Abbas Dehghan

List of Publications by Year
in descending order

301 papers	54,737 citations	2963 93 h-index	1489 219 g-index
327 all docs	327 docs citations	327 times ranked	66876 citing authors

#	Article	IF	Citations
1	Worldwide trends in body-mass index, underweight, overweight, and obesity from 1975 to 2016: a pooled analysis of 2416 population-based measurement studies in 128Â·9 million children, adolescents, and adults. Lancet, The, 2017, 390, 2627-2642.	6.3	5,010
2	Trends in adult body-mass index in 200 countries from 1975 to 2014: a pooled analysis of 1698 population-based measurement studies with 19Â·2 million participants. Lancet, The, 2016, 387, 1377-1396.	6.3	3,941
3	Worldwide trends in diabetes since 1980: a pooled analysis of 751 population-based studies with 4Â·4 million participants. Lancet, The, 2016, 387, 1513-1530.	6.3	2,842
4	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
5	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
6	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
7	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
8	Worldwide trends in blood pressure from 1975 to 2015: a pooled analysis of 1479 population-based measurement studies with 19Â·1 million participants. Lancet, The, 2017, 389, 37-55.	6.3	1,667
9	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
10	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
11	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	9.4	1,224
12	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
13	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
14	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
15	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
16	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
17	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet, The, 2008, 372, 1953-1961.	6.3	610
18	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	9.4	553

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19	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
20	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
21	High Serum Uric Acid as a Novel Risk Factor for Type 2 Diabetes. Diabetes Care, 2008, 31, 361-362.	4.3	484
22	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
23	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
24	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
25	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
26	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
27	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	9.4	363
28	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
29	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
30	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
31	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
32	High Bone Mineral Density and Fracture Risk in Type 2 Diabetes as Skeletal Complications of Inadequate Glucose Control. Diabetes Care, 2013, 36, 1619-1628.	4.3	309
33	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
34	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
35	Predictive Accuracy of a Polygenic Risk Scoreâ€“Enhanced Prediction Model vs a Clinical Risk Score for Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2020, 323, 636.	3.8	290
36	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	2.6	287

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37	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 523-530.	5.1	285
38	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
39	Predicting Type 2 Diabetes Based on Polymorphisms From Genome-Wide Association Studies. Diabetes, 2008, 57, 3122-3128.	0.3	265
40	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
41	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
42	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
43	Large-scale genomic studies reveal central role of ABO in sP-selectin and sICAM-1 levels. Human Molecular Genetics, 2010, 19, 1863-1872.	1.4	233
44	Maternal plasma folate impacts differential DNA methylation in an epigenome-wide meta-analysis of newborns. Nature Communications, 2016, 7, 10577.	5.8	219
45	Genome-wide association meta-analysis for total serum bilirubin levels. Human Molecular Genetics, 2009, 18, 2700-2710.	1.4	214
46	Genetic Variation, C-Reactive Protein Levels, and Incidence of Diabetes. Diabetes, 2007, 56, 872-878.	0.3	207
47	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	1.5	203
48	Genetic Variants Associated With Cardiac Structure and Function. JAMA - Journal of the American Medical Association, 2009, 302, 168.	3.8	202
49	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
50	Lifetime risk of developing impaired glucose metabolism and eventual progression from prediabetes to type 2 diabetes: a prospective cohort study. Lancet Diabetes and Endocrinology,the, 2016, 4, 44-51.	5.5	192
51	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	9.4	191
52	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. PLoS Genetics, 2010, 6, e1001045.	1.5	185
53	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
54	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176

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55	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. JAMA Psychiatry, 2017, 74, 1214.	6.0	174
56	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
57	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. PLoS Genetics, 2011, 7, e1002292.	1.5	172
58	Understanding the consequences of education inequality on cardiovascular disease: mendelian randomisation study. BMJ: British Medical Journal, 2019, 365, l1855.	2.4	172
59	Genetic Predisposition to High Blood Pressure and Lifestyle Factors. Circulation, 2018, 137, 653-661.	1.6	169
60	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
61	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
62	Subclinical Hypothyroidism and the Risk of Stroke Events and Fatal Stroke: An Individual Participant Data Analysis. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 2181-2191.	1.8	164
63	Common genetic loci influencing plasma homocysteine concentrations and their effect on risk of coronary artery disease. American Journal of Clinical Nutrition, 2013, 98, 668-676.	2.2	161
64	Genetic correlations among psychiatric and immuneâ€related phenotypes based on genomeâ€wide association data. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 641-657.	1.1	158
65	Polygenic dissection of major depression clinical heterogeneity. Molecular Psychiatry, 2016, 21, 516-522.	4.1	154
66	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
67	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
68	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	3.9	150
69	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
70	Uromodulin Levels Associate with a Common UMOD Variant and Risk for Incident CKD. Journal of the American Society of Nephrology: JASN, 2010, 21, 337-344.	3.0	146
71	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
72	The role of epigenetic modifications in cardiovascular disease: A systematic review. International Journal of Cardiology, 2016, 212, 174-183.	0.8	143

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73	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	1.5	142
74	Effects of diabetes definition on global surveillance of diabetes prevalence and diagnosis: a pooled analysis of 96 population-based studies with 331â€ˆ288 participants. Lancet Diabetes and Endocrinology,the, 2015, 3, 624-637.	5.5	139
75	Thyroid Function and the Risk of Nonalcoholic Fatty Liver Disease: The Rotterdam Study. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 3204-3211.	1.8	138
76	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
77	Common Genetic Variants Associate with Serum Phosphorus Concentration. Journal of the American Society of Nephrology: JASN, 2010, 21, 1223-1232.	3.0	123
78	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
79	Thyroid function and risk of type 2 diabetes: a population-based prospective cohort study. BMC Medicine, 2016, 14, 150.	2.3	123
80	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
81	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. PLoS Genetics, 2011, 7, e1002158.	1.5	117
82	Arterial Stiffness and Decline in Kidney Function. Clinical Journal of the American Society of Nephrology: CJASN, 2015, 10, 2190-2197.	2.2	117
83	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
84	Duffy antigen receptor for chemokines (Darc) polymorphism regulates circulating concentrations of monocyte chemoattractant protein-1 and other inflammatory mediators. Blood, 2010, 115, 5289-5299.	0.6	113
85	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	2.6	113
86	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	2.6	109
87	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
88	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	0.5	107
89	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	1.5	107
90	Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. European Heart Journal, 2019, 40, 2883-2896.	1.0	107

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91	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
92	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
93	Epigenome-wide association study (EWAS) on lipids: the Rotterdam Study. Clinical Epigenetics, 2017, 9, 15.	1.8	104
94	Associations of Steroid Sex Hormones and Sex Hormoneâ€“Binding Globulin With the Risk of Type 2 Diabetes in Women: A Population-Based Cohort Study and Meta-analysis. Diabetes, 2017, 66, 577-586.	0.3	103
95	What is new in the exposome?. Environment International, 2020, 143, 105887.	4.8	103
96	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
97	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. Journal of Clinical Investigation, 2013, 123, 4208-4218.	3.9	101
98	Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279.	1.6	99
99	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
100	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
101	A population-based phenome-wide association study of cardiac and aortic structure and function. Nature Medicine, 2020, 26, 1654-1662.	15.2	98
102	Genetic variation associated with plasma von Willebrand factor levels and the risk of incident venous thrombosis. Blood, 2011, 117, 6007-6011.	0.6	97
103	Variance heterogeneity analysis for detection of potentially interacting genetic loci: method and its limitations. BMC Genetics, 2010, 11, 92.	2.7	96
104	Thyroid Function and Cancer Risk: The Rotterdam Study. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 5030-5036.	1.8	96
105	Common Genetic Variation in the 3â€²- BCL11B Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
106	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	0.6	90
107	The Role of DNA Methylation and Histone Modifications in Neurodegenerative Diseases: A Systematic Review. PLoS ONE, 2016, 11, e0167201.	1.1	90
108	Eight genetic loci associated with variation in lipoprotein-associated phospholipase A2 mass and activity and coronary heart disease: meta-analysis of genome-wide association studies from five community-based studies. European Heart Journal, 2012, 33, 238-251.	1.0	89

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109	Thyroid Function and Sudden Cardiac Death. Circulation, 2016, 134, 713-722.	1.6	89
110	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
111	Common variants in the calcium-sensing receptor gene are associated with total serum calcium levels. Human Molecular Genetics, 2010, 19, 4296-4303.	1.4	86
112	Thyroid function and the risk of dementia. Neurology, 2016, 87, 1688-1695.	1.5	86
113	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	1.5	84
114	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
115	Circulating Levels of Interleukin 1-Receptor Antagonist and Risk of Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1222-1227.	1.1	81
116	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. American Journal of Epidemiology, 2019, 188, 991-1012.	1.6	81
117	Genomic Variation Associated With Mortality Among Adults of European and African Ancestry With Heart Failure. Circulation: Cardiovascular Genetics, 2010, 3, 248-255.	5.1	80
118	Normal Thyroid Function and the Risk of Atrial Fibrillation: the Rotterdam Study. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3718-3724.	1.8	80
119	Age at natural menopause and risk of type 2 diabetes: a prospective cohort study. Diabetologia, 2017, 60, 1951-1960.	2.9	80
120	Thyroid Function Characteristics and Determinants: The Rotterdam Study. Thyroid, 2016, 26, 1195-1204.	2.4	78
121	Association of Variation at the ABO Locus With Circulating Levels of Soluble Intercellular Adhesion Molecule-1, Soluble P-selectin, and Soluble E-selectin. Circulation: Cardiovascular Genetics, 2011, 4, 681-686.	5.1	77
122	Genome-Wide Association Analysis of Soluble ICAM-1 Concentration Reveals Novel Associations at the NFKBIK, PNPLA3, RELA, and SH2B3 Loci. PLoS Genetics, 2011, 7, e1001374.	1.5	76
123	Urate, Blood Pressure, and Cardiovascular Disease. Hypertension, 2021, 77, 383-392.	1.3	75
124	Iron Status and Risk of Stroke. Stroke, 2018, 49, 2815-2821.	1.0	74
125	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
126	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73

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127	Plasma lipids and risk of aortic valve stenosis: a Mendelian randomization study. European Heart Journal, 2020, 41, 3913-3920.	1.0	70
128	A genetic risk score based on direct associations with coronary heart disease improves coronary heart disease risk prediction in the Atherosclerosis Risk in Communities (ARIC), but not in the Rotterdam and Framingham Offspring, Studies. Atherosclerosis, 2012, 223, 421-426.	0.4	69
129	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
130	Resting Heart Rate and the Risk of Heart Failure in Healthy Adults. Circulation: Heart Failure, 2013, 6, 403-410.	1.6	69
131	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	1.1	69
132	Serum magnesium and the risk of prediabetes: a population-based cohort study. Diabetologia, 2017, 60, 843-853.	2.9	68
133	Bivariate genome-wide association study identifies novel pleiotropic loci for lipids and inflammation. BMC Genomics, 2016, 17, 443.	1.2	67
134	Thyroid Function Within the Reference Range and the Risk of Stroke: An Individual Participant Data Analysis. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4270-4282.	1.8	67
135	The association between serum uric acid and the incidence of prediabetes and type 2 diabetes mellitus: The Rotterdam Study. PLoS ONE, 2017, 12, e0179482.	1.1	67
136	An RBP4 promoter polymorphism increases risk of type 2 diabetes. Diabetologia, 2008, 51, 1423-1428.	2.9	66
137	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
138	Contributions of mean and shape of blood pressure distribution to worldwide trends and variations in raised blood pressure: a pooled analysis of 1018 population-based measurement studies with 88.6 million participants. International Journal of Epidemiology, 2018, 47, 872-883i.	0.9	65
139	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
140	The Relation of Uric Acid to Brain Atrophy and Cognition: The Rotterdam Scan Study. Neuroepidemiology, 2013, 41, 29-34.	1.1	64
141	Genome-Wide Association Studies. Methods in Molecular Biology, 2018, 1793, 37-49.	0.4	64
142	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
143	Blood pressure lowering and risk of new-onset type 2 diabetes: an individual participant data meta-analysis. Lancet, The, 2021, 398, 1803-1810.	6.3	64
144	Risk of Type 2 Diabetes Attributable to C-Reactive Protein and Other Risk Factors. Diabetes Care, 2007, 30, 2695-2699.	4.3	63

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145	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
146	Predicting Stroke Through Genetic Risk Functions. Stroke, 2014, 45, 403-412.	1.0	62
147	Metabolic syndrome is related to polyneuropathy and impaired peripheral nerve function: a prospective population-based cohort study. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, 1336-1342.	0.9	62
148	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	5.8	62
149	Vitamin D and C-Reactive Protein: A Mendelian Randomization Study. PLoS ONE, 2015, 10, e0131740.	1.1	61
150	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
151	EN-RAGE. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2695-2699.	1.1	60
152	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
153	Education protects against coronary heart disease and stroke independently of cognitive function: evidence from Mendelian randomization. International Journal of Epidemiology, 2019, 48, 1468-1477.	0.9	60
154	Genetically determined blood pressure, antihypertensive drug classes, and risk of stroke subtypes. Neurology, 2020, 95, e353-e361.	1.5	60
155	An Epigenome-Wide Association Study of Obesity-Related Traits. American Journal of Epidemiology, 2018, 187, 1662-1669.	1.6	59
156	Tobacco smoking is associated with methylation of genes related to coronary artery disease. Clinical Epigenetics, 2015, 7, 54.	1.8	58
157	The Association between Metabolic Syndrome, Bone Mineral Density, Hip Bone Geometry and Fracture Risk: The Rotterdam Study. PLoS ONE, 2015, 10, e0129116.	1.1	58
158	Genetic Variations in MicroRNA-Binding Sites Affect MicroRNA-Mediated Regulation of Several Genes Associated With Cardio-metabolic Phenotypes. Circulation: Cardiovascular Genetics, 2015, 8, 473-486.	5.1	57
159	Genetic variation associated with circulating monocyte count in the eMERGE Network. Human Molecular Genetics, 2013, 22, 2119-2127.	1.4	56
160	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
161	Subclinical thyroid dysfunction and the risk of stroke: a systematic review and meta-analysis. European Journal of Epidemiology, 2014, 29, 791-800.	2.5	54
162	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54

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163	Phosphodiesterase 1 regulation is a key mechanism in vascular aging. Clinical Science, 2015, 129, 1061-1075.	1.8	53
164	Thyroid function and age-related macular degeneration: a prospective population-based cohort study - the Rotterdam Study. BMC Medicine, 2015, 13, 94.	2.3	53
165	Genetic Variants in MicroRNAs and Their Binding Sites Are Associated with the Risk of Parkinson Disease. Human Mutation, 2016, 37, 292-300.	1.1	52
166	Identifying Novel Gene Variants in Coronary Artery Disease and Shared Genes With Several Cardiovascular Risk Factors. Circulation Research, 2016, 118, 83-94.	2.0	52
167	Epigenome-Wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. Gastroenterology, 2017, 153, 1096-1106.e2.	0.6	52
168	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
169	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	5.8	51
170	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	2.6	50
171	Kidney Function and Cerebral Blood Flow: The Rotterdam Study. Journal of the American Society of Nephrology: JASN, 2016, 27, 715-721.	3.0	50
172	Novel inflammatory markers for incident pre-diabetes and type 2 diabetes: the Rotterdam Study. European Journal of Epidemiology, 2017, 32, 217-226.	2.5	48
173	Associations of genetically determined iron status across the phenome: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002833.	3.9	48
174	Genetic analysis of over half a million people characterises C-reactive protein loci. Nature Communications, 2022, 13, 2198.	5.8	48
175	Novel metabolic indices and incident type 2 diabetes among women and men: the Rotterdam Study. Diabetologia, 2019, 62, 1581-1590.	2.9	46
176	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. Human Mutation, 2014, 35, 1524-1531.	1.1	45
177	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	2.6	45
178	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	1.4	45
179	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	2.6	45
180	Genetically Determined FXI (Factor XI) Levels and Risk of Stroke. Stroke, 2018, 49, 2761-2763.	1.0	45

#	Article	IF	Citations
181	Sleep, major depressive disorder, and Alzheimer disease. Neurology, 2020, 95, e1963-e1970.	1.5	45
182	SIRT1 genetic variation and mortality in type 2 diabetes: interaction with smoking and dietary niacin. Free Radical Biology and Medicine, 2009, 46, 836-841.	1.3	44
183	Risk Scores of Common Genetic Variants for Lipid Levels Influence Atherosclerosis and Incident Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2233-2239.	1.1	44
184	Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. International Journal of Epidemiology, 2015, 44, 682-688.	0.9	44
185	Serum Uric Acid and Chronic Kidney Disease: The Role of Hypertension. PLoS ONE, 2013, 8, e76827.	1.1	43
186	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	1.1	43
187	Pleiotropy among Common Genetic Loci Identified for Cardiometabolic Disorders and C-Reactive Protein. PLoS ONE, 2015, 10, e0118859.	1.1	43
188	Genome-wide identification of microRNA-related variants associated with risk of Alzheimerâ€™s disease. Scientific Reports, 2016, 6, 28387.	1.6	43
189	Tobacco smoking is associated with DNA methylation of diabetes susceptibility genes. Diabetologia, 2016, 59, 998-1006.	2.9	43
190	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	5.8	43
191	LDL cholesterol still a problem in old age? A Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 604-612.	0.9	42
192	Associations of Regional Brain Structural Differences With Aging, Modifiable Risk Factors for Dementia, and Cognitive Performance. JAMA Network Open, 2019, 2, e1917257.	2.8	42
193	Association of Rare Loss-Of-Function Alleles in HAL , Serum Histidine. Circulation: Cardiovascular Genetics, 2015, 8, 351-355.	5.1	41
194	The Influence of Serum Uric Acid on Bone Mineral Density, Hip Geometry, and Fracture Risk: The Rotterdam Study. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1113-1122.	1.8	41
195	Serum dehydroepiandrosterone levels are associated with lower risk of type 2 diabetes: the Rotterdam Study. Diabetologia, 2017, 60, 98-106.	2.9	41
196	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.3	41
197	Circulating inflammatory cytokines and risk of five cancers: a Mendelian randomization analysis. BMC Medicine, 2022, 20, 3.	2.3	41
198	Serum Levels of Apolipoproteins and Incident Type 2 Diabetes: A Prospective Cohort Study. Diabetes Care, 2017, 40, 346-351.	4.3	40

#	Article	IF	Citations
199	Polyunsaturated Fatty Acids and Serum C-Reactive Protein: The Rotterdam Study. American Journal of Epidemiology, 2015, 181, 846-856.	1.6	39
200	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.	3.0	39
201	Association of Uric Acid Genetic Risk Score With Blood Pressure. Hypertension, 2014, 64, 1061-1066.	1.3	38
202	Workflow for Integrated Processing of Multicohort Untargeted ¹H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. Journal of Proteome Research, 2016, 15, 4188-4194.	1.8	37
203	The clinical value of metabolic syndrome and risks of cardiometabolic events and mortality in the elderly: the Rotterdam study. Cardiovascular Diabetology, 2016, 15, 69.	2.7	37
204	Blood Pressure Parameters and Carotid Intraplaque Hemorrhage as Measured by Magnetic Resonance Imaging. Hypertension, 2013, 61, 76-81.	1.3	35
205	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	5.8	35
206	Kidney function and microstructural integrity of brain white matter. Neurology, 2015, 85, 154-161.	1.5	34
207	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.	1.5	34
208	The role of DNA methylation in dyslipidaemia: A systematic review. Progress in Lipid Research, 2016, 64, 178-191.	5.3	34
209	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
210	Intermittent fasting for the prevention of cardiovascular disease. The Cochrane Library, 2021, 2021, CD013496.	1.5	34
211	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. PLoS Genetics, 2016, 12, e1006034.	1.5	34
212	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	3.0	33
213	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. JAMA Cardiology, 2018, 3, 463.	3.0	33
214	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	1.4	32
215	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	2.1	31
216	Accelerated MRI-predicted brain ageing and its associations with cardiometabolic and brain disorders. Scientific Reports, 2020, 10, 19940.	1.6	31

#	Article	IF	Citations
217	The association of common polymorphisms in miR-196a2 with waist to hip ratio and miR-1908 with serum lipid and glucose. Obesity, 2015, 23, 495-503.	1.5	30
218	Genetic variants in microRNAs and their binding sites within gene 3â€²UTRs associate with susceptibility to age-related macular degeneration. Human Mutation, 2017, 38, 827-838.	1.1	30
219	Epigenetics and Inflammatory Markers: A Systematic Review of the Current Evidence. International Journal of Inflammation, 2019, 2019, 1-14.	0.9	30
220	Obesity and Life Expectancy with and without Diabetes in Adults Aged 55 Years and Older in the Netherlands: A Prospective Cohort Study. PLoS Medicine, 2016, 13, e1002086.	3.9	30
221	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	1.1	29
222	The association of thyroid function and the risk of kidney function decline: a population-based cohort study. European Journal of Endocrinology, 2016, 175, 653-660.	1.9	28
223	Could vitamin D reduce obesity-associated inflammation? Observational and Mendelian randomization study. American Journal of Clinical Nutrition, 2020, 111, 1036-1047.	2.2	28
224	Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203.	1.1	27
225	Lack of association of two common polymorphisms on 9p21 with risk of coronary heart disease and myocardial infarction; results from a prospective cohort study. BMC Medicine, 2008, 6, 30.	2.3	26
226	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
227	Low-risk susceptibility alleles in 40 human breast cancer cell lines. BMC Cancer, 2009, 9, 236.	1.1	25
228	A Genome-Wide Scan for MicroRNA-Related Genetic Variants Associated With Primary Open-Angle Glaucoma. , 2017, 58, 5368.		25
229	Blood Metabolomic Measures Associate With Present and Future Glycemic Control in Type 2 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4569-4579.	1.8	25
230	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	0.6	25
231	A serum 25-hydroxyvitamin D concentration-associated genetic variant in DHCR7 interacts with type 2 diabetes status to influence subclinical atherosclerosis (measured by carotid intimaâ€“media) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	24
232	Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. Blood, 2015, 125, 3949-3955.	0.6	24
233	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	3.0	24
234	GWAS for urinary sodium and potassium excretion highlights pathways shared with cardiovascular traits. Nature Communications, 2019, 10, 3653.	5.8	24

#	Article	IF	Citations
235	Comparison of Prognosis in Unrecognized Versus Recognized Myocardial Infarction in Men Versus Women >55 Years of Age (from the Rotterdam Study). American Journal of Cardiology, 2014, 113, 1-6.	0.7	23
236	ADAMTS13 activity as a novel risk factor for incident type 2 diabetes mellitus: a population-based cohort study. Diabetologia, 2017, 60, 280-286.	2.9	23
237	Effect of Religious Fasting in Ramadan on Blood Pressure: Results From LORANS (London Ramadan) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	23
238	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. Diabetes, 2016, 65, 3794-3804.	0.3	22
239	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
240	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	0.7	22
241	Fetuin-A and risk of coronary heart disease: A Mendelian randomization analysis and a pooled analysis of AHSG genetic variants in 7 prospective studies. Atherosclerosis, 2015, 243, 44-52.	0.4	21
242	Gamma-glutamyltransferase levels, prediabetes and type 2 diabetes: a Mendelian randomization study. International Journal of Epidemiology, 2017, 46, 1400-1409.	0.9	21
243	Estimated 24-Hour Urinary Sodium Excretion and Incident Cardiovascular Disease and Mortality Among 398 628 Individuals in UK Biobank. Hypertension, 2020, 76, 683-691.	1.3	21
244	Heritabilities, proportions of heritabilities explained by GWAS findings, and implications of cross-phenotype effects on PR interval. Human Genetics, 2015, 134, 1211-1219.	1.8	20
245	Gait patterns associated with thyroid function: The Rotterdam Study. Scientific Reports, 2016, 6, 38912.	1.6	19
246	Lifetime risk to progress from pre-diabetes to type 2 diabetes among women and men: comparison between American Diabetes Association and World Health Organization diagnostic criteria. BMJ Open Diabetes Research and Care, 2020, 8, e001529.	1.2	19
247	Lower microstructural integrity of brain white matter is related to higher mortality. Neurology, 2016, 87, 927-934.	1.5	18
248	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
249	Renal Function Is Related to Severity of Coronary Artery Calcification in Elderly Persons: The Rotterdam Study. PLoS ONE, 2011, 6, e16738.	1.1	17
250	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. Journal of Human Genetics, 2018, 63, 431-446.	1.1	17
251	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	1.6	17
252	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	1.1	17

#	Article	IF	Citations
253	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
254	Relation of antioxidant capacity of diet and markers of oxidative status with C-reactive protein and adipocytokines: a prospective study. Metabolism: Clinical and Experimental, 2017, 71, 171-181.	1.5	16
255	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
256	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	0.6	16
257	Identifying genetic risk variants for coronary heart disease in familial hypercholesterolemia: an extreme genetics approach. European Journal of Human Genetics, 2015, 23, 381-387.	1.4	15
258	Age-dependent association of thyroid function with brain morphology and microstructural organization: evidence from brain imaging. Neurobiology of Aging, 2018, 61, 44-51.	1.5	15
259	Trajectories of BMI Before Diagnosis of Type 2 Diabetes: The Rotterdam Study. Obesity, 2020, 28, 1149-1156.	1.5	15
260	Long-term prognosis after kidney donation: a propensity score matched comparison of living donors and non-donors from two population cohorts. European Journal of Epidemiology, 2020, 35, 699-707.	2.5	15
261	Gait characteristics in older adults with diabetes and impaired fasting glucose: The Rotterdam Study. Journal of Diabetes and Its Complications, 2016, 30, 61-66.	1.2	14
262	Intermittent fasting for the prevention of cardiovascular disease. The Cochrane Library, 0, , .	1.5	14
263	Genetic susceptibility, elevated blood pressure, and risk of atrial fibrillation: a Mendelian randomization study. Genome Medicine, 2021, 13, 38.	3.6	14
264	Investigating the relationships between unfavourable habitual sleep and metabolomic traits: evidence from multi-cohort multivariable regression and Mendelian randomization analyses. BMC Medicine, 2021, 19, 69.	2.3	14
265	Exploring the causal effect of maternal pregnancy adiposity on offspring adiposity: Mendelian randomisation using polygenic risk scores. BMC Medicine, 2022, 20, 34.	2.3	14
266	A frequent variant in the ABCA1 gene is associated with increased coronary heart disease risk and a better response to statin treatment in familial hypercholesterolemia patients. European Heart Journal, 2011, 32, 469-475.	1.0	12
267	Association of renal function with vascular stiffness in older adults: the Rotterdam study. Age and Ageing, 2014, 43, 827-833.	0.7	12
268	von Willebrand Factor, ADAMTS13 Activity, and Decline in Kidney Function: A Population-Based Cohort Study. American Journal of Kidney Diseases, 2016, 68, 726-732.	2.1	12
269	Kidney function, gait pattern and fall in the general population: a cohort study. Nephrology Dialysis Transplantation, 2018, 33, 2165-2172.	0.4	12
270	Dissecting the association of autophagy-related genes with cardiovascular diseases and intermediate vascular traits: A population-based approach. PLoS ONE, 2019, 14, e0214137.	1.1	12

#	Article	IF	Citations
271	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	1.9	12
272	Genetic correlation and causal relationships between cardio-metabolic traits and lung function impairment. Genome Medicine, 2021, 13, 104.	3.6	11
273	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
274	Higher thyrotropin leads to unfavorable lipid profile and somewhat higher cardiovascular disease risk: evidence from multi-cohort Mendelian randomization and metabolomic profiling. BMC Medicine, 2021, 19, 266.	2.3	11
275	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. European Journal of Epidemiology, 2021, 36, 1143-1155.	2.5	10
276	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
277	Impact of serum 25-hydroxyvitamin D 25(OH) on telomere attrition: A Mendelian Randomization study. Clinical Nutrition, 2020, 39, 2730-2733.	2.3	9
278	Early exposure to social disadvantages and later lifeÂbody mass index beyond genetic predisposition in three generations of Finnish birth cohorts. BMC Public Health, 2020, 20, 708.	1.2	9
279	Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. Diabetic Medicine, 2021, 38, e14639.	1.2	9
280	Finding Correspondence between Metabolomic Features in Untargeted Liquid Chromatographyâ€“Mass Spectrometry Metabolomics Datasets. Analytical Chemistry, 2022, 94, 5493-5503.	3.2	9
281	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	1.1	8
282	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
283	LOng-term follow-up after liVE kidney donation (LOVE) study: a longitudinal comparison study protocol. BMC Nephrology, 2016, 17, 14.	0.8	8
284	Prospective study of insulin-like growth factor-I, insulin-like growth factor-binding protein 3, genetic variants in the IGF1 and IGFBP3 genes and risk of coronary artery disease. International Journal of Molecular Epidemiology and Genetics, 2011, 2, 261-85.	0.4	8
285	Partnerâ€™s Smoking Status and Acute Coronary Syndrome: Population-based Case-control Study in Tirana, Albania. Croatian Medical Journal, 2008, 49, 751-756.	0.2	5
286	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
287	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	1.1	5
288	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5

#	Article	IF	Citations
289	Genetic and clinical determinants of abdominal aortic diameter: genome-wide association studies, exome array data and Mendelian randomization study. Human Molecular Genetics, 2022, 31, 3566-3579.	1.4	5
290	An Enrichment Analysis for Cardiometabolic Traits Suggests Non-Random Assignment of Genes to microRNAs. International Journal of Molecular Sciences, 2018, 19, 3666.	1.8	4
291	Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. Human Molecular Genetics, 2022, 31, 1171-1182.	1.4	4
292	Mass spectrometry in epidemiological studies: What are the key considerations?. European Journal of Epidemiology, 2016, 31, 715-716.	2.5	3
293	Epicardial fat volume and the risk of cardiometabolic diseases among women and men from the general population. European Journal of Preventive Cardiology, 2022, 28, e14-e16.	0.8	3
294	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. Atherosclerosis, 2017, 266, 196-204.	0.4	3
295	Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. Human Molecular Genetics, 2022, , .	1.4	3
296	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	1.4	3
297	Linking Metabolic Phenotyping and Genomic Information. , 2019, , 561-569.		2
298	Genetically Higher Level of Mannose Has No Impact on Cardiometabolic Risk Factors: Insight from Mendelian Randomization. Nutrients, 2021, 13, 2563.	1.7	1
299	The Association between Coffee and Caffeine Consumption and Renal Function: Insight from Individual-Level Data, Mendelian Randomization, and Meta-Analysis. Archives of Medical Science, 2021, , .	0.4	1
300	Sex-specific differences in the effects of local androgen metabolism in the heart as an indicator for the risk of myocardial infarction. Cardiovascular Endocrinology, 2014, 3, 134-141.	0.8	0
301	Effect of metabolic genetic variants on long-term disease comorbidity in patients with type 2 diabetes. Scientific Reports, 2021, 11, 2794.	1.6	0