Veikko Salomaa

List of Publications by Year
in descending order

383 papers	104,231 citations	298 139 h-index	265 298 g-index
428 all docs	428 docs citations	428 times ranked	81928 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
6	A comprehensive 1000 Genomesâ€"based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
7	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
8	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
9	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
10	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
11	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
12	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
13	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
14	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
15	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
16	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
17	Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. Nature Genetics, 2008, 40, 189-197.	9.4	1,286
18	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234

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19	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
20	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
21	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
22	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
23	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
24	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	9.4	990
25	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
26	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
27	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
28	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
29	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
30	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
31	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
32	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
33	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
34	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	1.5	796
35	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
36	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754

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37	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	3.9	753
38	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
39	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
40	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
41	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	6.3	668
42	Sequence variants at CHRNB3â€"CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
43	Association of Cardiometabolic Multimorbidity With Mortality. JAMA - Journal of the American Medical Association, 2015, 314, 52.	3.8	624
44	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
45	FINEMAP: efficient variable selection using summary data from genome-wide association studies. Bioinformatics, 2016, 32, 1493-1501.	1.8	584
46	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
47	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576
48	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	1.5	572
49	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
50	World Health Organization cardiovascular disease risk charts: revised models to estimate risk in 21 global regions. The Lancet Global Health, 2019, 7, e1332-e1345.	2.9	554
51	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
52	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
53	Metabolite Profiling and Cardiovascular Event Risk. Circulation, 2015, 131, 774-785.	1.6	547
54	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544

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55	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	9.4	537
56	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
57	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	9.4	516
58	A multilocus genetic risk score for coronary heart disease: case-control and prospective cohort analyses. Lancet, The, 2010, 376, 1393-1400.	6.3	503
59	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
60	DNA sequence diversity in a 9.7-kb region of the human lipoprotein lipase gene. Nature Genetics, 1998, 19, 233-240.	9.4	483
61	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nature Genetics, 2009, 41, 1182-1190.	9.4	481
62	Long term exposure to ambient air pollution and incidence of acute coronary events: prospective cohort study and meta-analysis in 11 European cohorts from the ESCAPE Project. BMJ, The, 2014, 348, f7412-f7412.	3.0	481
63	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
64	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
65	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
66	Non–Insulin-Dependent Diabetes Mellitus and Fasting Glucose and Insulin Concentrations Are Associated With Arterial Stiffness Indexes. Circulation, 1995, 91, 1432-1443.	1.6	458
67	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
68	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
69	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
70	Haplotype Structure and Population Genetic Inferences from Nucleotide-Sequence Variation in Human Lipoprotein Lipase. American Journal of Human Genetics, 1998, 63, 595-612.	2.6	439
71	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
72	Thirty-five-year trends in cardiovascular risk factors in Finland. International Journal of Epidemiology, 2010, 39, 504-518.	0.9	429

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73	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
74	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
75	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
76	Excess of rare variants in genes identified by genome-wide association study of hypertriglyceridemia. Nature Genetics, 2010, 42, 684-687.	9.4	414
77	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
78	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
79	Apolipoprotein E Variation at the Sequence Haplotype Level: Implications for the Origin and Maintenance of a Major Human Polymorphism. American Journal of Human Genetics, 2000, 67, 881-900.	2.6	377
80	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
81	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
82	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	1.1	369
83	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
84	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
85	Association of common variants in NPPA and NPPB with circulating natriuretic peptides and blood pressure. Nature Genetics, 2009, 41, 348-353.	9.4	361
86	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
87	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
88	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
89	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	6.3	345
90	Endotoxemia Is Associated With an Increased Risk of Incident Diabetes. Diabetes Care, 2011, 34, 392-397.	4.3	343

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91	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
92	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
93	Contribution of 30 Biomarkers to 10-Year Cardiovascular Risk Estimation in 2 Population Cohorts. Circulation, 2010, 121, 2388-2397.	1.6	320
94	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	5.5	319
95	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
96	Sex Differences and Similarities in Atrial Fibrillation Epidemiology, Risk Factors, and Mortality in Community Cohorts. Circulation, 2017, 136, 1588-1597.	1.6	307
97	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
98	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
99	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
100	Identification of heart rate–associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
101	Biomarker Profiling by Nuclear Magnetic Resonance Spectroscopy for the Prediction of All-Cause Mortality: An Observational Study of 17,345 Persons. PLoS Medicine, 2014, 11, e1001606.	3.9	281
102	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
103	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. Nature Medicine, 2020, 26, 549-557.	15.2	281
104	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	1.0	277
105	Metabolic Signatures of Adiposity in Young Adults: Mendelian Randomization Analysis and Effects of Weight Change. PLoS Medicine, 2014, 11, e1001765.	3.9	271
106	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
107	Common Missense Variant in the Glucokinase Regulatory Protein Gene Is Associated With Increased Plasma Triglyceride and C-Reactive Protein but Lower Fasting Glucose Concentrations. Diabetes, 2008, 57, 3112-3121.	0.3	264
108	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261

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109	Explaining the Decline in Coronary Heart Disease Mortality in Finland between 1982 and 1997. American Journal of Epidemiology, 2005, 162, 764-773.	1.6	257
110	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
111	Metabonomic, transcriptomic, and genomic variation of a population cohort. Molecular Systems Biology, 2010, 6, 441.	3.2	230
112	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
113	Prospective Study of Fibrinolytic Factors and Incident Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2001, 21, 611-617.	1.1	227
114	Soluble thrombomodulin as a predictor of incident coronary heart disease and symptomless carotid artery atherosclerosis in the Atherosclerosis Risk in Communities (ARIC) Study: a case-cohort study. Lancet, The, 1999, 353, 1729-1734.	6.3	220
115	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
116	Endotoxemia, Immune Response to Periodontal Pathogens, and Systemic Inflammation Associate With Incident Cardiovascular Disease Events. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 1433-1439.	1.1	218
117	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
118	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
119	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
120	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
121	Cohort Profile: The National FINRISK Study. International Journal of Epidemiology, 2018, 47, 696-696i.	0.9	214
122	Forty-year trends in cardiovascular risk factors in Finland. European Journal of Public Health, 2015, 25, 539-546.	0.1	208
123	Troponin I and cardiovascular risk prediction in the general population: the BiomarCaRE consortium. European Heart Journal, 2016, 37, 2428-2437.	1.0	200
124	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. American Journal of Human Genetics, 2017, 101, 539-551.	2.6	200
125	A metabolic view on menopause and ageing. Nature Communications, 2014, 5, 4708.	5.8	196
126	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191

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127	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	1.4	188
128	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. Nature Communications, 2019, 10, 3346.	5.8	188
129	Cardiovascular Risk Factors Associated With Venous Thromboembolism. JAMA Cardiology, 2019, 4, 163.	3.0	187
130	Genome-Wide Screen for Metabolic Syndrome Susceptibility Loci Reveals Strong Lipid Gene Contribution But No Evidence for Common Genetic Basis for Clustering of Metabolic Syndrome Traits. Circulation: Cardiovascular Genetics, 2012, 5, 242-249.	5.1	182
131	Association of branchedâ€chain amino acids and other circulating metabolites with risk of incident dementia and Alzheimer's disease: A prospective study in eight cohorts. Alzheimer's and Dementia, 2018, 14, 723-733.	0.4	182
132	The Biomarker GlycA Is Associated with Chronic Inflammation and Predicts Long-Term Risk of Severe Infection. Cell Systems, 2015, 1, 293-301.	2.9	179
133	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
134	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
135	Metabolomic Profiling of Statin Use and Genetic Inhibition of HMG-CoA Reductase. Journal of the American College of Cardiology, 2016, 67, 1200-1210.	1.2	173
136	The validity of the Finnish Hospital Discharge Register and Causes of Death Register data on coronary heart disease. European Journal of Cardiovascular Prevention and Rehabilitation, 2005, 12, 132-137.	3.1	173
137	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	1.5	171
138	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
139	High population prevalence of cardiac troponin I measured by a high-sensitivity assay and cardiovascular risk estimation: the MORGAM Biomarker Project Scottish Cohort. European Heart Journal, 2014, 35, 271-281.	1.0	160
140	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
141	Genome-wide physical activity interactions in adiposity â€ A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
142	Sequence Diversity and Large-Scale Typing of SNPs in the Human Apolipoprotein E Gene. Genome Research, 2000, 10, 1532-1545.	2.4	156
143	The validation of the Finnish Hospital Discharge Register and Causes of Death Register data on stroke diagnoses. European Journal of Cardiovascular Prevention and Rehabilitation, 2007, 14, 380-385.	3.1	152
144	Metabolic profiling of pregnancy: cross-sectional and longitudinal evidence. BMC Medicine, 2016, 14, 205.	2.3	150

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145	Thirty-One Novel Biomarkers as Predictors for Clinically Incident Diabetes. PLoS ONE, 2010, 5, e10100.	1.1	149
146	Genetic Risk Prediction and a 2-Stage Risk Screening Strategy for Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2261-2266.	1.1	147
147	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
148	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
149	Deletion of TOP3Î2, a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	7.1	144
150	Ischemic stroke is associated with the <i>ABO</i> locus: The EuroCLOT study. Annals of Neurology, 2013, 73, 16-31.	2.8	144
151	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.4	143
152	Circulating metabolites and the risk of type 2 diabetes: a prospective study of 11,896 young adults from four Finnish cohorts. Diabetologia, 2019, 62, 2298-2309.	2.9	141
153	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
154	metaCCA: summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis. Bioinformatics, 2016, 32, 1981-1989.	1.8	138
155	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	5.8	134
156	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
157	A Genome-Wide Association Study Identifies <i>LIPA</i> as a Susceptibility Gene for Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2011, 4, 403-412.	5.1	130
158	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	4.9	130
159	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
160	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
161	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
162	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119

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163	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
164	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
165	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	13.7	115
166	An Immune Response Network Associated with Blood Lipid Levels. PLoS Genetics, 2010, 6, e1001113.	1.5	112
167	Genome-Wide Association Studies of Asthma in Population-Based Cohorts Confirm Known and Suggested Loci and Identify an Additional Association near HLA. PLoS ONE, 2012, 7, e44008.	1.1	111
168	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
169	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. PLoS Genetics, 2015, 11, e1005498.	1.5	107
170	MORGAM (an international pooling of cardiovascular cohorts). International Journal of Epidemiology, 2004, 34, 21-27.	0.9	105
171	Endotoxemia, nutrition, and cardiometabolic disorders. Acta Diabetologica, 2015, 52, 395-404.	1.2	103
172	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102
173	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
174	Equalization of four cardiovascular risk algorithms after systematic recalibration: individual-participant meta-analysis of 86 prospective studies. European Heart Journal, 2019, 40, 621-631.	1.0	97
175	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
176	Genetic basis of lacunar stroke: a pooled analysis of individual patient data and genome-wide association studies. Lancet Neurology, The, 2021, 20, 351-361.	4.9	95
177	Primary prevention and risk factor reduction in coronary heart disease mortality among working aged men and women in eastern Finland over 40 years: population based observational study. BMJ, The, 2016, 352, i721.	3.0	93
178	Mendelian Randomization Study of B-Type Natriuretic Peptide and Type 2 Diabetes: Evidence of Causal Association from Population Studies. PLoS Medicine, 2011, 8, e1001112.	3.9	92
179	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
180	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90

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181	Metabolic profiling of alcohol consumption in 9778 young adults. International Journal of Epidemiology, 2016, 45, 1493-1506.	0.9	90
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