Markus Perola

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9499441/publications.pdf

Version: 2024-02-01

		5126	1551
232	56,886	86	223
papers	citations	h-index	g-index

247	247	247	63399
all docs	docs citations	times ranked	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 comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
6	Repurposed Antiviral Drugs for Covid-19 â€" Interim WHO Solidarity Trial Results. New England Journal of Medicine, 2021, 384, 497-511.	13.9	2,014
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	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
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	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
12	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
13	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
14	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
15	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
16	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
17	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
18	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

#	Article	IF	Citations
19	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
20	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
21	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
22	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
23	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
24	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576
25	Metabolite Profiling and Cardiovascular Event Risk. Circulation, 2015, 131, 774-785.	1.6	547
26	Heritability of Adult Body Height: A Comparative Study of Twin Cohorts in Eight Countries. Twin Research and Human Genetics, 2003, 6, 399-408.	1.5	544
27	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	9.4	516
28	A multilocus genetic risk score for coronary heart disease: case-control and prospective cohort analyses. Lancet, The, 2010, 376, 1393-1400.	6.3	503
29	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
30	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
31	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
32	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
33	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
34	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
35	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
36	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

#	Article	IF	Citations
37	Genome-wide Association Study Identifies 27 Loci Influencing Concentrations of Circulating Cytokines and Growth Factors. American Journal of Human Genetics, 2017, 100, 40-50.	2.6	360
38	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
39	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
40	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
41	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. International Journal of Epidemiology, 2015, 44, 1137-1147.	0.9	314
42	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
43	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
44	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
45	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
46	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
47	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	1.0	277
48	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
49	Metabonomic, transcriptomic, and genomic variation of a population cohort. Molecular Systems Biology, 2010, 6, 441.	3.2	230
50	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
51	Cohort Profile: The National FINRISK Study. International Journal of Epidemiology, 2018, 47, 696-696i.	0.9	214
52	A metabolic view on menopause and ageing. Nature Communications, 2014, 5, 4708.	5.8	196
53	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907.	4.9	191
54	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

#	Article	IF	Citations
55	DataSHIELD: taking the analysis to the data, not the data to the analysis. International Journal of Epidemiology, 2014, 43, 1929-1944.	0.9	188
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	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
58	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
59	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
60	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	1.5	171
61	The Three-Factor Eating Questionnaire, body mass index, and responses to sweet and salty fatty foods: a twin study of genetic and environmental associations. American Journal of Clinical Nutrition, 2008, 88, 263-271.	2.2	170
62	Age-Dependent Association of Apolipoprotein E Genotype With Coronary and Aortic Atherosclerosis in Middle-Aged Men. Circulation, 1999, 100, 608-613.	1.6	162
63	Sweet taste preferences are partly genetically determined: identification of a trait locus on chromosome 16. American Journal of Clinical Nutrition, 2007, 86, 55-63.	2.2	159
64	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
65	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
66	Association of serum cotinine level with a cluster of three nicotinic acetylcholine receptor genes (CHRNA3/CHRNA5/CHRNB4) on chromosome 15. Human Molecular Genetics, 2009, 18, 4007-4012.	1.4	151
67	Metabolic profiling of pregnancy: cross-sectional and longitudinal evidence. BMC Medicine, 2016, 14, 205.	2.3	150
68	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
69	Combined Genome Scans for Body Stature in 6,602 European Twins: Evidence for Common Caucasian Loci. PLoS Genetics, 2007, 3, e97.	1.5	145
70	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. Human Molecular Genetics, 2014, 23, 6961-6972.	1.4	143
71	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.4	143
72	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

#	Article	IF	Citations
73	Food Neophobia in Young Adults: Genetic Architecture and Relation to Personality, Pleasantness and Use Frequency of Foods, and Body Mass Indexâ€"A Twin Study. Behavior Genetics, 2011, 41, 512-521.	1.4	133
74	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
75	Food neophobia shows heritable variation in humans. Physiology and Behavior, 2007, 91, 573-578.	1.0	128
76	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
77	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
78	Association of FXIII Val34Leu with decreased risk of myocardial infarction in Finnish males. Atherosclerosis, 1999, 142, 295-300.	0.4	122
79	Heritability and risk factors of uterine fibroids â€" The Finnish Twin Cohort Study. Maturitas, 2000, 37, 15-26.	1.0	119
80	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
81	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
82	Evaluation of O2PLS in Omics data integration. BMC Bioinformatics, 2016, 17, 11.	1.2	113
83	An Immune Response Network Associated with Blood Lipid Levels. PLoS Genetics, 2010, 6, e1001113.	1.5	112
84	MORGAM (an international pooling of cardiovascular cohorts). International Journal of Epidemiology, 2004, 34, 21-27.	0.9	105
85	Data harmonization and federated analysis of population-based studies: the BioSHaRE project. Emerging Themes in Epidemiology, 2013, 10, 12.	1.2	105
86	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
87	Coronary Artery Complicated Lesion Area Is Related to Functional Polymorphism of Matrix Metalloproteinase 9 Gene. Arteriosclerosis, Thrombosis, and Vascular Biology, 2001, 21, 1446-1450.	1.1	96
88	Risks of Light and Moderate Alcohol Use in Fatty Liver Disease: Followâ€Up of Population Cohorts. Hepatology, 2020, 71, 835-848.	3.6	96
89	Neolithic dairy farming at the extreme of agriculture in northern Europe. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140819.	1.2	92
90	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

#	Article	IF	Citations
91	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
92	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
93	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. Human Molecular Genetics, 2012, 21, 1444-1455.	1.4	89
94	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
95	Same genetic components underlie different measures of sweet taste preference. American Journal of Clinical Nutrition, 2007, 86, 1663-1669.	2.2	88
96	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
97	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	0.8	86
98	Genetic and environmental contributions to food use patterns of young adult twins. Physiology and Behavior, 2008, 93, 235-242.	1.0	84
99	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	1.4	84
100	Comprehensive catalog of European biobanks. Nature Biotechnology, 2011, 29, 795-797.	9.4	83
101	Sex hormone-binding globulin associations with circulating lipids and metabolites and the risk for type 2 diabetes: observational and causal effect estimates. International Journal of Epidemiology, 2015, 44, 623-637.	0.9	83
102	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
103	Gender Differences in Genetic Risk Profiles for Cardiovascular Disease. PLoS ONE, 2008, 3, e3615.	1.1	81
104	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	5.8	81
105	Platelet Glycoprotein Ibî± HPA-2 Met/VNTR B Haplotype as a Genetic Predictor of Myocardial Infarction and Sudden Cardiac Death. Circulation, 2001, 104, 876-880.	1.6	77
106	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
107	Glycoprotein IIIa Pl ^A Polymorphism Associates With Progression of Coronary Artery Disease and With Myocardial Infarction in an Autopsy Series of Middle-Aged Men Who Died Suddenly. Arteriosclerosis, Thrombosis, and Vascular Biology, 1999, 19, 2573-2578.	1.1	74
108	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74

#	Article	IF	Citations
109	BBMRI-ERIC as a resource for pharmaceutical and life science industries: the development of biobank-based Expert Centres. European Journal of Human Genetics, 2015, 23, 893-900.	1.4	71
110	Low galactosylation of IgG associates with higher risk for future diagnosis of rheumatoid arthritis during 10â€¯years of follow-up. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2034-2039.	1.8	66
111	Chronic disease research in Europe and the need for integrated population cohorts. European Journal of Epidemiology, 2017, 32, 741-749.	2.5	65
112	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
113	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
114	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
115	Platelet membrane collagen receptor glycoprotein VI polymorphism is associated with coronary thrombosis and fatal myocardial infarction in middle-aged men. Atherosclerosis, 2004, 176, 95-99.	0.4	62
116	Chromosome X-Wide Association Study Identifies Loci for Fasting Insulin and Height and Evidence for Incomplete Dosage Compensation. PLoS Genetics, 2014, 10, e1004127.	1.5	61
117	Glycoprotein IIIa PlA1/A2 polymorphism and sudden cardiac death. Journal of the American College of Cardiology, 2000, 36, 1317-1323.	1.2	59
118	Identifying flavor preference subgroups. Genetic basis and related eating behavior traits. Appetite, 2014, 75, 1-10.	1.8	59
119	European lactase persistence genotype shows evidence of association with increase in body mass index. Human Molecular Genetics, 2010, 19, 1129-1136.	1.4	58
120	USF1 deficiency activates brown adipose tissue and improves cardiometabolic health. Science Translational Medicine, 2016, 8, 323ra13.	5.8	58
121	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
122	Cohort Profile: The Corogene study. International Journal of Epidemiology, 2012, 41, 1265-1271.	0.9	55
123	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	1.5	55
124	Intertumoral heterogeneity in patient-specific drug sensitivities in treatment-naÃ¯ve glioblastoma. BMC Cancer, 2019, 19, 628.	1.1	55
125	Risk Alleles of USF1 Gene Predict Cardiovascular Disease of Women in Two Prospective Studies. PLoS Genetics, 2006, 2, e69.	1.5	51
126	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51

#	Article	IF	Citations
127	OSBPL10, a novel candidate gene for high triglyceride trait in dyslipidemic Finnish subjects, regulates cellular lipid metabolism. Journal of Molecular Medicine, 2009, 87, 825-835.	1.7	50
128	Common Genetic Variants, QT Interval, and Sudden Cardiac Death in a Finnish Population-Based Study. Circulation: Cardiovascular Genetics, 2011, 4, 305-311.	5.1	50
129	A Genome-Wide Association Study of Monozygotic Twin-Pairs Suggests a Locus Related to Variability of Serum High-Density Lipoprotein Cholesterol. Twin Research and Human Genetics, 2012, 15, 691-699.	0.3	50
130	Same genetic components underlie different measures of sweet taste preference. American Journal of Clinical Nutrition, 2007, 86, 1663-1669.	2.2	48
131	Food neophobia associates with poorer dietary quality, metabolic risk factors, and increased disease outcome risk in population-based cohorts in a metabolomics study. American Journal of Clinical Nutrition, 2019, 110, 233-245.	2.2	47
132	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. Genome Biology, 2017, 18, 146.	3.8	46
133	Appetitive traits as behavioural pathways in genetic susceptibility to obesity: a population-based cross-sectional study. Scientific Reports, 2015, 5, 14726.	1.6	45
134	Genomeâ€wide association study of sleep duration in the <scp>F</scp>innish population. Journal of Sleep Research, 2014, 23, 609-618.	1.7	44
135	The GPIIIa (Î²3 integrin) PlA polymorphism in the early development of coronary atherosclerosis. Atherosclerosis, 2001, 154, 721-727.	0.4	42
136	Genetic Association and Interaction Analysis of USF1 and APOA5 on Lipid Levels and Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 346-352.	1.1	42
137	Metaâ€analysis on blood transcriptomic studies identifies consistently coexpressed proteinâ€“protein interaction modules as robust markers of human aging. Aging Cell, 2014, 13, 216-225.	3.0	42
138	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. Scientific Reports, 2016, 6, 20092.	1.6	42
139	The Molecular Genetic Architecture of Self-Employment. PLoS ONE, 2013, 8, e60542.	1.1	41
140	Genetic Determinants of Circulating Interleukin-1 Receptor Antagonist Levels and Their Association With Glycemic Traits. Diabetes, 2014, 63, 4343-4359.	0.3	40
141	Protective Low-Frequency Variants for Preeclampsia in the Fms Related Tyrosine Kinase 1 Gene in the Finnish Population. Hypertension, 2017, 70, 365-371.	1.3	37
142	Common Genetic Variants Associated with Sudden Cardiac Death: The FinSCDgen Study. PLoS ONE, 2012, 7, e41675.	1.1	37
143	ACE gene and physical activity, blood pressure, and hypertension: a population study in Finland. Journal of Applied Physiology, 2002, 92, 2508-2512.	1.2	34
144	Environmental Effects Exceed Genetic Effects on Perceived Intensity and Pleasantness of Several Odors: A Three-Population Twin Study. Behavior Genetics, 2008, 38, 484-492.	1.4	34

#	Article	IF	Citations
145	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
146	Association of Variation in the Interleukin-1 Gene Family with Diabetes and Glucose Homeostasis. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4575-4583.	1.8	33
147	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. Hypertension, 2020, 76, 195-205.	1.3	33
148	Metabolic profiling of angiopoietin-like protein 3 and 4 inhibition: a drug-target Mendelian randomization analysis. European Heart Journal, 2021, 42, 1160-1169.	1.0	33
149	Plasminogen Activator Inhibitor-1 (PAI-1) 4G/5G Polymorphism, Coronary Thrombosis, and Myocardial Infarction in Middle-aged Finnish Men who Died Suddenly. Thrombosis and Haemostasis, 2000, 84, 78-82.	1.8	32
150	Genetic component of identification, intensity and pleasantness of odours: a Finnish family study. European Journal of Human Genetics, 2007, 15, 596-602.	1.4	32
151	Genetic contribution to sour taste preference. Appetite, 2012, 58, 687-694.	1.8	32
152	A distinctive DNA methylation pattern in insufficient sleep. Scientific Reports, 2019, 9, 1193.	1.6	32
153	Abuse of Alcohol in Sudden Out-of-Hospital Deaths in Finland. Alcoholism: Clinical and Experimental Research, 1994, 18, 255-260.	1.4	31
154	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.	2.6	31
155	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. PLoS Genetics, 2020, 16, e1008682.	1.5	31
156	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. PLoS Genetics, 2011, 7, e1002333.	1.5	29
157	Low-Expression Variant of Fatty Acidâ€“Binding Protein 4 Favors Reduced Manifestations of Atherosclerotic Disease and Increased Plaque Stability. Circulation: Cardiovascular Genetics, 2014, 7, 588-598.	5.1	28
158	An epigenome-wide association study of metabolic syndrome and its components. Scientific Reports, 2020, 10, 20567.	1.6	27
159	The Role of Inflammatory Cytokines as Intermediates in the Pathway from Increased Adiposity to Disease. Obesity, 2021, 29, 428-437.	1.5	27
160	Association of the endothelial nitric oxide synthase gene polymorphism with risk of coronary artery disease and myocardial infarction in middle-aged men. Journal of Molecular Medicine, 2002, 80, 605-609.	1.7	26
161	Association Analysis of Allelic Variants of USF1 in Coronary Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 983-989.	1.1	26
162	AUTOGSCAN: Powerful Tools for Automated Genome-Wide Linkage and Linkage Disequilibrium Analysis. Twin Research and Human Genetics, 2005, 8, 16-21.	0.3	25

#	Article	IF	Citations
163	Combined Effects of Thrombosis Pathway Gene Variants Predict Cardiovascular Events. PLoS Genetics, 2007, 3, e120.	1.5	25
164	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
165	Association of Circulating Metabolites in Plasma or Serum and Risk of Stroke. Neurology, 2021, 96, .	1.5	24
166	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	1.6	24
167	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. PLoS ONE, 2016, 11, e0163877.	1.1	23
168	ADAM8 and its single nucleotide polymorphism 2662 T/G are associated with advanced atherosclerosis and fatal myocardial infarction: Tampere vascular study. Annals of Medicine, 2009, 41, 497-507.	1.5	22
169	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
170	Transnational access to large prospective cohorts in Europe: Current trends and unmet needs. New Biotechnology, 2019, 49, 98-103.	2.4	22
171	Combined Effects of Alcohol and Metabolic Disorders in Patients With Chronic Liver Disease. Clinical Gastroenterology and Hepatology, 2020, 18, 995-997.e2.	2.4	22
172	Genetic Risk Scores Predict Recurrence of Acute Coronary Syndrome. Circulation: Cardiovascular Genetics, 2016, 9, 172-178.	5.1	21
173	Genetic Variants Contributing to Circulating Matrix Metalloproteinase 8 Levels and Their Association With Cardiovascular Diseases. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	21
174	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
175	Angiotensin-converting enzyme genotypes in the high- and low-risk area for coronary heart disease in Finland. Genetic Epidemiology, 1995, 12, 391-399.	0.6	20
176	Feasibility study of using highâ€throughput drug sensitivity testing to target recurrent glioblastoma stem cells for individualized treatment. Clinical and Translational Medicine, 2019, 8, 33.	1.7	20
177	Polymorphisms in the nephrin gene and diabetic nephropathy in type 1 diabetic patients. Kidney International, 2003, 63, 1205-1210.	2.6	19
178	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. Endocrinology, 2019, 160, 1731-1742.	1.4	19
179	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
180	Genetic variation of the interleukin-1 family and nongenetic factors determining the interleukin-1 receptor antagonist phenotypes. Metabolism: Clinical and Experimental, 2010, 59, 1520-1527.	1.5	17

#	Article	IF	Citations
181	Associations of Nicotine Intake Measures With CHRN Genes in Finnish Smokers. Nicotine and Tobacco Research, 2011, 13, 686-690.	1.4	17
182	Evaluating Whole Genome Amplification via Multiply-Primed Rolling Circle Amplification for SNP Genotyping of Samples With Low DNA Yield. Twin Research and Human Genetics, 2005, 8, 368-375.	0.3	16
183	Genome-wide linkage screen for stature and body mass index in 3.032 families: evidence for sex- and population-specific genetic effects. European Journal of Human Genetics, 2009, 17, 258-266.	1.4	16
184	Thyroid cancer and co-occurring RET mutations in Hirschsprung disease. Endocrine-Related Cancer, 2013, 20, 595-602.	1.6	16
185	BMI is positively associated with accelerated epigenetic aging in twin pairs discordant for body mass index. Journal of Internal Medicine, 2022, 292, 627-640.	2.7	15
186	Astringency Perception and Heritability Among Young Finnish Twins. Chemosensory Perception, 2011, 4, 134-144.	0.7	14
187	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
188	Genetics of Human Stature: Lessons from Genome-Wide Association Studies. Hormone Research in Paediatrics, 2011, 76, 10-10.	0.8	13
189	Noncoding RET variants explain the strong association with Hirschsprung disease in patients without rare coding sequence variant. European Journal of Medical Genetics, 2019, 62, 229-234.	0.7	13
190	Age-dependent association between hepatic lipase gene C-480T polymorphism and the risk of pre-hospital sudden cardiac death: The Helsinki Sudden Death Study. Atherosclerosis, 2007, 192, 421-427.	0.4	12
191	Longitudinal profiling of metabolic ageing trends in two population cohorts of young adults. International Journal of Epidemiology, 2022, 51, 1970-1983.	0.9	12
192	Testing Genetic Susceptibility Loci for Alcoholic Heart Muscle Disease. Alcoholism: Clinical and Experimental Research, 2001, 25, 1409-1413.	1.4	11
193	Platelet collagen receptor GPIa (C807T/HPA-5) haplotype is not associated with an increased risk of fatal coronary events in middle-aged men. Atherosclerosis, 2002, 165, 111-118.	0.4	11
194	Dopamine D3 receptor gene polymorphisms, blood pressure and nephropathy in type 1 diabetic patients. Nephrology Dialysis Transplantation, 2004, 19, 1432-1436.	0.4	11
195	Bayesian Variable Selection in Searching for Additive and Dominant Effects in Genome-Wide Data. PLoS ONE, 2012, 7, e29115.	1.1	11
196	Birthplace predicts risk for prehospital sudden cardiac death in middle-aged men who migrated to metropolitan area: The Helsinki Sudden Death Study. Annals of Medicine, 2009, 41, 57-65.	1.5	10
197	Genome-wide association approaches for identifying loci for human height genes. Best Practice and Research in Clinical Endocrinology and Metabolism, 2011, 25, 19-23.	2.2	10
198	Evaluating whole genome amplification via multiply-primed rolling circle amplification for SNP genotyping of samples with low DNA yield. Twin Research and Human Genetics, 2005, 8, 368-75.	0.3	10

#	Article	IF	Citations
199	Role of Academic Biobanks in Publicâ€“Private Partnerships in the European Biobanking and BioMolecular Resources Research Infrastructure Community. Biopreservation and Biobanking, 2019, 17, 46-51.	0.5	9
200	Genetic Profile of Endotoxemia Reveals an Association With Thromboembolism and Stroke. Journal of the American Heart Association, 2021, 10, e022482.	1.6	9
201	Comprehensive biomarker profiling of hypertension in 36â€Š985 Finnish individuals. Journal of Hypertension, 2022, 40, 579-587.	0.3	9
202	A Functional variant of the iNOS gene flanking region is associated with LAD coronary artery disease: an autopsy study. European Journal of Clinical Investigation, 2003, 33, 1032-1037.	1.7	8
203	A common variant near the KCNJ2 gene is associated with T-peak to T-end interval. Heart Rhythm, 2012, 9, 1099-1103.	0.3	8
204	Changes in the fine-scale genetic structure of Finland through the 20th century. PLoS Genetics, 2021, 17, e1009347.	1.5	8
205	A Web Portal for Communicating Polygenic Risk Score Results for Health Care Useâ€”The P5 Study. Frontiers in Genetics, 2021, 12, 763159.	1.1	8
206	Circulating Metabolic Biomarkers Are Consistently Associated With Type 2 Diabetes Risk in Asian and European Populations. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2751-e2761.	1.8	8
207	Spline Methods for the Comparison of Physical and Genetic Maps. Journal of Computational Biology, 2002, 9, 465-475.	0.8	7
208	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. JAMA Ophthalmology, 2021, 139, 762.	1.4	7
209	MixFit: Methodology for Computing Ancestry-Related Genetic Scores at the Individual Level and Its Application to the Estonian and Finnish Population Studies. PLoS ONE, 2017, 12, e0170325.	1.1	7
210	Pharmacoepigenetics of hypertension: genome-wide methylation analysis of responsiveness to four classes of antihypertensive drugs using a double-blind crossover study design. Epigenetics, 2022, , 1-14.	1.3	7
211	Genetic Variants on Chromosome 1p13.3 Are Associated with Non-ST Elevation Myocardial Infarction and the Expression of DRAM2 in the Finnish Population. PLoS ONE, 2015, 10, e0140576.	1.1	6
212	Novel 6p21.3 Risk Haplotype Predisposes to Acute Coronary Syndrome. Circulation: Cardiovascular Genetics, 2016, 9, 55-63.	5.1	6
213	A polymorphism in the protein kinase C gene PRKCB is associated with Î±2-adrenoceptor-mediated vasoconstriction. Pharmacogenetics and Genomics, 2013, 23, 127-134.	0.7	5
214	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	1.6	5
215	Mitochondrial bioenergetic pathways in blood leukocyte transcriptome decrease after intensive weight loss but are rescued following weight regain in female physique athletes. FASEB Journal, 2021, 35, e21484.	0.2	5
216	Birthplace in area with high coronary heart disease mortality predicts the severity of coronary atherosclerosis among middle-aged Finnish men who had migrated to capital area: The Helsinki Sudden Death Study. Annals of Medicine, 2010, 42, 286-295.	1.5	4

#	Article	IF	Citations
217	The Detection of Metabolite-Mediated Gene Module Co-Expression Using Multivariate Linear Models. PLoS ONE, 2016, 11, e0150257.	1.1	4
218	Association of paraoxonase-1 M55L genotype and alcohol consumption with coronary atherosclerosis. Pharmacogenetics and Genomics, 2004, 14, 479-485.	5.7	3
219	Age-dependent interaction of apolipoprotein E gene with eastern birthplace in Finland affects severity of coronary atherosclerosis and risk of fatal myocardial infarctionâ€"Helsinki Sudden Death Study. Annals of Medicine, 2013, 45, 213-219.	1.5	3
220	Testing genetic susceptibility loci for alcoholic heart muscle disease. Alcoholism: Clinical and Experimental Research, 2001, 25, 1409-13.	1.4	3
221	Mendelian randomisation analysis of clustered causal effects of body mass on cardiometabolic biomarkers. BMC Bioinformatics, 2018, 19, 195.	1.2	2
222	On the Combination of Omics Data for Prediction of Binary Outcomes. , 2017, , 259-275.		2
223	Reaching for Precision Healthcare in Finland via Use of Genomic Data. Frontiers in Genetics, 2022, 13, 877891.	1.1	1
224	Genetics of Platelet Glycoprotein Receptors: Risk of Thrombotic Events and Pharmacogenetic Implications. Clinical and Applied Thrombosis/Hemostasis, 2005, 11, 113-125.	0.7	0
225	Genome-wide search for QTLs for apolipoprotein A-I level in elderly Swedish DZ twins: evidence of female-specific locus on 15q11â€"13. European Journal of Human Genetics, 2008, 16, 1103-1110.	1.4	0
226	A multivariate linear model for investigating the association between gene-module co-expression and a continuous covariate. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.2	0
227	HDL-Mediated Cholesterol Efflux Associates with Incident Kidney Disease. Clinical Chemistry, 2021, 67, 689-691.	1.5	0
228	Combined Effects of Thrombosis Pathway Gene Variants Predict Cardiovascular Events. PLoS Genetics, 2005, preprint, e120.	1.5	0
229	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
230	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
231	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
232	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0