Adam Butterworth

List of Publications by Year
in descending order

159 papers	34,945 citations	10070 75 h-index	6177 164 g-index
224 all docs	224 docs citations	224 times ranked	44637 citing authors

#	Article	IF	Citations
1	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	1.4	9
2	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.	0.5	1
3	Milk intake and incident stroke and CHD in populations of European descent: a Mendelian randomisation study. British Journal of Nutrition, 2022, 128, 1789-1797.	1.2	2
4	An Expanded Genome-Wide Association Study of Fructosamine Levels Identifies RCN3 as a Replicating Locus and Implicates FCGRT as the Effector Transcript. Diabetes, 2022, 71, 359-364.	0.3	1
5	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.	1.6	2
6	Higher body mass index raises immature platelet count: potential contribution to obesity-related thrombosis. Platelets, 2022, 33, 869-878.	1.1	9
7	Machine learning optimized polygenic scores for blood cell traits identify sex-specific trajectories and genetic correlations with disease. Cell Genomics, 2022, 2, 100086.	3.0	9
8	Physical activity attenuates but does not eliminate coronary heart disease risk amongst adults with risk factors: EPIC-CVD case-cohort study. European Journal of Preventive Cardiology, 2022, 29, 1618-1629.	0.8	8
9	Measurement and initial characterization of leukocyte telomere length in 474,074 participants in UK Biobank. Nature Aging, 2022, 2, 170-179.	5.3	75
10	Association of shorter leucocyte telomere length with risk of frailty. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 1741-1751.	2.9	13
11	Genetically Determined Reproductive Aging and Coronary Heart Disease: A Bidirectional 2-sample Mendelian Randomization. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2952-e2961.	1.8	13
12	Doseâ€“response relationships for vitamin D and all-cause mortality â€“ Authors' reply. Lancet Diabetes and Endocrinology,the, 2022, 10, 158-159.	5.5	0
13	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
14	Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American Journal of Human Genetics, 2022, 109, 1038-1054.	2.6	17
15	Modifiable traits, healthy behaviours, and leukocyte telomere length: a population-based study in UK Biobank. The Lancet Healthy Longevity, 2022, 3, e321-e331.	2.0	27
16	Flashfm-ivis: interactive visualization for fine-mapping of multiple quantitative traits. Bioinformatics, 2022, 38, 4238-4242.	1.8	2
17	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.	0.9	12
18	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. Diabetes Care, 2021, 44, 98-106.	4.3	68

#	Article	IF	Citations
19	Metabolic profiling of angiopoietin-like protein 3 and 4 inhibition: a drug-target Mendelian randomization analysis. European Heart Journal, 2021, 42, 1160-1169.	1.0	33
20	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	9.4	117
21	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	3.9	95
22	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
23	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	15.2	120
24	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
25	SCORE2 risk prediction algorithms: new models to estimate 10-year risk of cardiovascular disease in Europe. European Heart Journal, 2021, 42, 2439-2454.	1.0	491
26	Plasma Proteomics of Renal Function: A Transethnic Meta-Analysis and Mendelian Randomization Study. Journal of the American Society of Nephrology: JASN, 2021, 32, 1747-1763.	3.0	16
27	Effects of adiposity on the human plasma proteome: observational and Mendelian randomisation estimates. International Journal of Obesity, 2021, 45, 2221-2229.	1.6	31
28	Shorter leukocyte telomere length is associated with adverse COVID-19 outcomes: A cohort study in UK Biobank. EBioMedicine, 2021, 70, 103485.	2.7	36
29	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	15.2	40
30	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci. BMC Medicine, 2021, 19, 232.	2.3	25
31	The blood metabolome of incident kidney cancer: A caseâ€“control study nested within the MetKid consortium. PLoS Medicine, 2021, 18, e1003786.	3.9	16
32	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.	2.6	14
33	Risk factors and prediction models for incident heart failure with reduced and preserved ejection fraction. ESC Heart Failure, 2021, , .	1.4	9
34	204Effects of adiposity on the human proteome: Mendelian randomization study using individual-level data. International Journal of Epidemiology, 2021, 50, .	0.9	0
35	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.	0.9	52
36	Polygenic basis and biomedical consequences of telomere length variation. Nature Genetics, 2021, 53, 1425-1433.	9.4	145

#	Article	IF	Citations
37	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. Nature Metabolism, 2021, 3, 1476-1483.	5.1	43
38	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. Nutrients, 2021, 13, 4164.	1.7	3
39	Dietary Fatty Acids, Macronutrient Substitutions, Food Sources and Incidence of Coronary Heart Disease: Findings From the EPICâ€CVD Caseâ€Cohort Study Across Nine European Countries. Journal of the American Heart Association, 2021, 10, e019814.	1.6	29
40	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
41	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
42	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: AÂmeta-analysis and Mendelian randomisation analysis. PLoS Medicine, 2020, 17, e1003394.	3.9	45
43	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
44	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
45	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. Communications Biology, 2020, 3, 703.	2.0	40
46	Validation of a Genome-Wide PolygenicÂScore for Coronary ArteryÂDisease inÂSouth Asians. Journal of the American College of Cardiology, 2020, 76, 703-714.	1.2	76
47	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506.	2.5	31
48	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
49	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131.	9.4	298
50	Lipoprotein(a) in Alzheimer, Atherosclerotic, Cerebrovascular, Thrombotic, and Valvular Disease. Circulation, 2020, 141, 1826-1828.	1.6	56
51	The influence of rare variants in circulating metabolic biomarkers. PLoS Genetics, 2020, 16, e1008605.	1.5	9
52	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.	3.0	75
53	Glycemic index, glycemic load, and risk of coronary heart disease: a pan-European cohort study. American Journal of Clinical Nutrition, 2020, 112, 631-643.	2.2	19
54	The associations of major foods and fibre with risks of ischaemic and haemorrhagic stroke: a prospective study of 418Â329 participants in the EPIC cohort across nine European countries. European Heart Journal, 2020, 41, 2632-2640.	1.0	60

#	Article	IF	Citations
55	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
56	Lifestyle factors and risk of multimorbidity of cancer and cardiometabolic diseases: a multinational cohort study. BMC Medicine, 2020, 18, 5.	2.3	148
57	Neurology-related protein biomarkers are associated with cognitive ability and brain volume in older age. Nature Communications, 2020, 11, 800.	5.8	42
58	ACE inhibition and cardiometabolic risk factors, lungACE2andTMPRSS2gene expression, and plasma ACE2 levels: a Mendelian randomization study. Royal Society Open Science, 2020, 7, 200958.	1.1	12
59	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
60	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
61	Association of Triglyceride-Lowering LPL Variants and LDL-Câ€“Lowering LDLR Variants With Risk of Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2019, 321, 364.	3.8	460
62	PhenoScanner V2: an expanded tool for searching human genotypeâ€“phenotype associations. Bioinformatics, 2019, 35, 4851-4853.	1.8	1,036
63	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
64	Consumption of Meat, Fish, Dairy Products, and Eggs and Risk of Ischemic Heart Disease. Circulation, 2019, 139, 2835-2845.	1.6	103
65	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.	1.8	55
66	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.	1.8	25
67	Body mass index and all cause mortality in HUNT and UK Biobank studies: linear and non-linear mendelian randomisation analyses. BMJ: British Medical Journal, 2019, 364, l1042.	2.4	125
68	Assessing the causal association of glycine with risk of cardio-metabolic diseases. Nature Communications, 2019, 10, 1060.	5.8	85
69	Mendelian Randomization Study of ACLY and Cardiovascular Disease. New England Journal of Medicine, 2019, 380, 1033-1042.	13.9	216
70	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.	1.2	34
71	Association of menopausal characteristics and risk of coronary heart disease: a pan-European caseâ€“cohort analysis. International Journal of Epidemiology, 2019, 48, 1275-1285.	0.9	47
72	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. Circulation Genomic and Precision Medicine, 2019, 12, e002413.	1.6	46

#	Article	IF	Citations
73	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
74	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
75	Lipoprotein signatures of cholesteryl ester transfer protein and HMG-CoA reductase inhibition. PLoS Biology, 2019, 17, e3000572.	2.6	29
76	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. Nature Communications, 2019, 10, 5819.	5.8	124
77	Genetic Determinants of Lipids and Cardiovascular Disease Outcomes. Circulation Genomic and Precision Medicine, 2019, 12, e002711.	1.6	83
78	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. Nature Communications, 2019, 10, 5741.	5.8	110
79	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	0.8	30
80	Cardiovascular Risk Factors Associated With Venous Thromboembolism. JAMA Cardiology, 2019, 4, 163.	3.0	187
81	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
82	ProGeM: a framework for the prioritization of candidate causal genes at molecular quantitative trait loci. Nucleic Acids Research, 2019, 47, e3-e3.	6.5	90
83	Identification of Novel Variants Associated with Fetal Hemoglobin Levels in Healthy Donors (the) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.6	0
84	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
85	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599â€˜912 current drinkers in 83 prospective studies. Lancet, The, 2018, 391, 1513-1523.	6.3	858
86	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	5.8	295
87	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.	1.0	209
88	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	5.8	33
89	Metabolomic Consequences of Genetic Inhibition of PCSK9 Compared With Statin Treatment. Circulation, 2018, 138, 2499-2512.	1.6	69
90	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	1.2	557

#	Article	IF	Citations
91	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
92	Alcohol intake in relation to non-fatal and fatal coronary heart disease and stroke: EPIC-CVD case-cohort study. BMJ: British Medical Journal, 2018, 361, k934.	2.4	70
93	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. Lancet Haematology,the, 2018, 5, e241-e251.	2.2	70
94	Genomeâ€wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. Nature Communications, 2018, 9, 3268.	5.8	221
95	Genomic atlas of the human plasma proteome. Nature, 2018, 558, 73-79.	13.7	1,180
96	Association ofLPAVariants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies. JAMA Cardiology, 2018, 3, 619.	3.0	428
97	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
98	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
99	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
100	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.	1.6	403
101	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. European Journal of Preventive Cardiology, 2017, 24, 492-504.	0.8	22
102	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
103	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.	1.4	45
104	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
105	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
106	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
107	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.	4.9	191
108	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48

#	Article	IF	Citations
109	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
110	Coffee Drinking and Mortality in 10 European Countries. Annals of Internal Medicine, 2017, 167, 236-247.	2.0	168
111	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
112	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
113	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
114	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.	3.8	247
115	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	9.4	218
116	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
117	Parity, breastfeeding and risk of coronary heart disease: A pan-European caseâ€“cohort study. European Journal of Preventive Cardiology, 2016, 23, 1755-1765.	0.8	58
118	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
119	Natriuretic peptides and integrated risk assessment for cardiovascular disease: an individual-participant-data meta-analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 840-849.	5.5	159
120	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
121	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
122	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
123	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
124	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
125	PhenoScanner: a database of human genotypeâ€“phenotype associations. Bioinformatics, 2016, 32, 3207-3209.	1.8	983
126	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438

#	Article	IF	Citations
127	Association of Multiple Biomarkers of Iron Metabolism and Type 2 Diabetes: The EPIC-InterAct Study. Diabetes Care, 2016, 39, 572-581.	4.3	65
128	Beyond Mendelian randomization: how to interpret evidence of shared genetic predictors. Journal of Clinical Epidemiology, 2016, 69, 208-216.	2.4	77
129	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, 1331-1340.	1.2	25
130	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.	1.2	13
131	Association of Cardiometabolic Multimorbidity With Mortality. JAMA - Journal of the American Medical Association, 2015, 314, 52.	3.8	624
132	The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design. European Journal of Epidemiology, 2015, 30, 577-587.	2.5	25
133	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2015, 3, 243-253.	5.5	115
134	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, 3582-3594.	1.4	53
135	Network Mendelian randomization: using genetic variants as instrumental variables to investigate mediation in causal pathways. International Journal of Epidemiology, 2015, 44, 484-495.	0.9	263
136	Leucocyte Telomere Length and Risk of Type 2 Diabetes Mellitus: New Prospective Cohort Study and Literature-Based Meta-Analysis. PLoS ONE, 2014, 9, e112483.	1.1	174
137	Leucocyte telomere length and risk of cardiovascular disease: systematic review and meta-analysis. BMJ, The, 2014, 349, g4227-g4227.	3.0	693
138	Assessing Risk Prediction Models Using Individual Participant Data From Multiple Studies. American Journal of Epidemiology, 2014, 179, 621-632.	1.6	47
139	Glycated Hemoglobin Measurement and Prediction of Cardiovascular Disease. JAMA - Journal of the American Medical Association, 2014, 311, 1225.	3.8	179
140	Association of Dietary, Circulating, and Supplement Fatty Acids With Coronary Risk. Annals of Internal Medicine, 2014, 160, 398.	2.0	997
141	Inflammatory cytokines and risk of coronary heart disease: new prospective study and updated meta-analysis. European Heart Journal, 2014, 35, 578-589.	1.0	483
142	Mendelian Randomization Analysis With Multiple Genetic Variants Using Summarized Data. Genetic Epidemiology, 2013, 37, 658-665.	0.6	2,705
143	Functional IL6R 358Ala Allele Impairs Classical IL-6 Receptor Signaling and Influences Risk of Diverse Inflammatory Diseases. PLoS Genetics, 2013, 9, e1003444.	1.5	234
144	GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm. PLoS Genetics, 2013, 9, e1003657.	1.5	58

#	Article	IF	Citations
145	Lipid-Related Markers and Cardiovascular Disease Prediction. JAMA - Journal of the American Medical Association, 2012, 307, 2499-506.	3.8	352
146	Clinical Utility of Genetic Variants for Cardiovascular Risk Prediction. Circulation: Cardiovascular Genetics, 2012, 5, 387-390.	5.1	16
147	C-Reactive Protein, Fibrinogen, and Cardiovascular Disease Prediction. New England Journal of Medicine, 2012, 367, 1310-1320.	13.9	909
148	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, 1419-1433.	0.9	230
149	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	6.3	668
150	Use of Mendelian randomisation to assess potential benefit of clinical intervention. BMJ, The, 2012, 345, e7325-e7325.	3.0	212
151	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	1.5	203
152	Association of the 9p21.3 Locus With Risk of First-Ever Myocardial Infarction in Pakistanis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 1467-1473.	1.1	48
153	Genetic Determinants of Major Blood Lipids in Pakistanis Compared With Europeans. Circulation: Cardiovascular Genetics, 2010, 3, 348-357.	5.1	25
154	Triglyceride-mediated pathways and coronary disease: collaborative analysis of 101 studies. Lancet, The, 2010, 375, 1634-1639.	6.3	606
155	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, 139-146.	1.1	186
156	Genome-wide association studies, field synopses, and the development of the knowledge base on genetic variation and human diseases. , 2009, , 227-246.		0
157	Seven Lipoprotein Lipase Gene Polymorphisms, Lipid Fractions, and Coronary Disease: A HuGE Association Review and Meta-Analysis. American Journal of Epidemiology, 2008, 168, 1233-1246.	1.6	117
158	Turning the Pump Handle: Evolving Methods for Integrating the Evidence on Gene-Disease Association. American Journal of Epidemiology, 2007, 166, 863-866.	1.6	25
159	Relative and absolute risk of colorectal cancer for individuals with a family history: A meta-analysis. European Journal of Cancer, 2006, 42, 216-227.	1.3	377