Veikko Salomaa

List of Publications by Year
in descending order

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383	104,231	354	309
papers	citations	139 h-index	298 g-index

428	428	428	89235
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Alcohol intake and total mortality in 142â€‰960 individuals from the MORGAM Project: a populationâ€based study. Addiction, 2022, 117, 312-325.	1.7	22
2	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. JAMA Psychiatry, 2022, 79, 260.	6.0	44
3	Gut Microbiome Composition Is Predictive of Incident Type 2 Diabetes in a Population Cohort of 5,572 Finnish Adults. Diabetes Care, 2022, 45, 811-818.	4.3	47
4	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
5	Integration of questionnaire-based risk factors improves polygenic risk scores for human coronary heart disease and type 2 diabetes. Communications Biology, 2022, 5, 158.	2.0	18
6	Development and validation of a model to predict incident chronic liver disease in the general population: The CLivD score. Journal of Hepatology, 2022, 77, 302-311.	1.8	21
7	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
8	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
9	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
10	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. European Journal of Human Genetics, 2021, 29, 615-624.	1.4	17
11	Association of Circulating Metabolites in Plasma or Serum and Risk of Stroke. Neurology, 2021, 96, .	1.5	24
12	Endotoxemia is associated with an adverse metabolic profile. Innate Immunity, 2021, 27, 3-14.	1.1	21
13	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. European Respiratory Journal, 2021, 57, 2003091.	3.1	85
14	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. European Journal of Human Genetics, 2021, 29, 309-324.	1.4	19
15	Joint association between education and polygenic risk score for incident coronary heart disease events: a longitudinal population-based study of 26 203 men and women. Journal of Epidemiology and Community Health, 2021, 75, 651-657.	2.0	6
16	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
17	Alcohol consumption, cardiac biomarkers, and risk of atrial fibrillation and adverse outcomes. European Heart Journal, 2021, 42, 1170-1177.	1.0	79
18	Polygenic burden has broader impact on health, cognition, and socioeconomic outcomes than most rare and high-risk copy number variants. Molecular Psychiatry, 2021, 26, 4884-4895.	4.1	8

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19	Polygenic Risk Scores Predict Hypertension Onset and Cardiovascular Risk. Hypertension, 2021, 77, 1119-1127.	1.3	61
20	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. PLoS Genetics, 2021, 17, e1009501.	1.5	28
21	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
22	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. Nature Communications, 2021, 12, 2671.	5.8	55
23	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
24	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. JAMA Ophthalmology, 2021, 139, 762.	1.4	7
25	Predictive Accuracy of a Clinical and Genetic Risk Model for Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, e003355.	1.6	13
26	The Role of Inflammatory Cytokines as Intermediates in the Pathway from Increased Adiposity to Disease. Obesity, 2021, 29, 428-437.	1.5	27
27	Association of iron deficiency with incident cardiovascular diseases and mortality in the general population. ESC Heart Failure, 2021, 8, 4584-4592.	1.4	13
28	Genetic Profile of Endotoxemia Reveals an Association With Thromboembolism and Stroke. Journal of the American Heart Association, 2021, 10, e022482.	1.6	9
29	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	1.6	24
30	Metabolic Biomarker Discovery for Risk of Peripheral Artery Disease Compared With Coronary Artery Disease: Lipoprotein and Metabolite Profiling of 31 657 Individuals From 5 Prospective Cohorts. Journal of the American Heart Association, 2021, 10, e021995.	1.6	25
31	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
32	Is Brain Derived Neurotrophic Factor (Bdnf) Associated With Smoking Initiation? Replication Using a Large Finnish Population Sample. Nicotine and Tobacco Research, 2020, 22, 293-296.	1.4	5
33	Genetic and Environmental Contributions to Cardiovascular Risk: Lessons From North Karelia and FINRISK. Global Heart, 2020, 11, 229.	0.9	2
34	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
35	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
36	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466

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37	REPLY:. Hepatology, 2020, 71, 1888-1889.	3.6	1
38	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
39	Assessment of causality of natriuretic peptides and atrial fibrillation and heart failure: a Mendelian randomization study in the FINRISK cohort. Europace, 2020, 22, 1463-1469.	0.7	14
40	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
41	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	1.6	5
42	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
43	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	13.7	115
44	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. Hypertension, 2020, 76, 195-205.	1.3	33
45	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	1.6	60
46	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
47	A Platelet Function Modulator of Thrombin Activation Is Causally Linked to Cardiovascular Disease and Affects PAR4 Receptor Signaling. American Journal of Human Genetics, 2020, 107, 211-221.	2.6	26
48	Genetic Associations of Chronotype in the Finnish General Population. Journal of Biological Rhythms, 2020, 35, 501-511.	1.4	18
49	Genomic prediction of alcohol-related morbidity and mortality. Translational Psychiatry, 2020, 10, 23.	2.4	19
50	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
51	Apolipoprotein A-I concentrations and risk of coronary artery disease: A Mendelian randomization study. Atherosclerosis, 2020, 299, 56-63.	0.4	47
52	Comparison of Cardiovascular Risk Factors in European Population Cohorts for Predicting Atrial Fibrillation and Heart Failure, Their Subsequent Onset, and Death. Journal of the American Heart Association, 2020, 9, e015218.	1.6	13
53	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
54	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34

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55	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	4.1	44
56	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
57	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. BMJ: British Medical Journal, 2019, 366, l4292.	2.4	28
58	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
59	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Populationâ€Ascertained Hyperlipidemias. Journal of the American Heart Association, 2019, 8, e012415.	1.6	24
60	Machine learning of human plasma lipidomes for obesity estimation in a large population cohort. PLoS Biology, 2019, 17, e3000443.	2.6	51
61	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
62	Association of Circulating Metabolites With Risk of Coronary Heart Disease in a European Population. JAMA Cardiology, 2019, 4, 1270.	3.0	39
63	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
64	Elevated serum alpha-1 antitrypsin is a major component of GlycA-associated risk for future morbidity and mortality. PLoS ONE, 2019, 14, e0223692.	1.1	14
65	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
66	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
67	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
68	Contribution of rare and common variants to intellectual disability in a sub-isolate of Northern Finland. Nature Communications, 2019, 10, 410.	5.8	32
69	Genome-wide association study identifies seven novel loci associating with circulating cytokines and cell adhesion molecules in Finns. Journal of Medical Genetics, 2019, 56, 607-616.	1.5	46
70	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
71	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. American Journal of Human Genetics, 2019, 104, 1169-1181.	2.6	90
72	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549

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73	Genome-wide association study of white-coat effect in hypertensive patients. Blood Pressure, 2019, 28, 239-249.	0.7	6
74	Sex-Specific Epidemiology of Heart Failure Risk and Mortality in Europe. JACC: Heart Failure, 2019, 7, 204-213.	1.9	54
75	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
76	Lipoprotein signatures of cholesteryl ester transfer protein and HMG-CoA reductase inhibition. PLoS Biology, 2019, 17, e3000572.	2.6	29
77	Serum lipopolysaccharides predict advanced liver disease in the general population. JHEP Reports, 2019, 1, 345-352.	2.6	27
78	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
79	Cardiovascular Risk Factors Associated With Venous Thromboembolism. JAMA Cardiology, 2019, 4, 163.	3.0	187
80	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
81	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
82	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
83	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
84	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
85	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.4	143
86	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
87	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	2.6	57
88	Cohort Profile: The National FINRISK Study. International Journal of Epidemiology, 2018, 47, 696-696i.	0.9	214
89	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	2.3	26
90	Nuclear magnetic resonanceâ€based metabolomics identifies phenylalanine as a novel predictor of incident heart failure hospitalisation: results from PROSPER and FINRISK 1997. European Journal of Heart Failure, 2018, 20, 663-673.	2.9	47

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91	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59
92	Metabolomic Consequences of Genetic Inhibition of PCSK9 Compared With Statin Treatment. Circulation, 2018, 138, 2499-2512.	1.6	69
93	Biomarker Glycoprotein Acetyls Is Associated With the Risk of a Wide Spectrum of Incident Diseases and Stratifies Mortality Risk in Angiography Patients. Circulation Genomic and Precision Medicine, 2018, 11, e002234.	1.6	38
94	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	5.8	134
95	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
96	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
97	Adverse lipid profile elevates risk for subarachnoid hemorrhage: AÂprospective population-based cohort study. Atherosclerosis, 2018, 274, 112-119.	0.4	9
98	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
99	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
100	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
101	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
102	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
103	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
104	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
105	High-sensitivity cardiac troponin I and NT-proBNP as predictors of incident dementia and Alzheimerâ€™s disease: the FINRISK Study. Journal of Neurology, 2017, 264, 503-511.	1.8	20
106	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
107	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	1.4	60
108	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

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109	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
110	Circulating Levels of Interleukin 1-Receptor Antagonist and Risk of Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1222-1227.	1.1	81
111	Matrix metalloproteinase-8 and tissue inhibitor of matrix metalloproteinase-1 predict incident cardiovascular disease events and all-cause mortality in a population-based cohort. European Journal of Preventive Cardiology, 2017, 24, 1136-1144.	0.8	25
112	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
113	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
114	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
115	Association of the DBH Polymorphism rs3025343 With Smoking Cessation in a Large Population-Based Sample. Nicotine and Tobacco Research, 2017, 19, 1112-1115.	1.4	6
116	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	2.3	76
117	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
118	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
119	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
120	Soluble HLA-DR serum levels are associated with smoking but not with acute coronary syndrome. Atherosclerosis, 2017, 266, 58-63.	0.4	2
121	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
122	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
123	Sex Differences and Similarities in Atrial Fibrillation Epidemiology, Risk Factors, and Mortality in Community Cohorts. Circulation, 2017, 136, 1588-1597.	1.6	307
124	Increased plasma N-glycome complexity is associated with higher risk of type 2 diabetes. Diabetologia, 2017, 60, 2352-2360.	2.9	78
125	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
126	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

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127	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
128	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. Diabetes, 2017, 66, 543-550.	0.3	45
129	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
130	Genome-Wide Association Study Implicates Atrial Natriuretic Peptide Rather Than B-Type Natriuretic Peptide in the Regulation of Blood Pressure in the General Population. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	26
131	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
132	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	0.8	86
133	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. Genome Biology, 2017, 18, 146.	3.8	46
134	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
135	Genetic Variants Contributing to Circulating Matrix Metalloproteinase 8 Levels and Their Association With Cardiovascular Diseases. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	21
136	Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns. Journal of Lipid Research, 2017, 58, 1471-1481.	2.0	49
137	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
138	Low MMP-8/TIMP-1 reflects left ventricle impairment in takotsubo cardiomyopathy and high TIMP-1 may help to differentiate it from acute coronary syndrome. PLoS ONE, 2017, 12, e0173371.	1.1	10
139	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
140	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	1.5	48
141	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
142	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
143	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	2.9	57
144	Family history and perceived risk of diabetes, cardiovascular disease, cancer, and depression. Preventive Medicine, 2016, 90, 177-183.	1.6	28

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145	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
146	Troponin I and cardiovascular risk prediction in the general population: the BiomarCaRE consortium. European Heart Journal, 2016, 37, 2428-2437.	1.0	200
147	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
148	Insomnia does not mediate or modify the association between MTNR1B risk variant rs10830963 and glucose levels. Diabetologia, 2016, 59, 1070-1072.	2.9	3
149	Cardiovascular Risk Factors and Ischemic Heart Disease. Circulation: Cardiovascular Genetics, 2016, 9, 279-286.	5.1	5
150	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
151	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
152	Effects of hormonal contraception on systemic metabolism: cross-sectional and longitudinal evidence. International Journal of Epidemiology, 2016, 45, 1445-1457.	0.9	62
153	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
154	Apolipoproteins and HDL cholesterol do not associate with the risk of future dementia and Alzheimerâ€™s disease: the National Finnish population study (FINRISK). Age, 2016, 38, 465-473.	3.0	28
155	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	1.0	277
156	Prediction of Blood Pressure and Blood Pressure Change With a Genetic Risk Score. Journal of Clinical Hypertension, 2016, 18, 181-186.	1.0	27
157	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
158	Genetic support for the causal role of insulin in coronary heart disease. Diabetologia, 2016, 59, 2369-2377.	2.9	14
159	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
160	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. International Journal of Epidemiology, 2016, 45, 1469-1481.	0.9	19
161	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
162	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

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163	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	1.6	25
164	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
165	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576
166	Prolonged sleep restriction induces changes in pathways involved in cholesterol metabolism and inflammatory responses. Scientific Reports, 2016, 6, 24828.	1.6	72
167	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. Scientific Reports, 2016, 6, 20092.	1.6	42
168	Metabolic profiling of alcohol consumption in 9778 young adults. International Journal of Epidemiology, 2016, 45, 1493-1506.	0.9	90
169	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
170	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
171	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
172	Metabolic profiling of pregnancy: cross-sectional and longitudinal evidence. BMC Medicine, 2016, 14, 205.	2.3	150
173	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
174	USF1 deficiency activates brown adipose tissue and improves cardiometabolic health. Science Translational Medicine, 2016, 8, 323ra13.	5.8	58
175	Novel 6p21.3 Risk Haplotype Predisposes to Acute Coronary Syndrome. Circulation: Cardiovascular Genetics, 2016, 9, 55-63.	5.1	6
176	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
177	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
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