Leo-Pekka LyytikÃ¤inen

List of Publications by Year
in descending order

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166 papers	26,707 citations	15504 65 h-index	7950 149 g-index
178 all docs	178 docs citations	178 times ranked	33746 citing authors

#	Article	IF	Citations
1	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
2	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
4	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
5	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
6	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
7	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
8	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
9	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
10	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
11	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	21.4	516
12	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
13	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
14	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.	3.5	419
15	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
16	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
17	miR-21, miR-210, miR-34a, and miR-146a/b are up-regulated in human atherosclerotic plaques in the Tampere Vascular Study. Atherosclerosis, 2011, 219, 211-217.	0.8	402
18	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402

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19	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
20	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
21	Genome-wide Association Study Identifies 27 Loci Influencing Concentrations of Circulating Cytokines and Growth Factors. American Journal of Human Genetics, 2017, 100, 40-50.	6.2	360
22	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
23	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
24	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.	6.2	326
25	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
26	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
27	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.	21.4	294
28	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
29	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
30	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
31	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
32	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
33	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
34	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	3.5	240
35	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
36	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210

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37	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
38	Genetic Determinants of Serum Testosterone Concentrations in Men. PLoS Genetics, 2011, 7, e1002313.	3.5	178
39	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	3.5	171
40	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
41	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
42	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
43	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
44	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
45	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
46	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
47	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.6	116
48	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
49	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
50	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
51	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
52	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.	6.2	109
53	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
54	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108

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55	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	3.5	100
56	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
57	Toll-Like Receptor 7 Protects From Atherosclerosis by Constraining â€œInflammatoryâ€•Macrophage Activation. Circulation, 2012, 126, 952-962.	1.6	92
58	Pulse Wave Velocity Predicts the Progression of Blood Pressure and Development of Hypertension in Young Adults. Hypertension, 2018, 71, 451-456.	2.7	91
59	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. Human Molecular Genetics, 2014, 23, 3054-3068.	2.9	90
60	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. Human Molecular Genetics, 2012, 21, 1444-1455.	2.9	89
61	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
62	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
63	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
64	Uncovering the complex genetics of human character. Molecular Psychiatry, 2020, 25, 2295-2312.	7.9	77
65	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
66	Proprotein convertases in human atherosclerotic plaques: The overexpression of FURIN and its substrate cytokines BAFF and APRIL. Atherosclerosis, 2011, 219, 799-806.	0.8	72
67	Uncovering the complex genetics of human temperament. Molecular Psychiatry, 2020, 25, 2275-2294.	7.9	72
68	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. Archives of General Psychiatry, 2012, 69, 854.	12.3	71
69	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
70	Associations between serum uric acid and markers of subclinical atherosclerosis in young adults. The cardiovascular risk in Young Finns study. Atherosclerosis, 2012, 223, 497-503.	0.8	69
71	Blood microRNA profile associates with the levels of serum lipids and metabolites associated with glucose metabolism and insulin resistance and pinpoints pathways underlying metabolic syndrome. Molecular and Cellular Endocrinology, 2014, 391, 41-49.	3.2	65
72	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64

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73	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolismâ€"The Young Finns Study. Scientific Reports, 2016, 6, 38262.	3.3	62
74	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
75	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
76	A meta-analysis of genome-wide association studies of the electrocardiographic early repolarization pattern. Heart Rhythm, 2012, 9, 1627-1634.	0.7	58
77	Three geneticâ€"environmental networks for human personality. Molecular Psychiatry, 2021, 26, 3858-3875.	7.9	58
78	Palmitoylethanolamide Promotes a Proresolving Macrophage Phenotype and Attenuates Atherosclerotic Plaque Formation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 2562-2575.	2.4	57
79	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. Scientific Reports, 2019, 9, 8887.	3.3	55
80	Genome-Wide Association Study Identifies 3 Genomic Loci Significantly Associated With Serum Levels of Homoarginine. Circulation: Cardiovascular Genetics, 2013, 6, 505-513.	5.1	54
81	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
82	Differentially expressed genes and canonical pathway expression in human atherosclerotic plaques â€" Tampere Vascular Study. Scientific Reports, 2017, 7, 41483.	3.3	52
83	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.	6.2	50
84	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	12.8	49
85	A longitudinal analysis on associations of adiponectin levels with metabolic syndrome and carotid artery intima-media thickness. The Cardiovascular Risk in Young Finns Study. Atherosclerosis, 2011, 217, 234-239.	0.8	46
86	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.	7.9	44
87	Extensive phenotype data and machine learning in prediction of mortality in acute coronary syndrome â€" the MADDEC study. Annals of Medicine, 2019, 51, 156-163.	3.8	44
88	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. Scientific Reports, 2016, 6, 20092.	3.3	42
89	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
90	Serotonin receptor 1B genotype and hostility, anger and aggressive behavior through the lifespan: the Young Finns study. Journal of Behavioral Medicine, 2013, 36, 583-590.	2.1	40

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91	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.	6.1	39
92	Genetic Variants and Their Interactions in the Prediction of Increased Pre-Clinical Carotid Atherosclerosis: The Cardiovascular Risk in Young Finns Study. PLoS Genetics, 2010, 6, e1001146.	3.5	38
93	Melanocortin 1 Receptor Signaling Regulates Cholesterol Transport in Macrophages. Circulation, 2017, 136, 83-97.	1.6	35
94	Risk factors associated with acute kidney injury in a cohort of 20,575 arthroplasty patients. Monthly Notices of the Royal Astronomical Society: Letters, 2017, 88, 370-376.	3.3	35
95	Association of Neuroimmune Guidance Cue Netrin-1 and Its Chemorepulsive Receptor UNC5B With Atherosclerotic Plaque Expression Signatures and Stability in Human(s). Circulation: Cardiovascular Genetics, 2013, 6, 579-587.	5.1	33
96	Genome-wide association study on dimethylarginines reveals novel AGXT2 variants associated with heart rate variability but not with overall mortality. European Heart Journal, 2014, 35, 524-531.	2.2	33
97	Distinct Loci in the CHRNA5/CHRNA3/CHRNB4 Gene Cluster Are Associated With Onset of Regular Smoking. Genetic Epidemiology, 2013, 37, 846-859.	1.3	32
98	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. American Journal of Human Genetics, 2019, 105, 1076-1090.	6.2	31
99	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
100	A genome-wide expression quantitative trait loci analysis of proprotein convertase subtilisin/kexin enzymes identifies a novel regulatory gene variant for FURIN expression and blood pressure. Human Genetics, 2015, 134, 627-636.	3.8	29
101	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
102	C-type lectin receptor CLEC4A2 promotes tissue adaptation of macrophages and protects against atherosclerosis. Nature Communications, 2022, 13, 215.	12.8	28
103	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
104	Polymorphism in the C-reactive protein (CRP) gene affects CRP levels in plasma and one early marker of atherosclerosis in men: The Health 2000 Survey. Scandinavian Journal of Clinical and Laboratory Investigation, 2011, 71, 353-361.	1.2	26
105	Genetic Profiling Using Genome-Wide Significant Coronary Artery Disease Risk Variants Does Not Improve the Prediction of Subclinical Atherosclerosis: The Cardiovascular Risk in Young Finns Study, the Bogalusa Heart Study and the Health 2000 Survey â€“ A Meta-Analysis of Three Independent Studies. PLoS ONE, 2012, 7, e28931.	2.5	26
106	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. European Heart Journal, 2015, 36, 1669-1675.	2.2	26
107	Does Bone Resorption Stimulate Periosteal Expansion? A Cross-Sectional Analysis of Î²-C-telopeptides of Type I Collagen (CTX), Genetic Markers of the RANKL Pathway, and Periosteal Circumference as Measured by pQCT. Journal of Bone and Mineral Research, 2014, 29, 1015-1024.	2.8	24
108	Genome-Wide Association Study Pinpoints a New Functional Apolipoprotein B Variant Influencing Oxidized Low-Density Lipoprotein Levels But Not Cardiovascular Events. Circulation: Cardiovascular Genetics, 2013, 6, 73-81.	5.1	22

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109	Pro-opiomelanocortin and its Processing Enzymes Associate with Plaque Stability in Human Atherosclerosis â€“ Tampere Vascular Study. Scientific Reports, 2018, 8, 15078.	3.3	22
110	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
111	Upstream Transcription Factor 1 (USF1) allelic variants regulate lipoprotein metabolism in women and USF1 expression in atherosclerotic plaque. Scientific Reports, 2014, 4, 4650.	3.3	20
112	Associations of functional alanine-glyoxylate aminotransferase 2 gene variants with atrial fibrillation and ischemic stroke. Scientific Reports, 2016, 6, 23207.	3.3	20
113	Differentially expressed genes and canonical pathways in the ascending thoracic aortic aneurysm â€“ The Tampere Vascular Study. Scientific Reports, 2017, 7, 12127.	3.3	20
114	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
115	Pre-Operative Masseter Area is an Independent Predictor of Long-Term Survival after Carotid Endarterectomy. European Journal of Vascular and Endovascular Surgery, 2019, 57, 331-338.	1.5	19
116	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
117	The prognostic significance of Tâ€wave inversion according to ECG lead group during longâ€term followâ€up in the general population. Annals of Noninvasive Electrocardiology, 2021, 26, e12799.	1.1	18
118	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
119	A comparison of the accuracy of Illumina HumanHT-12 v3 Expression BeadChip and TaqMan qRT-PCR gene expression results in patient samples from the Tampere Vascular Study. Atherosclerosis, 2013, 226, 149-152.	0.8	17
120	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	3.6	17
121	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
122	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
123	Novel associations for coronary artery disease derived from genome wide association studies are not associated with increased carotid intima-media thickness, suggesting they do not act via early atherosclerosis or vessel remodeling. Atherosclerosis, 2011, 219, 684-689.	0.8	16
124	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. Heart Rhythm, 2014, 11, 471-477.	0.7	16
125	The association between charlson comorbidity index and mortality in acute coronary syndrome â€“ the MADDEC study. Scandinavian Cardiovascular Journal, 2020, 54, 146-152.	1.2	16
126	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	3.3	15

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127	A Genome-Wide Association Study Identifies UGT1A1 as a Regulator of Serum Cell-Free DNA in Young Adults: The Cardiovascular Risk in Young Finns Study. PLoS ONE, 2012, 7, e35426.	2.5	13
128	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
129	Methylation status of nc886 epiallele reflects periconceptional conditions and is associated with glucose metabolism through nc886 RNAs. Clinical Epigenetics, 2021, 13, 143.	4.1	13
130	Association of the novel single-nucleotide polymorphism which increases oxidized low-density lipoprotein levels with cerebrovascular disease events. Atherosclerosis, 2014, 234, 214-217.	0.8	12
131	Combination of low blood pressure response, low exercise capacity and slow heart rate recovery during an exercise test significantly increases mortality risk. Annals of Medicine, 2019, 51, 390-396.	3.8	12
132	Left ventricular ejection fraction adds value over the GRACE score in prediction of 6-month mortality after ACS: the MADDEC study. Open Heart, 2019, 6, e001007.	2.3	12
133	Histaminergic gene polymorphisms associated with sedation in clozapine-treated patients. European Neuropsychopharmacology, 2017, 27, 442-449.	0.7	11
134	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
135	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
136	Fatty liver is associated with blood pathways of inflammatory response, immune system activation and prothrombotic state in Young Finns Study. Scientific Reports, 2018, 8, 10358.	3.3	10
137	The prevalence and prognostic significance of interatrial block in the general population. Annals of Medicine, 2020, 52, 63-73.	3.8	10
138	Adulthood blood levels of hsa-miR-29b-3p associate with preterm birth and adult metabolic and cognitive health. Scientific Reports, 2021, 11, 9203.	3.3	10
139	Tissue inhibitor of matrix metalloproteinases 4 (TIMP4) in a population of young adults: Relations to cardiovascular risk markers and carotid artery intima-media thickness. The Cardiovascular Risk in Young Finns Study. Scandinavian Journal of Clinical and Laboratory Investigation, 2012, 72, 540-546.	1.2	9
140	Longâ€term outcome of intraventricular conduction delays in the general population. Annals of Noninvasive Electrocardiology, 2021, 26, e12788.	1.1	9
141	Complementary prediction of cardiovascular events by estimated apo- and lipoprotein concentrations in the working age population. The Health 2000 Study. Annals of Medicine, 2013, 45, 141-148.	3.8	8
142	INSIG2polymorphism and weight gain, dyslipidemia and serum adiponectin in Finnish patients with schizophrenia treated with clozapine. Pharmacogenomics, 2016, 17, 1987-1997.	1.3	7
143	Examining the effect of mitochondrial DNA variants on blood pressure in two Finnish cohorts. Scientific Reports, 2021, 11, 611.	3.3	7
144	Impedance plethysmography-based method in the assessment of subclinical atherosclerosis. Atherosclerosis, 2021, 319, 101-107.	0.8	7

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145	Vascular cell adhesion molecule 1, soluble Fas and hepatocyte growth factor as predictors of mortality in nonagenarians: The Vitality 90 + study. Experimental Gerontology, 2013, 48, 1167-1172.	2.8	6
146	Cardiorespiratory fitness and heart rate recovery predict sudden cardiac death independent of ejection fraction. Heart, 2020, 106, 434-440.	2.9	6
147	Magical thinking in individuals with high polygenic risk for schizophrenia but no non-affective psychosesâ€"a general population study. Molecular Psychiatry, 2022, 27, 3286-3293.	7.9	6
148	No Association of nineteen COX-2 gene variants to preclinical markers of atherosclerosis The Cardiovascular Risk in Young Finns Study. BMC Medical Genetics, 2012, 13, 32.	2.1	4
149	Influence of Genetic Variation in PDE3A on Endothelial Function and Stroke. Hypertension, 2020, 75, 365-371.	2.7	4
150	Functional Polymorphisms in Oxytocin and Dopamine Pathway Genes and the Development of Dispositional Compassion Over Time: The Young Finns Study. Frontiers in Psychology, 2021, 12, 576346.	2.1	4
151	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
152	Blood pathway analyses reveal differences between prediabetic subjects with or without dyslipidaemia. The Cardiovascular Risk in Young Finns Study. Diabetes/Metabolism Research and Reviews, 2017, 33, e2914.	4.0	3
153	Fasting Glucose and the Risk of Depressive Symptoms: Instrumental-Variable Regression in the Cardiovascular Risk in Young Finns Study. International Journal of Behavioral Medicine, 2017, 24, 901-907.	1.7	3
154	Discovery of mitochondrial DNA variants associated with genome-wide blood cell gene expression: a population-based mtDNA sequencing study. Human Molecular Genetics, 2019, 28, 1381-1391.	2.9	3
155	Long-term prognostic significance of the ST level and ST slope in the 12â€lead ECG in the general population. Journal of Electrocardiology, 2020, 58, 176-183.	0.9	3
156	Relation of intraventricular conduction delay to risk of new-onset heart failure and structural heart disease in the general population. IJC Heart and Vasculature, 2020, 31, 100639.	1.1	3
157	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
158	EEG sources of noise in intraoperative somatosensory evoked potential monitoring during propofol anesthesia. Journal of Clinical Monitoring and Computing, 2009, 23, 237-242.	1.6	2
159	Common Genetic Variation in Relation to Brachial Vascular Dimensions and Flow-Mediated Vasodilation. Circulation Genomic and Precision Medicine, 2019, 12, e002409.	3.6	2
160	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
161	Serum apolipoprotein A-I concentration differs in coronary and peripheral artery disease. Scandinavian Journal of Clinical and Laboratory Investigation, 2020, 80, 370-374.	1.2	1
162	Prehospital Adenosine Diphosphate Receptor Blocker Use, Culprit Artery Flow, and Mortality in STEMI: The MADDEC Study. Clinical Drug Investigation, 2021, 41, 605-613.	2.2	1

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163	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
164	Interatrial block and P terminal force in the general population â€“ Longitudinal changes, risk factors and prognosis. Journal of Electrocardiology, 2022, 73, 12-20.	0.9	1
165	Genetic differential susceptibility to the parentâ€“child relationship quality and the life span development of compassion. Developmental Psychobiology, 2021, 63, e22184.	1.6	0
166	Prevalence and long-term prognostic implications of prolonged QRS duration in left ventricular hypertrophy: a population-based observational cohort study. BMJ Open, 2022, 12, e053477.	1.9	0