Archie Campbell

List of Publications by Citations

170 papers	6,680 citations	41 h-index	79 g-index
203 ext. papers	10,401 ext. citations	11 avg, IF	4.85 L-index

#	Paper	IF	Citations
170	Genomic insights into the origin of farming in the ancient Near East. *Nature*, **2016**, 536, 419-24	50.4	485
169	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
168	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
167	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	36.3	257
166	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	7.8	237
165	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
164	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 97-105	18.1	225
163	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112 117). *Molecular Psychiatry*, **2017**, 22, 1376-1384	15.1	225
162	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. *Cell Systems*, **2020**, 11, 11-24.e4	10.6	219
161	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
160	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
159	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	36.3	170
158	Molecular genetic contributions to socioeconomic status and intelligence. *Intelligence*, **2014**, 44, 26-32	3	131
157	Mental health before and during the COVID-19 pandemic in two longitudinal UK population cohorts. *British Journal of Psychiatry*, **2020**, 1-10	5.4	123
156	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
155	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
154	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. *BMJ Open*, **2014**, 4, e006141	3	115

153	Cardiac Troponin T and Troponin I in the General Population. *Circulation*, **2019**, 139, 2754-2764	16.7	90
152	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
151	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. *Diabetes*, **2016**, 65, 2448-60	0.9	86
150	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. *Genome Medicine*, **2017**, 9, 23	14.4	85
149	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
148	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81
147	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
146	Epigenetic prediction of complex traits and death. *Genome Biology*, **2018**, 19, 136	18.3	77
145	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	3.7	75
144	Effect of Smoking on Blood Pressure and Resting Heart Rate: A Mendelian Randomization Meta-Analysis in the CARTA Consortium. *Circulation: Cardiovascular Genetics*, **2015**, 8, 832-41		70
143	Comparison between High-Sensitivity Cardiac Troponin T and Cardiac Troponin I in a Large General Population Cohort. *Clinical Chemistry*, **2018**, 64, 1607-1616	5.5	61
142	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. *PLoS Genetics*, **2018**, 14, e1007601	6	60
141	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
140	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	11	59
139	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	5.2	57
138	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. *PLoS Genetics*, **2016**, 12, e1005804	6	50
137	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. *European Journal of Human Genetics*, **2016**, 24, 919-23	5.3	47
136	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	0.9	46

135	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
134	An epigenome-wide association study of sex-specific chronological ageing. *Genome Medicine*, **2019**, 12, 1	14.4	43
133	Mental health during the COVID-19 pandemic in two longitudinal UK population cohorts		42
132	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
131	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	41
130	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	11.6	41
129	Exploring causality in the association between circulating 25-hydroxyvitamin D and colorectal cancer risk: a large Mendelian randomisation study. *BMC Medicine*, **2018**, 16, 142	11.4	40
128	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
127	Stratification by smoking status reveals an association of CHRNA5-A3-B4 genotype with body mass index in never smokers. *PLoS Genetics*, **2014**, 10, e1004799	6	40
126	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	3.7	40
125	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. *Clinical Epigenetics*, **2020**, 12, 115	7.7	40
124	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
123	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. *BMJ Open*, **2015**, 5, e008808	3	39
122	Self-reported medication use validated through record linkage to national prescribing data. *Journal of Clinical Epidemiology*, **2018**, 94, 132-142	5.7	38
121	A meta-analysis of genome-wide association studies of epigenetic age acceleration. *PLoS Genetics*, **2019**, 15, e1008104	6	38
120	Epigenetic signatures of starting and stopping smoking. *EBioMedicine*, **2018**, 37, 214-220	8.8	36
119	Recent genomic heritage in Scotland. *BMC Genomics*, **2015**, 16, 437	4.5	33
118	Factors associated with sharing e-mail information and mental health survey participation in large population cohorts. *International Journal of Epidemiology*, **2020**, 49, 410-421	7.8	32

117	A time-resolved proteomic and prognostic map of COVID-19. *Cell Systems*, **2021**, 12, 780-794.e7	10.6	32
116	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
115	and 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	12.7	30
114	Common genetic variants explain the majority of the correlation between height and intelligence: the generation Scotland study. *Behavior Genetics*, **2014**, 44, 91-6	3.2	30
113	Quantifying the extent to which index event biases influence large genetic association studies. *Human Molecular Genetics*, **2017**, 26, 1018-1030	5.6	30
112	Assessing the genetic overlap between BMI and cognitive function. *Molecular Psychiatry*, **2016**, 21, 1477-82	13.1	29
111	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
110	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
109	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. *EBioMedicine*, **2016**, 14, 161-167	8.8	26
108	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
107	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
106	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	3.5	24
105	The Dementias Platform UK (DPUK) Data Portal. *European Journal of Epidemiology*, **2020**, 35, 601-611	12.1	23
104	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. *Nature Communications*, **2019**, 10, 2373	17.4	22
103	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. *Nature Communications*, **2019**, 10, 1383	17.4	21
102	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. *Journal of Alzheimer's Disease* , **2017**, 57, 275-283	4.3	21
101	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. *Scientific Reports*, **2015**, 5, 16286	4.9	21
100	Blunted medial prefrontal cortico-limbic reward-related effective connectivity and depression. *Brain*, **2020**, 143, 1946-1956	11.2	19

99	Dissection of major depressive disorder using polygenic risk scores for schizophrenia in two independent cohorts. *Translational Psychiatry*, **2016**, 6, e938	8.6	19
98	Bayesian reassessment of the epigenetic architecture of complex traits. *Nature Communications*, **2020**, 11, 2865	17.4	18
97	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. *Human Molecular Genetics*, **2015**, 24, 5464-74	5.6	18
96	Novel Urinary Peptidomic Classifier Predicts Incident Heart Failure. *Journal of the American Heart Association*, **2017**, 6,	6	17
95	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
94	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. *Clinical Epigenetics*, **2020**, 12, 113	7.7	15
93	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
92	Within-sibship GWAS improve estimates of direct genetic effects		14
91	Urinary peptides in heart failure: a link to molecular pathophysiology. *European Journal of Heart Failure*, **2021**, 23, 1875-1887	12.3	14
90	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. *Brain, Behavior, and Immunity*, **2021**, 92, 39-48	16.6	14
89	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. *EBioMedicine*, **2019**, 43, 576-586	8.8	13
88	Polygenic risk of ischemic stroke is associated with cognitive ability. *Neurology*, **2016**, 86, 611-8	6.5	13
87	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	13
86	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	5.5	12
85	Regional variation in health is predominantly driven by lifestyle rather than genetics. *Nature Communications*, **2017**, 8, 801	17.4	11
84	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	11
83	Identification of epigenome-wide DNA methylation differences between carriers of APOE 4 and APOE 2 alleles. *Genome Medicine*, **2021**, 13, 1	14.4	11
82	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	11.5	10

81	Current versus lifetime depression, APOE variation, and their interaction on cognitive performance in younger and older adults. *Psychosomatic Medicine*, **2015**, 77, 480-92	3.7	10
80	Sex-Differences in the Metabolic Health of Offspring of Parents with Diabetes: A Record-Linkage Study. *PLoS ONE*, **2015**, 10, e0134883	3.7	10
79	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	4.8	10
78	A genome-wide association study finds genetic variants associated with neck or shoulder pain in UK Biobank. *Human Molecular Genetics*, **2020**, 29, 1396-1404	5.6	10
77	Electronic health record and genome-wide genetic data in Generation Scotland participants. *Wellcome Open Research*, **2017**, 2, 85	4.8	9
76	Insights into the genetic basis of retinal detachment. *Human Molecular Genetics*, **2020**, 29, 689-702	5.6	9
75	Genetic stratification of depression in UK Biobank. *Translational Psychiatry*, **2020**, 10, 163	8.6	8
74	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. *Clinical Epigenetics*, **2020**, 12, 49	7.7	8
73	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. *BMC Cardiovascular Disorders*, **2019**, 19, 240	2.3	8
72	Investigating genetic links between grapheme-colour synaesthesia and neuropsychiatric traits. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2019**, 374, 20190026	5.8	8
71	Assessment of dried blood spots for DNA methylation profiling. *Wellcome Open Research*, **2019**, 4, 44	4.8	8
70	Epigenetic clocks predict prevalence and incidence of leading causes of death and disease burden		8
69	Genetic comorbidity between major depression and cardio-metabolic traits, stratified by age at onset of major depression. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 309-330	3.5	8
68	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. *Translational Psychiatry*, **2018**, 8, 63	8.6	7
67	Birth weight associations with DNA methylation differences in an adult population. *Epigenetics*, **2021**, 16, 783-796	5.7	7
66	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	15.1	7
65	CovidLife: a resource to understand mental health, well-being and behaviour during the COVID-19 pandemic in the UK. *Wellcome Open Research*,6, 176	4.8	7
64	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7

63	Exome sequencing to detect rare variants associated with general cognitive ability: a pilot study. *Twin Research and Human Genetics*, **2015**, 18, 117-25	2.2	6
62	A proteomic survival predictor for COVID-19 patients in intensive care **2022**, 1, e0000007		6
61	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
60	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
59	Genetic stratification of depression in UK Biobank suggests a subgroup linked to age of natural menopause		6
58	Prescreening for European Prevention of Alzheimer Dementia (EPAD) trial-ready cohort: impact of AD risk factors and recruitment settings. *Alzheimers Research and Therapy*, **2020**, 12, 8	9	6
57	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
56	Birth weight associations with psychiatric and physical health, cognitive function, and DNA methylation differences in an adult population		5
55	Genome-wide association study of cardiac troponin I in the general population. *Human Molecular Genetics*, **2021**, 30, 2027-2039	5.6	5
54	Early life predictors of late life cerebral small vessel disease in four prospective cohort studies. *Brain*, **2021**,	11.2	5
53	Acute COVID-19 severity and mental health morbidity trajectories in patient populations of six nations: an observational study.. *Lancet Public Health, The*, **2022**,	22.4	5
52	Molecular Genetic Risk for Psychosis Is Associated With Psychosis Risk Symptoms in a Population-Based UK Cohort: Findings From Generation Scotland. *Schizophrenia Bulletin*, **2020**,	1.3	4
51	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
50	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. *Molecular Psychiatry*, **2021**, 26, 4344-4354	15.1	4
49	Pharmaco-epidemiology of antidepressant exposure in a UK cohort record-linkage study. *Journal of Psychopharmacology*, **2019**, 33, 482-493	4.6	3
48	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
47	Using tree-based methods for detection of gene-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	7.2	3
46	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PLoS ONE*, **2021**, 16, e0255402	3.7	3

45	Genome-Wide Association Study of NAFLD Using Electronic Health Records. *Hepatology Communications*, **2021**,	6	3
44	Epigenetic scores for the circulating proteome as tools for disease prediction.. *ELife*, **2022**, 11,	8.9	2
43	Cohort Profile: COVIDMENT: COVID-19 cohorts on mental health across six nations.. *International Journal of Epidemiology*, **2021**,	7.8	2
42	TeenCovidLife: a resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. *Wellcome Open Research*,6, 277	4.8	2
41	Creating and validating a DNA methylation-based proxy for Interleukin-6		2
40	Generation Scotland participant survey on data collection. *Wellcome Open Research*, **2019**, 4, 111	4.8	2
39	Electronic Health Record and Genome-wide Genetic Data in Generation Scotland Participants		2
38	Epigenetic scores for the circulating proteome as tools for disease prediction		2
37	A meta-analysis of genome-wide association studies of epigenetic age acceleration		2
36	Blood-based epigenome-wide analyses of cognitive abilities		2
35	Sex Differences in Cardiac Troponin I and T and the Prediction of Cardiovascular Events in the General Population. *Clinical Chemistry*, **2021**, 67, 1351-1360	5.5	2
34	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin.. *Journal of the American Society of Nephrology: JASN*, **2022**, 33, 511-529	12.7	2
33	Blood-based epigenome-wide analyses of cognitive abilities.. *Genome Biology*, **2022**, 23, 26	18.3	1
32	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. *EBioMedicine*, **2021**, 74, 103730	8.8	1
31	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
30	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. *Molecular Psychiatry*, **2021**,	15.1	1
29	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability		1
28	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population		1

27	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. *Alzheimers and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2020**, 12, e12078	5.2	1
26	Socioeconomic position and mental health during the COVID-19 pandemic: a cross-sectional analysis of the CovidLife study. *Wellcome Open Research*,6, 139	4.8	1
25	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	6.4	1
24	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. *PLoS Genetics*, **2021**, 17, e1009750	6	1
23	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. *Molecular Psychiatry*, **2021**,	15.1	1
22	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
21	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
20	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. *Epigenetics*, **2021**, 1-17	5.7	0
19	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. *JAMA Network Open*, **2021**, 4, e2136560	10.4	0
18	Hair glucocorticoids are associated with childhood adversity, depressive symptoms and reduced global and lobar grey matter in Generation Scotland. *Translational Psychiatry*, **2021**, 11, 523	8.6	0
17	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
16	Genome-wide association study of susceptibility to hospitalised respiratory infections. *Wellcome Open Research*,6, 290	4.8	0
15	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
14	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*,4, 185	4.8	0
13	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	3.5	0
12	Identification of plasma proteins relating to brain neurodegeneration and vascular pathology in cognitively normal individuals. *Alzheimers and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2021**, 13, e12240	5.2	0
11	Complex trait methylation scores in the prediction of major depressive disorder.. *EBioMedicine*, **2022**, 79, 104000	8.8	0
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0

9	TeenCovidLife: a resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. *Wellcome Open Research*,6, 277	4.8	0
8	A Computer Based Follow-up of Hypertension in the Community: Baseline Characteristics of 502 Patients. *Clinical Science*, **1988**, 74, 17P-17P		
7	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits.. *Frontiers in Genetics*, **2021**, 12, 791712	4.5	
6	RuralCovidLife: Study protocol and description of the data. *Wellcome Open Research*,6, 317	4.8	
5	Generation Scotland participant survey on data collection. *Wellcome Open Research*,4, 111	4.8	
4	Face covering adherence is positively associated with better mental health and wellbeing: a longitudinal analysis of the CovidLife surveys. *Wellcome Open Research*,6, 62	4.8	
3	General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52	2.6	
2	Genome- and epigenome-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	5.2	
1	RuralCovidLife: A new resource for the impact of the pandemic on rural Scotland.. *Wellcome Open Research*,6, 317	4.8	