cohort profile for the STratifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 2019, 4, 185.	1.8	27
89	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	2.9	26
90	Dissection of major depressive disorder using polygenic risk scores for schizophrenia in two independent cohorts. Translational Psychiatry, 2016, 6, e938-e938.	4.8	25

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91	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. International Journal of Obesity, 2019, 43, 1795-1802.	3.4	25
92	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
93	The genetic landscape of Scotland and the Isles. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19064-19070.	7.1	24
94	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. Molecular Psychiatry, 2022, 27, 1111-1119.	7.9	24
95	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
96	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. EBioMedicine, 2019, 43, 576-586.	6.1	21
97	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	7.9	21
98	Early life predictors of late life cerebral small vessel disease in four prospective cohort studies. Brain, 2021, 144, 3769-3778.	7.6	21
99	Assessment of dried blood spots for DNA methylation profiling. Wellcome Open Research, 2019, 4, 44.	1.8	20
100	Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26.	8.8	20
101	Genetic stratification of depression in UK Biobank. Translational Psychiatry, 2020, 10, 163.	4.8	19
102	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
103	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	1.8	19
104	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
105	Birth weight associations with DNA methylation differences in an adult population. Epigenetics, 2021, 16, 783-796.	2.7	18
106	Epigenome-wide association study of alcohol consumption in Nâ€‰=â€‰8161 individuals and relevance to alcohol use disorder pathophysiology: identification of the cystine/glutamate transporter SLC7A11 as a top target. Molecular Psychiatry, 2022, 27, 1754-1764.	7.9	18
107	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
108	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. Clinical Epigenetics, 2020, 12, 49.	4.1	17

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109	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
110	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 2284-2292.	3.6	16
111	Cohort Profile: COVIDMENT: COVID-19 cohorts on mental health across six nations. International Journal of Epidemiology, 2022, 51, e108-e122.	1.9	16
112	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. JAMA Network Open, 2021, 4, e2136560.	5.9	16
113	Regional variation in health is predominantly driven by lifestyle rather than genetics. Nature Communications, 2017, 8, 801.	12.8	15
114	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	1.8	15
115	Polygenic risk of ischemic stroke is associated with cognitive ability. Neurology, 2016, 86, 611-618.	1.1	14
116	Electronic health record and genome-wide genetic data in Generation Scotland participants. Wellcome Open Research, 2017, 2, 85.	1.8	14
117	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	6.1	14
118	CovidLife: a resource to understand mental health, well-being and behaviour during the COVID-19 pandemic in the UK. Wellcome Open Research, 0, 6, 176.	1.8	13
119	Hair glucocorticoids are associated with childhood adversity, depressive symptoms and reduced global and lobar grey matter in Generation Scotland. Translational Psychiatry, 2021, 11, 523.	4.8	13
120	Sex-Differences in the Metabolic Health of Offspring of Parents with Diabetes: A Record-Linkage Study. PLoS ONE, 2015, 10, e0134883.	2.5	12
121	Investigating genetic links between graphemeâ€“colour synaesthesia and neuropsychiatric traits. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190026.	4.0	12
122	Prescreening for European Prevention of Alzheimer Dementia (EPAD) trial-ready cohort: impact of AD risk factors and recruitment settings. Alzheimer's Research and Therapy, 2020, 12, 8.	6.2	12
123	Molecular Genetic Risk for Psychosis Is Associated With Psychosis Risk Symptoms in a Population-Based UK Cohort: Findings From Generation Scotland. Schizophrenia Bulletin, 2020, 46, 1045-1052.	4.3	12
124	Cohort profile for the STratifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 0, 4, 185.	1.8	12
125	Genomeâ€wide analysis identifies gallstoneâ€susceptibility loci including genes regulating gastrointestinal motility. Hepatology, 2022, 75, 1081-1094.	7.3	12
126	Current Versus Lifetime Depression, APOE Variation, and Their Interaction on Cognitive Performance in Younger and Older Adults. Psychosomatic Medicine, 2015, 77, 480-492.	2.0	11

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127	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. Translational Psychiatry, 2018, 8, 63.	4.8	11
128	Pharmaco-epidemiology of antidepressant exposure in a UK cohort record-linkage study. Journal of Psychopharmacology, 2019, 33, 482-493.	4.0	11
129	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	2.9	11
130	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
131	Using tree-based methods for detection of geneâ€“gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. Bioinformatics, 2019, 35, 181-188.	4.1	10
132	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. Molecular Psychiatry, 2021, 26, 4344-4354.	7.9	10
133	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. Molecular Psychiatry, 2022, 27, 1647-1657.	7.9	10
134	Epigenomeâ€wide analyses identify DNA methylation signatures of dementia risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12078.	2.4	8
135	Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study. Twin Research and Human Genetics, 2015, 18, 117-125.	0.6	7
136	Methylome-wide association study of early life stressors and adult mental health. Human Molecular Genetics, 2022, 31, 651-664.	2.9	7
137	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. PLoS Genetics, 2021, 17, e1009750.	3.5	7
138	TeenCovidLife:Âa resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. Wellcome Open Research, 0, 6, 277.	1.8	7
139	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. Molecular Psychiatry, 2022, 27, 3875-3884.	7.9	7
140	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	2.5	6
141	Socioeconomic position and mental health during the COVID-19 pandemic: a cross-sectional analysis of the CovidLife study. Wellcome Open Research, 0, 6, 139.	1.8	5
142	Spectral clustering based on structural magnetic resonance imaging and its relationship with major depressive disorder and cognitive ability. European Journal of Neuroscience, 2021, 54, 6281-6303.	2.6	5
143	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. EBioMedicine, 2021, 74, 103730.	6.1	5
144	Identification of plasma proteins relating to brain neurodegeneration and vascular pathology in cognitively normal individuals. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2021, 13, e12240.	2.4	4

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145	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
146	Genomeâ€•and epigenomeâ€wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12280.	2.4	4
147	Complex trait methylation scores in the prediction of major depressive disorder. EBioMedicine, 2022, 79, 104000.	6.1	4
148	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
149	Genome-wide association study of susceptibility to hospitalised respiratory infections. Wellcome Open Research, 0, 6, 290.	1.8	3
150	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. Epigenetics, 2022, 17, 1143-1158.	2.7	3
151	Generation Scotland participant survey on data collection. Wellcome Open Research, 2019, 4, 111.	1.8	2
152	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits. Frontiers in Genetics, 2021, 12, 791712.	2.3	2
153	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
154	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
155	TeenCovidLife:Âa resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. Wellcome Open Research, 0, 6, 277.	1.8	1
156	A Computer Based Follow-up of Hypertension in the Community: Baseline Characteristics of 502 Patients. Clinical Science, 1988, 74, 17P-17P.	0.0	0
157	General Framework for Metaâ€Analysis of Haplotype Association Tests. Genetic Epidemiology, 2016, 40, 244-252.	1.3	0
158	Face covering adherence is positively associated with better mental health and wellbeing: a longitudinal analysis of the CovidLife surveys. Wellcome Open Research, 0, 6, 62.	1.8	0
159	Generation Scotland participant survey on data collection. Wellcome Open Research, 0, 4, 111.	1.8	0
160	RuralCovidLife: Study protocol and description of the data. Wellcome Open Research, 0, 6, 317.	1.8	0
161	RuralCovidLife: A new resource for the impact of the pandemic on rural Scotland.. Wellcome Open Research, 0, 6, 317.	1.8	0