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	C-type lectin receptor CLEC4A2 promotes tissue adaptation of macrophages and protects against atherosclerosis. Nature Communications, 2022, 13, 215.	12.8	28
2	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
3	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
4	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
5	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
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
7	Three geneticâ€“environmental networks for human personality. Molecular Psychiatry, 2021, 26, 3858-3875.	7.9	58
8	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
9	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
10	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
11	Longâ€term outcome of intraventricular conduction delays in the general population. Annals of Noninvasive Electrocardiology, 2021, 26, e12788.	1.1	9
12	Examining the effect of mitochondrial DNA variants on blood pressure in two Finnish cohorts. Scientific Reports, 2021, 11, 611.	3.3	7
13	Impedance plethysmography-based method in the assessment of subclinical atherosclerosis. Atherosclerosis, 2021, 319, 101-107.	0.8	7
14	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
15	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
16	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
17	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
18	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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19	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
20	Genetic differential susceptibility to the parentâ€“child relationship quality and the life span development of compassion. Developmental Psychobiology, 2021, 63, e22184.	1.6	0
21	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
22	Uncovering the complex genetics of human character. Molecular Psychiatry, 2020, 25, 2295-2312.	7.9	77
23	Uncovering the complex genetics of human temperament. Molecular Psychiatry, 2020, 25, 2275-2294.	7.9	72
24	Cardiorespiratory fitness and heart rate recovery predict sudden cardiac death independent of ejection fraction. Heart, 2020, 106, 434-440.	2.9	6
25	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
26	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
27	Influence of Genetic Variation in PDE3A on Endothelial Function and Stroke. Hypertension, 2020, 75, 365-371.	2.7	4
28	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
29	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
30	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
31	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
32	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
33	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
34	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
35	The prevalence and prognostic significance of interatrial block in the general population. Annals of Medicine, 2020, 52, 63-73.	3.8	10
36	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3

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37	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
38	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
39	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
40	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
41	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
42	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
43	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
44	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
45	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
46	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	12.8	49
47	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
48	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
49	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
50	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
51	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
52	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
53	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
54	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549

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55	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	3.6	17
56	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
57	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
58	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
59	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
60	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
61	Common Genetic Variation in Relation to Brachial Vascular Dimensions and Flow-Mediated Vasodilation. Circulation Genomic and Precision Medicine, 2019, 12, e002409.	3.6	2
62	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
63	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
64	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
65	Pulse Wave Velocity Predicts the Progression of Blood Pressure and Development of Hypertension in Young Adults. Hypertension, 2018, 71, 451-456.	2.7	91
66	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
67	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
68	Palmitoylethanolamide Promotes a Proresolving Macrophage Phenotype and Attenuates Atherosclerotic Plaque Formation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 2562-2575.	2.4	57
69	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
70	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
71	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
72	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484

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73	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
74	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
75	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
76	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
77	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
78	Differentially expressed genes and canonical pathway expression in human atherosclerotic plaques â€“ Tampere Vascular Study. Scientific Reports, 2017, 7, 41483.	3.3	52
79	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
80	Histaminergic gene polymorphisms associated with sedation in clozapine-treated patients. European Neuropsychopharmacology, 2017, 27, 442-449.	0.7	11
81	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
82	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
83	Melanocortin 1 Receptor Signaling Regulates Cholesterol Transport in Macrophages. Circulation, 2017, 136, 83-97.	1.6	35
84	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
85	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
86	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
87	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
88	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
89	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
90	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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91	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
92	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
93	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
94	INSIG2polymorphism and weight gain, dyslipidemia and serum adiponectin in Finnish patients with schizophrenia treated with clozapine. Pharmacogenomics, 2016, 17, 1987-1997.	1.3	7
95	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
96	Associations of functional alanine-glyoxylate aminotransferase 2 gene variants with atrial fibrillation and ischemic stroke. Scientific Reports, 2016, 6, 23207.	3.3	20
97	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
98	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
99	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
100	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
101	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
102	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
103	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. Scientific Reports, 2016, 6, 20092.	3.3	42
104	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
105	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
106	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
107	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
108	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412

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109	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
110	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
111	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
112	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. European Heart Journal, 2015, 36, 1669-1675.	2.2	26
113	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
114	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
115	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
116	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
117	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
118	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
119	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
120	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
121	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
122	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
123	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. Heart Rhythm, 2014, 11, 471-477.	0.7	16
124	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
125	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
126	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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127	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
128	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
129	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
130	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
131	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
132	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
133	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	3.5	100
134	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
135	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
136	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
137	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
138	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
139	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
140	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
141	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
142	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	3.5	171
143	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
144	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	3.5	240

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145	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. Archives of General Psychiatry, 2012, 69, 854.	12.3	71
146	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
147	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
148	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
149	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	21.4	516
150	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. Human Molecular Genetics, 2012, 21, 1444-1455.	2.9	89
151	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
152	A meta-analysis of genome-wide association studies of the electrocardiographic early repolarization pattern. Heart Rhythm, 2012, 9, 1627-1634.	0.7	58
153	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
154	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
155	Toll-Like Receptor 7 Protects From Atherosclerosis by Constraining â€œInflammatoryâ€•Macrophage Activation. Circulation, 2012, 126, 952-962.	1.6	92
156	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
157	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
158	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
159	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
160	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
161	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
162	Genetic Determinants of Serum Testosterone Concentrations in Men. PLoS Genetics, 2011, 7, e1002313.	3.5	178

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163	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
164	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
165	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
166	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1