Adam Butterworth

List of Publications by Citations

177 papers	19,183 citations	62 h-index	138 g-index
224 ext. papers	27,598 ext. citations	16.7 avg, IF	6.24 L-index

#	Paper	IF	Citations
177	Mendelian randomization analysis with multiple genetic variants using summarized data. *Genetic Epidemiology*, **2013**, 37, 658-65	2.6	1047
176	Association of dietary, circulating, and supplement fatty acids with coronary risk: a systematic review and meta-analysis. *Annals of Internal Medicine*, **2014**, 160, 398-406	8	763
175	C-reactive protein, fibrinogen, and cardiovascular disease prediction. *New England Journal of Medicine*, **2012**, 367, 1310-20	59.2	750
174	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
173	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
172	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
171	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599 912 current drinkers in 83 prospective studies. *Lancet, The*, **2018**, 391, 1513-1523	40	530
170	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
169	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
168	Triglyceride-mediated pathways and coronary disease: collaborative analysis of 101 studies. *Lancet, The*, **2010**, 375, 1634-9	40	520
167	Leucocyte telomere length and risk of cardiovascular disease: systematic review and meta-analysis. *BMJ, The*, **2014**, 349, g4227	5.9	501
166	PhenoScanner: a database of human genotype-phenotype associations. *Bioinformatics*, **2016**, 32, 3207-3209	7.9	430
165	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
164	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
163	Association of Cardiometabolic Multimorbidity With Mortality. *JAMA - Journal of the American Medical Association*, **2015**, 314, 52-60	27.4	365
162	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
161	Inflammatory cytokines and risk of coronary heart disease: new prospective study and updated meta-analysis. *European Heart Journal*, **2014**, 35, 578-89	9.5	344

160	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
159	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
158	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
157	Relative and absolute risk of colorectal cancer for individuals with a family history: a meta-analysis. *European Journal of Cancer*, **2006**, 42, 216-27	7.5	295
156	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention. *Journal of the American College of Cardiology*, **2018**, 72, 1883-1893	15.1	285
155	Lipid-related markers and cardiovascular disease prediction. *JAMA - Journal of the American Medical Association*, **2012**, 307, 2499-506	27.4	271
154	Association of Triglyceride-Lowering LPL Variants and LDL-C-Lowering LDLR Variants With Risk of Coronary Heart Disease. *JAMA - Journal of the American Medical Association*, **2019**, 321, 364-373	27.4	263
153	PhenoScanner V2: an expanded tool for searching human genotype-phenotype associations. *Bioinformatics*, **2019**, 35, 4851-4853	7.2	260
152	Polygenic Risk Score Identifies Subgroup With Higher Burden of Atherosclerosis and Greater Relative Benefit From Statin Therapy in the Primary Prevention Setting. *Circulation*, **2017**, 135, 2091-2101	16.7	244
151	Association of LPA Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies: A Mendelian Randomization Analysis. *JAMA Cardiology*, **2018**, 3, 619-627	16.2	235
150	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
149	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
148	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
147	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
146	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
145	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
144	Adult height and the risk of cause-specific death and vascular morbidity in 1 million people: individual participant meta-analysis. *International Journal of Epidemiology*, **2012**, 41, 1419-33	7.8	178
143	Large-scale gene-centric analysis identifies novel variants for coronary artery disease. *PLoS Genetics* , **2011**, 7, e1002260	6	175

142	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
141	Functional IL6R 358Ala allele impairs classical IL-6 receptor signaling and influences risk of diverse inflammatory diseases. *PLoS Genetics*, **2013**, 9, e1003444	6	170
140	Association of Genetic Variants Related to CETP Inhibitors and Statins With Lipoprotein Levels and Cardiovascular Risk. *JAMA - Journal of the American Medical Association*, **2017**, 318, 947-956	27.4	169
139	Array CGH in patients with learning disability (mental retardation) and congenital anomalies: updated systematic review and meta-analysis of 19 studies and 13,926 subjects. *Genetics in Medicine*, **2009**, 11, 139-46	8.1	164
138	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
137	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
136	Separate and combined associations of obesity and metabolic health with coronary heart disease: a pan-European case-cohort analysis. *European Heart Journal*, **2018**, 39, 397-406	9.5	146
135	Network Mendelian randomization: using genetic variants as instrumental variables to investigate mediation in causal pathways. *International Journal of Epidemiology*, **2015**, 44, 484-95	7.8	144
134	Leucocyte telomere length and risk of type 2 diabetes mellitus: new prospective cohort study and literature-based meta-analysis. *PLoS ONE*, **2014**, 9, e112483	3.7	144
133	Glycated hemoglobin measurement and prediction of cardiovascular disease. *JAMA - Journal of the American Medical Association*, **2014**, 311, 1225-33	27.4	136
132	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*, **2017**, 49, 1450-1457	36.3	136
131	Use of Mendelian randomisation to assess potential benefit of clinical intervention. *BMJ, The*, **2012**, 345, e7325	5.9	133
130	Coffee Drinking and Mortality in 10 European Countries: A Multinational Cohort Study. *Annals of Internal Medicine*, **2017**, 167, 236-247	8	127
129	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
128	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. *Lancet Neurology, The*, **2017**, 16, 898-907	24.1	121
127	Mendelian Randomization Study of and Cardiovascular Disease. *New England Journal of Medicine*, **2019**, 380, 1033-1042	59.2	116
126	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. *Nature Communications*, **2018**, 9, 3268	17.4	111
125	Natriuretic peptides and integrated risk assessment for cardiovascular disease: an individual-participant-data meta-analysis. *Lancet Diabetes and Endocrinology,the*, **2016**, 4, 840-9	18.1	108

124	Cardiovascular Risk Factors Associated With Venous Thromboembolism. *JAMA Cardiology*, **2019**, 4, 163-173	16.2	102
123	Seven lipoprotein lipase gene polymorphisms, lipid fractions, and coronary disease: a HuGE association review and meta-analysis. *American Journal of Epidemiology*, **2008**, 168, 1233-46	3.8	98
122	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
121	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
120	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 243-53	18.1	81
119	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
118	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. *Nature Genetics*, **2020**, 52, 1122-1131	36.3	75
117	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
116	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
115	Body mass index and all cause mortality in HUNT and UK Biobank studies: linear and non-linear mendelian randomisation analyses. *BMJ, The*, **2019**, 364, l1042	5.9	58
114	SCORE2 risk prediction algorithms: new models to estimate 10-year risk of cardiovascular disease in Europe. *European Heart Journal*, **2021**, 42, 2439-2454	9.5	58
113	Beyond Mendelian randomization: how to interpret evidence of shared genetic predictors. *Journal of Clinical Epidemiology*, **2016**, 69, 208-16	5.7	54
112	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. *Nature Communications*, **2019**, 10, 5819	17.4	54
111	Consumption of Meat, Fish, Dairy Products, and Eggs and Risk of Ischemic Heart Disease. *Circulation* , **2019**, 139, 2835-2845	16.7	52
110	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
109	Association of Multiple Biomarkers of Iron Metabolism and Type 2 Diabetes: The EPIC-InterAct Study. *Diabetes Care*, **2016**, 39, 572-81	14.6	48
108	GUESS-ing polygenic associations with multiple phenotypes using a GPU-based evolutionary stochastic search algorithm. *PLoS Genetics*, **2013**, 9, e1003657	6	45
107	Association of the 9p21.3 locus with risk of first-ever myocardial infarction in Pakistanis: case-control study in South Asia and updated meta-analysis of Europeans. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 1467-73	9.4	45

106	ProGeM: a framework for the prioritization of candidate causal genes at molecular quantitative trait loci. *Nucleic Acids Research*, **2019**, 47, e3	20.1	45
105	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
104	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
103	Alcohol intake in relation to non-fatal and fatal coronary heart disease and stroke: EPIC-CVD case-cohort study. *BMJ, The*, **2018**, 361, k934	5.9	44
102	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
101	Lifestyle factors and risk of multimorbidity of cancer and cardiometabolic diseases: a multinational cohort study. *BMC Medicine*, **2020**, 18, 5	11.4	43
100	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. *Nature Communications*, **2019**, 10, 5741	17.4	42
99	Genetic Determinants of Lipids and Cardiovascular Disease Outcomes: A Wide-Angled Mendelian Randomization Investigation. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002711	5.2	41
98	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. *American Journal of Human Genetics*, **2020**, 106, 389-404	11	40
97	Parity, breastfeeding and risk of coronary heart disease: A pan-European case-cohort study. *European Journal of Preventive Cardiology*, **2016**, 23, 1755-1765	3.9	39
96	An Unbiased Lipid Phenotyping Approach To Study the Genetic Determinants of Lipids and Their Association with Coronary Heart Disease Risk Factors. *Journal of Proteome Research*, **2019**, 18, 2397-2410	5.6	38
95	Assessing the causal association of glycine with risk of cardio-metabolic diseases. *Nature Communications*, **2019**, 10, 1060	17.4	38
94	Assessing risk prediction models using individual participant data from multiple studies. *American Journal of Epidemiology*, **2014**, 179, 621-32	3.8	36
93	Metabolomic Consequences of Genetic Inhibition of PCSK9 Compared With Statin Treatment. *Circulation*, **2018**, 138, 2499-2512	16.7	36
92	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
91	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. *Lancet Haematology,the*, **2018**, 5, e241-e251	14.6	35
90	Contribution of common non-synonymous variants in PCSK1 to body mass index variation and risk of obesity: a systematic review and meta-analysis with evidence from up to 331 175 individuals. *Human Molecular Genetics*, **2015**, 24, 3582-94	5.6	34
89	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33

88	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, **2017**, 7, 4394	4.9	31
87	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058	17.4	30
86	Lipoprotein(a) in Alzheimer, Atherosclerotic, Cerebrovascular, Thrombotic, and Valvular Disease: Mendelian Randomization Investigation. *Circulation*, **2020**, 141, 1826-1828	16.7	29
85	The associations of major foods and fibre with risks of ischaemic and haemorrhagic stroke: a prospective study of 418 329 participants in the EPIC cohort across nine European countries. *European Heart Journal*, **2020**, 41, 2632-2640	9.5	28
84	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. *PLoS Medicine*, **2021**, 18, e1003498	11.6	27
83	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
82	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002413	5.2	25
81	Association of plasma biomarkers of fruit and vegetable intake with incident type 2 diabetes: EPIC-InterAct case-cohort study in eight European countries. *BMJ, The*, **2020**, 370, m2194	5.9	24
80	A comparison of Cox and logistic regression for use in genome-wide association studies of cohort and case-cohort design. *European Journal of Human Genetics*, **2017**, 25, 854-862	5.3	23
79	Association of menopausal characteristics and risk of coronary heart disease: a pan-European case-cohort analysis. *International Journal of Epidemiology*, **2019**, 48, 1275-1285	7.8	23
78	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
77	Validation of a Genome-Wide Polygenic Score for Coronary Artery Disease in South Asians. *Journal of the American College of Cardiology*, **2020**, 76, 703-714	15.1	22
76	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases		21
75	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. *Diabetes Care*, **2021**, 44, 98-106	14.6	21
74	Genetic determinants of major blood lipids in Pakistanis compared with Europeans. *Circulation: Cardiovascular Genetics*, **2010**, 3, 348-57		20
73	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. *Nature Medicine*, **2021**, 27, 668-676	50.5	19
72	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. *Nature Communications*, **2018**, 9, 4674	17.4	19
71	A cross-platform approach identifies genetic regulators of human metabolism and health. *Nature Genetics*, **2021**, 53, 54-64	36.3	18

70	Association of Plasma Vitamin D Metabolites With Incident Type 2 Diabetes: EPIC-InterAct Case-Cohort Study. *Journal of Clinical Endocrinology and Metabolism*, **2019**, 104, 1293-1303	5.6	17
69	Estimating dose-response relationships for vitamin D with coronary heart disease, stroke, and all-cause mortality: observational and Mendelian randomisation analyses. *Lancet Diabetes and Endocrinology,the*, **2021**, 9, 837-846	18.1	17
68	Genomic risk prediction of coronary artery disease in nearly 500,000 adults: implications for early screening and primary prevention		17
67	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. *European Journal of Preventive Cardiology*, **2017**, 24, 492-504	3.9	16
66	The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design. *European Journal of Epidemiology*, **2015**, 30, 577-87	12.1	16
65	Comparative validity of vitamin C and carotenoids as indicators of fruit and vegetable intake: a systematic review and meta-analysis of randomised controlled trials. *British Journal of Nutrition*, **2015**, 114, 1331-40	3.6	15
64	Polygenic basis and biomedical consequences of telomere length variation. *Nature Genetics*, **2021**, 53, 1425-1433	36.3	15
63	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: A meta-analysis and Mendelian randomisation analysis. *PLoS Medicine*, **2020**, 17, e1003394	11.6	15
62	Lipoprotein signatures of cholesteryl ester transfer protein and HMG-CoA reductase inhibition. *PLoS Biology*, **2019**, 17, e3000572	9.7	15
61	Effect of communicating phenotypic and genetic risk of coronary heart disease alongside web-based lifestyle advice: the INFORM Randomised Controlled Trial. *Heart*, **2019**, 105, 982-989	5.1	14
60	Shorter leukocyte telomere length is associated with adverse COVID-19 outcomes: A cohort study in UK Biobank. *EBioMedicine*, **2021**, 70, 103485	8.8	13
59	High-throughput multivariable Mendelian randomization analysis prioritizes apolipoprotein B as key lipid risk factor for coronary artery disease. *International Journal of Epidemiology*, **2021**, 50, 893-901	7.8	12
58	Development and evaluation of a transfusion medicine genome wide genotyping array. *Transfusion*, **2019**, 59, 101-111	2.9	12
57	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. *Communications Biology*, **2020**, 3, 703	6.7	11
56	Metabolic profiling of angiopoietin-like protein 3 and 4 inhibition: a drug-target Mendelian randomization analysis. *European Heart Journal*, **2021**, 42, 1160-1169	9.5	11
55	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. *Communications Biology*, **2021**, 4, 156	6.7	11
54	Glycemic index, glycemic load, and risk of coronary heart disease: a pan-European cohort study. *American Journal of Clinical Nutrition*, **2020**, 112, 631-643	7	10
53	Consequences of natural perturbations in the human plasma proteome		10

52	Information and Risk Modification Trial (INFORM): design of a randomised controlled trial of communicating different types of information about coronary heart disease risk, alongside lifestyle advice, to achieve change in health-related behaviour. *BMC Public Health*, **2015**, 15, 868	4.1	9
51	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. *Nature Communications*, **2020**, 11, 800	17.4	8
50	Cross-platform genetic discovery of small molecule products of metabolism and application to clinical outcomes		8
49	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. *Blood Advances*, **2020**, 4, 3495-3506	7.8	7
48	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. *Nature Metabolism*, **2021**, 3, 1476-1483	14.6	6
47	ACE inhibition and cardiometabolic risk factors, lung and gene expression, and plasma ACE2 levels: a Mendelian randomization study. *Royal Society Open Science*, **2020**, 7, 200958	3.3	6
46	Genomic evaluation of circulating proteins for drug target characterisation and precision medicine		5
45	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries		5
44	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
43	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5
42	Plant foods, dietary fibre and risk of ischaemic heart disease in the European Prospective Investigation into Cancer and Nutrition (EPIC) cohort. *International Journal of Epidemiology*, **2021**, 50, 212-222	7.8	5
41	Measurement and initial characterization of leukocyte telomere length in 474,074 participants in UK Biobank. *Nature Aging*, **2022**, 2, 170-179		5
40	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
39	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
38	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases		4
37	ACE inhibition and cardiometabolic risk factors, lung ACE2 and TMPRSS2 gene expression, and plasma ACE2 levels: a Mendelian randomization study		4
36	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. *Nature Medicine*, **2021**, 27, 1564-1575	50.5	4
35	The influence of rare variants in circulating metabolic biomarkers. *PLoS Genetics*, **2020**, 16, e1008605	6	3

34	Dietary Fatty Acids, Macronutrient Substitutions, Food Sources and Incidence of Coronary Heart Disease: Findings From the EPIC-CVD Case-Cohort Study Across Nine European Countries. *Journal of the American Heart Association*, **2021**, 10, e019814	6	3
33	Genetic Analyses of Blood Cell Structure for Biological and Pharmacological Inference		3
32	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
31	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci. *BMC Medicine*, **2021**, 19, 232	11.4	3
30	Quality control and removal of technical variation of NMR metabolic biomarker data in ~120,000 UK Biobank participants		3
29	Modifiable traits, healthy behaviours, and leukocyte telomere length: a population-based study in UK Biobank. *The Lancet Healthy Longevity*, **2022**, 3, e321-e331	9.5	3
28	ProGeM: A framework for the prioritisation of candidate causal genes at molecular quantitative trait loci		2
27	Effects of adiposity on the human plasma proteome: observational and Mendelian randomisation estimates. *International Journal of Obesity*, **2021**, 45, 2221-2229	5.5	2
26	Risk factors and prediction models for incident heart failure with reduced and preserved ejection fraction. *ESC Heart Failure*, **2021**,	3.7	2
25	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. *Human Molecular Genetics*, **2021**,	5.6	2
24	Higher body mass index raises immature platelet count: potential contribution to obesity-related thrombosis.. *Platelets*, **2022**, 1-10	3.6	1
23	Machine learning optimized polygenic scores for blood cell traits identify sex-specific trajectories and genetic correlations with disease.. *Cell Genomics*, **2022**, 2, None		1
22	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. *Nutrients*, **2021**, 13,	6.7	1
21	Investigating Genetic and Other Determinants of First-Onset Myocardial Infarction in Malaysia: Protocol for the Malaysian Acute Vascular Events Risk Study.. *JMIR Research Protocols*, **2022**, 11, e31885[2]		1
20	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits		1
19	Genetic determinants of lipids and cardiovascular disease outcomes: a wide-angled Mendelian randomization investigation		1
18	High-throughput multivariable Mendelian randomization analysis prioritizes apolipoprotein B as key lipid risk factor for coronary artery disease		1
17	Learning polygenic scores for human blood cell traits		1

16	Effects of adiposity on the human plasma proteome: Observational and Mendelian randomization estimates		1
15	Genome-wide analysis of blood lipid metabolites in over 5,000 South Asians reveals biological insights at cardiometabolic disease loci		1
14	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19		1
13	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
12	Lipoprotein Signatures of Cholesteryl Ester Transfer Protein and HMG-CoA Reductase Inhibition		1
11	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
10	Interleukin-6 Receptor Signalling and Abdominal Aortic Aneurysm Growth Rates		1
9	Genetic analysis identifies molecular systems and biological pathways associated with household income		1
8	Plasma Proteomics of Renal Function: A Trans-ethnic Meta-analysis and Mendelian Randomization Study. *Journal of the American Society of Nephrology: JASN*, **2021**,	12.7	1
7	The blood metabolome of incident kidney cancer: A case-control study nested within the MetKid consortium. *PLoS Medicine*, **2021**, 18, e1003786	11.6	1
6	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 1836-1851	11	1
5	Association of shorter leucocyte telomere length with risk of frailty.. *Journal of Cachexia, Sarcopenia and Muscle*, **2022**,	10.3	1
4	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations.. *Scientific Reports*, **2022**, 12, 1131	4.9	0
3	Milk intake and incident stroke and coronary heart disease in populations of European descent: A Mendelian Randomization study. *British Journal of Nutrition*, **2021**, 1-25	3.6	0
2	Identification of Novel Variants Associated with Fetal Hemoglobin Levels in Healthy Donors (the INTERVAL study). *Blood*, **2019**, 134, 2243-2243	2.2	
1	Dose-response relationships for vitamin D and all-cause mortality - AuthorsUreply.. *Lancet Diabetes and Endocrinology,the*, **2022**, 10, 158-159	18.1	