

Samuli Ripatti

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/2635810/samuli-ripatti-publications-by-year.pdf>
Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

279 papers	46,646 citations	85 h-index	215 g-index
315 ext. papers	59,305 ext. citations	13.2 avg, IF	5.95 L-index

#	Paper	IF	Citations
279	How Communicating Polygenic and Clinical Risk for Atherosclerotic Cardiovascular Disease Impacts Health Behavior: an Observational Follow-up Study.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , CIRCGEN121003459	5.2	4
278	Multiparametric platform for profiling lipid trafficking in human leukocytes.. <i>Cell Reports Methods</i> , 2022 , 2, 100166		0
277	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles.. <i>Nature Genetics</i> , 2022 , 54, 152-160	36.3	13
276	Integration of questionnaire-based risk factors improves polygenic risk scores for human coronary heart disease and type 2 diabetes.. <i>Communications Biology</i> , 2022 , 5, 158	6.7	0
275	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci.. <i>Nature Communications</i> , 2022 , 13, 1644	17.4	5
274	A genome-wide association study of outcome from traumatic brain injury.. <i>EBioMedicine</i> , 2022 , 77, 1039138	33.8	0
273	Genome-wide association meta-analysis of nicotine metabolism and cigarette consumption measures in smokers of European descent. <i>Molecular Psychiatry</i> , 2021 , 26, 2212-2223	15.1	22
272	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
271	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021 , 27, 1876-1884	50.5	25
270	Multimomics and digital monitoring during lifestyle changes reveal independent dimensions of human biology and health. <i>Cell Systems</i> , 2021 ,	10.6	3
269	Polygenic risk provides biological validity for the ICHD-3 criteria among Finnish migraine families. <i>Cephalalgia</i> , 2021 , 3331024211045651	6.1	1
268	Changes in the fine-scale genetic structure of Finland through the 20th century. <i>PLoS Genetics</i> , 2021 , 17, e1009347	6	2
267	Association of structural variation with cardiometabolic traits in Finns. <i>American Journal of Human Genetics</i> , 2021 , 108, 583-596	11	3
266	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. <i>PLoS Genetics</i> , 2021 , 17, e1009501	6	8
265	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021 , 12, 2182	17.4	5
264	Genome-Wide Association Study and Identification of a Protective Missense Variant on Lipoprotein(a) Concentration: Protective Missense Variant on Lipoprotein(a) Concentration-Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021 , 41, 1792-1800	9.4	8
263	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. <i>Human Genomics</i> , 2021 , 15, 34	6.8	2

262	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. <i>JAMA Ophthalmology</i> , 2021 , 139, 762-768	3.9	0
261	The relation of severe malocclusion to patients' mental and behavioral disorders, growth, and speech problems. <i>European Journal of Orthodontics</i> , 2021 , 43, 159-164	3.3	4
260	Genetic Influences on Patient-Oriented Outcomes in Traumatic Brain Injury: A Living Systematic Review of Non-Apolipoprotein E Single-Nucleotide Polymorphisms. <i>Journal of Neurotrauma</i> , 2021 , 38, 1107-1123	5.4	24
259	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021 , 5, 59-70	12.8	33
258	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. <i>European Journal of Human Genetics</i> , 2021 , 29, 615-624	5.3	5
257	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. <i>European Respiratory Journal</i> , 2021 , 57,	13.6	17
256	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. <i>European Journal of Human Genetics</i> , 2021 , 29, 309-324	5.3	6
255	Joint association between education and polygenic risk score for incident coronary heart disease events: a longitudinal population-based study of 26 203 men and women. <i>Journal of Epidemiology and Community Health</i> , 2021 ,	5.1	2
254	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021 , 53, 185-194	36.3	78
253	Sleep apnoea is a risk factor for severe COVID-19. <i>BMJ Open Respiratory Research</i> , 2021 , 8,	5.6	37
252	Polygenic burden has broader impact on health, cognition, and socioeconomic outcomes than most rare and high-risk copy number variants. <i>Molecular Psychiatry</i> , 2021 , 26, 4884-4895	15.1	1
251	Accuracy of 1-Hour Plasma Glucose During the Oral Glucose Tolerance Test in Diagnosis of Type 2 Diabetes in Adults: A Meta-analysis. <i>Diabetes Care</i> , 2021 , 44, 1062-1069	14.6	9
250	Lifetime risk of rheumatoid arthritis-associated interstitial lung disease in mutation carriers. <i>Annals of the Rheumatic Diseases</i> , 2021 , 80, 1530-1536	2.4	3
249	Clinical Conditions and Their Impact on Utility of Genetic Scores for Prediction of Acute Coronary Syndrome. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003283	5.2	2
248	Childhood adversities are associated with shorter leukocyte telomere length at adult age in a population-based study. <i>Psychoneuroendocrinology</i> , 2021 , 130, 105276	5	1
247	Predictive Accuracy of a Clinical and Genetic Risk Model for Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003355	5.2	2
246	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
245	Polygenic Score for Physical Activity Is Associated with Multiple Common Diseases. <i>Medicine and Science in Sports and Exercise</i> , 2021 ,	1.2	2

244	The Role of Inflammatory Cytokines as Intermediates in the Pathway from Increased Adiposity to Disease. <i>Obesity</i> , 2021 , 29, 428-437	8	6
243	Integrating lipidomics and genomics: emerging tools to understand cardiovascular diseases. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 2565-2584	10.3	8
242	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
241	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
240	MetaPhat: Detecting and Decomposing Multivariate Associations From Univariate Genome-Wide Association Statistics. <i>Frontiers in Genetics</i> , 2020 , 11, 431	4.5	5
239	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002725	5.2	26
238	Genomic prediction of alcohol-related morbidity and mortality. <i>Translational Psychiatry</i> , 2020 , 10, 23	8.6	7
237	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. <i>Nature Medicine</i> , 2020 , 26, 549-557	50.5	109
236	Effects of TM6SF2 E167K on hepatic lipid and very low-density lipoprotein metabolism in humans. <i>JCI Insight</i> , 2020 , 5,	9.9	13
235	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020 , 7, 1032-1045	23.3	43
234	Human essential hypertension: no significant association of polygenic risk scores with antihypertensive drug responses. <i>Scientific Reports</i> , 2020 , 10, 11940	4.9	3
233	A data-driven medication score predicts 10-year mortality among aging adults. <i>Scientific Reports</i> , 2020 , 10, 15760	4.9	1
232	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020 , 69, 2806-2818	0.9	10
231	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
230	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. <i>Nature Communications</i> , 2020 , 11, 6383	17.4	23
229	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. <i>Nature Communications</i> , 2019 , 10, 4329	17.4	58
228	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019 , 105, 15-28	11	12
227	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. <i>American Journal of Human Genetics</i> , 2019 , 104, 1169-1181	11	50

226	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019 , 10, 2154	17.4	81
225	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019 , 51, 1207-1214	36.3	303
224	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019 , 572, 323-338	38.4	69
223	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Population-Ascertained Hyperlipidemias. <i>Journal of the American Heart Association</i> , 2019 , 8, e012415	6	11
222	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019 , 109, 276-287	7	24
221	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. <i>American Journal of Human Genetics</i> , 2019 , 105, 1076-1090	11	16
220	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 58-66	15.1	86
219	Genome-wide association study in Finnish twins highlights the connection between nicotine addiction and neurotrophin signaling pathway. <i>Addiction Biology</i> , 2019 , 24, 549-561	4.6	7
218	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018 , 9, 260	17.4	174
217	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. <i>Neuron</i> , 2018 , 98, 743-753.e4	13.9	42
216	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <i>American Journal of Human Genetics</i> , 2018 , 102, 760-775	11	34
215	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018 , 142, 540-546	7.5	21
214	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018 , 360,	33.3	666
213	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018 , 9, 2606	17.4	53
212	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018 , 9, 3391	17.4	90
211	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018 , 21, 1656-1669	25.5	257
210	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018 , 9, 4285	17.4	76
209	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386

208	Obstructive sleep apnoea and the risk for coronary heart disease and type 2 diabetes: a longitudinal population-based study in Finland. <i>BMJ Open</i> , 2018 , 8, e022752	3	27
207	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. <i>American Journal of Human Genetics</i> , 2018 , 102, 1204-1211	11	59
206	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. <i>European Journal of Human Genetics</i> , 2017 , 25, 477-484	5.3	41
205	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. <i>European Journal of Human Genetics</i> , 2017 , 25, 869-876	5.3	82
204	Family aggregation of cardiovascular disease mortality: a register-based prospective study of pooled Nordic twin cohorts. <i>International Journal of Epidemiology</i> , 2017 , 46, 1223-1229	7.8	5
203	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	29.02	414
202	Does expecting more pain make it more intense? Factors associated with the first week pain trajectories after breast cancer surgery. <i>Pain</i> , 2017 , 158, 922-930	8	32
201	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. <i>International Journal of Cancer</i> , 2017 , 140, 2701-2708	7.5	50
200	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
199	Genome-wide Association Study Identifies 27 Loci Influencing Concentrations of Circulating Cytokines and Growth Factors. <i>American Journal of Human Genetics</i> , 2017 , 100, 40-50	11	133
198	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2017 , 101, 539-551	11	111
197	biMM: efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements. <i>Bioinformatics</i> , 2017 , 33, 2405-2407	7.2	6
196	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <i>Genome Biology</i> , 2017 , 18, 146	18.3	27
195	Clinical Prediction Model and Tool for Assessing Risk of Persistent Pain After Breast Cancer Surgery. <i>Journal of Clinical Oncology</i> , 2017 , 35, 1660-1667	2.2	54
194	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. <i>European Journal of Cancer</i> , 2017 , 84, 228-238	7.5	56
193	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
192	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017 , 8, 15927	17.4	37
191	Fine-Scale Genetic Structure in Finland. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3459-3468	3.2	50

190	Genetic loci associated with coronary artery disease harbor evidence of selection and antagonistic pleiotropy. <i>PLoS Genetics</i> , 2017 , 13, e1006328	6	39
189	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , 2017 , 49, 1450-1457	36.3	136
188	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
187	Genetic support for the causal role of insulin in coronary heart disease. <i>Diabetologia</i> , 2016 , 59, 2369-2377	10.3	11
186	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016 , 17, 874	4.5	56
185	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
184	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016 , 6, 35278	4.9	18
183	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016 , 7, 11122	17.4	335
182	USF1 deficiency activates brown adipose tissue and improves cardiometabolic health. <i>Science Translational Medicine</i> , 2016 , 8, 323ra13	17.5	46
181	Variation at 2q35 (PNKD and TMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2016 , 25, 2349-2359	5.6	27
180	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
179	metaCCA: summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis. <i>Bioinformatics</i> , 2016 , 32, 1981-9	7.2	76
178	FINEMAP: efficient variable selection using summary data from genome-wide association studies. <i>Bioinformatics</i> , 2016 , 32, 1493-501	7.2	303
177	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016 , 24, 521-8	5.3	19
176	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. <i>PLoS Genetics</i> , 2016 , 12, e1006327	6	38
175	Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. <i>PLoS Genetics</i> , 2016 , 12, e1006379	6	14
174	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. <i>PLoS ONE</i> , 2016 , 11, e0163877	3.7	15
173	The Contribution of GWAS Loci in Familial Dyslipidemias. <i>PLoS Genetics</i> , 2016 , 12, e1006078	6	38

172	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016 , 115, 266-72	8.7	39
171	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016 , 53, 441-9	5.8	27
170	Genetic Risk Scores Predict Recurrence of Acute Coronary Syndrome. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 172-8		16
169	Genomic prediction of coronary heart disease. <i>European Heart Journal</i> , 2016 , 37, 3267-3278	9.5	184
168	Genome-wide time-to-event analysis on smoking progression stages in a family-based study. <i>Brain and Behavior</i> , 2016 , 6, e00462	3.4	12
167	Metabolite profiling and cardiovascular event risk: a prospective study of 3 population-based cohorts. <i>Circulation</i> , 2015 , 131, 774-85	16.7	367
166	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. <i>Diabetes</i> , 2015 , 64, 1841-52	5.29	50
165	Hierarchical Bayesian model for rare variant association analysis integrating genotype uncertainty in human sequence data. <i>Genetic Epidemiology</i> , 2015 , 39, 89-100	2.6	8
164	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
163	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
162	Genetically determined height and coronary artery disease. <i>New England Journal of Medicine</i> , 2015 , 372, 1608-18	59.2	152
161	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
160	The Biomarker GlycA Is Associated with Chronic Inflammation and Predicts Long-Term Risk of Severe Infection. <i>Cell Systems</i> , 2015 , 1, 293-301	10.6	113
159	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
158	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
157	Mondo-Mlx Mediates Organismal Sugar Sensing through the Gli-Similar Transcription Factor Sugarbabe. <i>Cell Reports</i> , 2015 , 13, 350-64	10.6	56
156	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015 , 11, e1005230	6	59
155	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. <i>PLoS Genetics</i> , 2015 , 11, e1005498	5.498	80

154	Genetic Loci Associated with Allergic Sensitization in Lithuanians. <i>PLoS ONE</i> , 2015 , 10, e0134188	3.7	3
153	Genetic Variants on Chromosome 1p13.3 Are Associated with Non-ST Elevation Myocardial Infarction and the Expression of DRAM2 in the Finnish Population. <i>PLoS ONE</i> , 2015 , 10, e0140576	3.7	5
152	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2015 , 44, 578-86	7.8	97
151	Pharmacogenomics of hypertension: a genome-wide, placebo-controlled cross-over study, using four classes of antihypertensive drugs. <i>Journal of the American Heart Association</i> , 2015 , 4, e001521	6	54
150	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015 , 6, 8658	17.4	79
149	Comparative Analysis of Whole-Genome Sequences of Influenza A(H1N1)pdm09 Viruses Isolated from Hospitalized and Nonhospitalized Patients Identifies Missense Mutations That Might Be Associated with Patient Hospital Admissions in Finland during 2009 to 2014. <i>Genome Announcements</i> , 2015 , 5, e00001-5		5
148	Genome-Wide Analysis of Evolutionary Markers of Human Influenza A(H1N1)pdm09 and A(H3N2) Viruses May Guide Selection of Vaccine Strain Candidates. <i>Genome Biology and Evolution</i> , 2015 , 7, 3472-83	3.9	14
147	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31
146	Targeted resequencing of the pericentromere of chromosome 2 linked to constitutional delay of growth and puberty. <i>PLoS ONE</i> , 2015 , 10, e0128524	3.7	8
145	Allele-specific regulation of DISC1 expression by miR-135b-5p. <i>European Journal of Human Genetics</i> , 2014 , 22, 840-3	5.3	14
144	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. <i>Human Molecular Genetics</i> , 2014 , 23, 4452-64	5.6	66
143	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014 , 46, 669-77	36.3	104
142	Towards a molecular systems model of coronary artery disease. <i>Current Cardiology Reports</i> , 2014 , 16, 488	4.2	16
141	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2014 , 2, 719-29	18.1	250
140	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
139	Assessing multivariate gene-metabolome associations with rare variants using Bayesian reduced rank regression. <i>Bioinformatics</i> , 2014 , 30, 2026-34	7.2	18
138	Regularized machine learning in the genetic prediction of complex traits. <i>PLoS Genetics</i> , 2014 , 10, e1004054	4.54	86
137	Metabolic signatures of adiposity in young adults: Mendelian randomization analysis and effects of weight change. <i>PLoS Medicine</i> , 2014 , 11, e1001765	11.6	193

136	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
135	Chromosome X-wide association study identifies Loci for fasting insulin and height and evidence for incomplete dosage compensation. <i>PLoS Genetics</i> , 2014 , 10, e1004127	6	46
134	High risk population isolate reveals low frequency variants predisposing to intracranial aneurysms. <i>PLoS Genetics</i> , 2014 , 10, e1004134	6	43
133	Bayesian latent variable collapsing model for detecting rare variant interaction effect in twin study. <i>Genetic Epidemiology</i> , 2014 , 38, 310-24	2.6	1
132	Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. <i>PLoS Genetics</i> , 2014 , 10, e1004147	6	42
131	Biomarker profiling by nuclear magnetic resonance spectroscopy for the prediction of all-cause mortality: an observational study of 17,345 persons. <i>PLoS Medicine</i> , 2014 , 11, e1001606	11.6	206
130	The challenges of genome-wide interaction studies: lessons to learn from the analysis of HDL blood levels. <i>PLoS ONE</i> , 2014 , 9, e109290	3.7	12
129	Deletion of TOP3 β component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. <i>Nature Neuroscience</i> , 2013 , 16, 1228-1237	25.5	110
128	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
127	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597
126	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. <i>Human Molecular Genetics</i> , 2013 , 22, 2735-47	5.6	138
125	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013 , 45, 1238-1243	36.3	1244
124	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
123	Diagnostic efficacy of myeloperoxidase to identify acute coronary syndrome in subjects with chest pain. <i>Annals of Medicine</i> , 2013 , 45, 322-7	1.5	6
122	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013 , 45, 145-54	36.3	505
121	From genetic discovery to future personalized health research. <i>New Biotechnology</i> , 2013 , 30, 291-5	6.4	19
120	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013 , 45, 422-7, 427e1-2	36.3	624
119	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437

118	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563
117	Genetic risk prediction and a 2-stage risk screening strategy for coronary heart disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013 , 33, 2261-6	9.4	105
116	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
115	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. <i>PLoS Medicine</i> , 2013 , 10, e1001474	11.6	144
114	Genomic, transcriptomic, and lipidomic profiling highlights the role of inflammation in individuals with low high-density lipoprotein cholesterol. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013 , 33, 847-57	9.4	33
113	Genomic association analysis of common variants influencing antihypertensive response to hydrochlorothiazide. <i>Hypertension</i> , 2013 , 62, 391-7	8.5	79
112	How could use of genetic markers prevent coronary heart disease events?. <i>Personalized Medicine</i> , 2013 , 10, 769-771	2.2	1
111	The molecular genetic architecture of self-employment. <i>PLoS ONE</i> , 2013 , 8, e60542	3.7	28
110	A genome-wide analysis of populations from European Russia reveals a new pole of genetic diversity in northern Europe. <i>PLoS ONE</i> , 2013 , 8, e58552	3.7	24
109	Partial sleep restriction activates immune response-related gene expression pathways: experimental and epidemiological studies in humans. <i>PLoS ONE</i> , 2013 , 8, e77184	3.7	53
108	Pain in 1,000 women treated for breast cancer: a prospective study of pain sensitivity and postoperative pain. <i>Anesthesiology</i> , 2013 , 119, 1410-21	4.3	69
107	Effect of catechol-o-methyltransferase-gene (COMT) variants on experimental and acute postoperative pain in 1,000 women undergoing surgery for breast cancer. <i>Anesthesiology</i> , 2013 , 119, 1422-33	4.3	47
106	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. <i>Lancet, The</i> , 2012 , 380, 572-80	40	1523
105	A common variant near the KCNJ2 gene is associated with T-peak to T-end interval. <i>Heart Rhythm</i> , 2012 , 9, 1099-103	6.7	8
104	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
103	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012 , 21, 4805-15	5.6	24
102	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. <i>Nature Genetics</i> , 2012 , 44, 269-76	36.3	441
101	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. <i>Human Molecular Genetics</i> , 2012 , 21, 1444-55	5.6	74

100	Adipose tissue gene expression analysis reveals changes in inflammatory, mitochondrial respiratory and lipid metabolic pathways in obese insulin-resistant subjects. <i>BMC Medical Genomics</i> , 2012 , 5, 9	3.7	53
99	Impact of common variation in bone-related genes on type 2 diabetes and related traits. <i>Diabetes</i> , 2012 , 61, 2176-86	0.9	25
98	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012 , 490, 267-72	50.4	304
97	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--a meta-analysis of three independent studies. <i>PLoS ONE</i> , 2012 , 7, e28931	3.7	25
96	Work-related exhaustion and telomere length: a population-based study. <i>PLoS ONE</i> , 2012 , 7, e40186	3.7	61
95	Genome-wide screen for metabolic syndrome susceptibility Loci reveals strong lipid gene contribution but no evidence for common genetic basis for clustering of metabolic syndrome traits. <i>Circulation: Cardiovascular Genetics</i> , 2012 , 5, 242-9		153
94	Support for involvement of glutamate decarboxylase 1 and neuropeptide Y in anxiety susceptibility. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012 , 159B, 316-27 ^{3.5}		30
93	Metabolic signatures of insulin resistance in 7,098 young adults. <i>Diabetes</i> , 2012 , 61, 1372-80	0.9	224
92	Analysis of detailed phenotype profiles reveals CHRNA5-CHRNA3-CHRNA4 gene cluster association with several nicotine dependence traits. <i>Nicotine and Tobacco Research</i> , 2012 , 14, 720-33	4.9	48
91	Novel Loci for metabolic networks and multi-tissue expression studies reveal genes for atherosclerosis. <i>PLoS Genetics</i> , 2012 , 8, e1002907	6	125
90	Increased genetic vulnerability to smoking at CHRNA5 in early-onset smokers. <i>Archives of General Psychiatry</i> , 2012 , 69, 854-60		65
89	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
88	Pubertal timing and growth influences cardiometabolic risk factors in adult males and females. <i>Diabetes Care</i> , 2012 , 35, 850-6	14.6	85
87	A genome-wide association study of monozygotic twin-pairs suggests a locus related to variability of serum high-density lipoprotein cholesterol. <i>Twin Research and Human Genetics</i> , 2012 , 15, 691-9	2.2	25
86	The rocky road to personalized medicine: computational and statistical challenges. <i>Personalized Medicine</i> , 2012 , 9, 109-114	2.2	4
85	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011 , 43, 753-60	36.3	237
84	SNPs and coronary heart disease [Authors' reply]. <i>Lancet, The</i> , 2011 , 377, 379-380	40	
83	The genetic structure of the Swedish population. <i>PLoS ONE</i> , 2011 , 6, e22547	3.7	53

82	Genetic architecture of circulating lipid levels. <i>European Journal of Human Genetics</i> , 2011 , 19, 813-9	5.3	19
81	Psychiatric comorbidity in couples: a longitudinal study of 202,959 married and cohabiting individuals. <i>Social Psychiatry and Psychiatric Epidemiology</i> , 2011 , 46, 623-33	4.5	26
80	Missing value imputation in longitudinal measures of alcohol consumption. <i>International Journal of Methods in Psychiatric Research</i> , 2011 , 20, 50-61	4.3	27
79	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. <i>Circulation</i> , 2011 , 123, 731-8	16.7	395
78	Associations of nicotine intake measures with CHRN genes in Finnish smokers. <i>Nicotine and Tobacco Research</i> , 2011 , 13, 686-90	4.9	15
77	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung disease, and their joint effects on lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011 , 184, 786-95	10.2	112
76	SAIL--a software system for sample and phenotype availability across biobanks and cohorts. <i>Bioinformatics</i> , 2011 , 27, 589-91	7.2	12
75	Genetic variants and blood pressure in a population-based cohort: the Cardiovascular Risk in Young Finns study. <i>Hypertension</i> , 2011 , 58, 1079-85	8.5	43
74	Association of known loci with lipid levels among children and prediction of dyslipidemia in adults. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 673-80		33
73	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011 , 43, 1082-90	36.3	313
72	Phenotype mining in CNV carriers from a population cohort. <i>Human Molecular Genetics</i> , 2011 , 20, 2686-95	5.6	13
71	A genome-wide screen for interactions reveals a new locus on 4p15 modifying the effect of waist-to-hip ratio on total cholesterol. <i>PLoS Genetics</i> , 2011 , 7, e1002333	6	25
70	NordicDB: a Nordic pool and portal for genome-wide control data. <i>European Journal of Human Genetics</i> , 2010 , 18, 1322-6	5.3	12
69	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
68	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
67	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010 , 42, 36-44	36.3	430
66	Sequence variants at CHRNA3-CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010 , 42, 448-53	36.3	582
65	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724

64	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
63	Childhood adversities are associated with shorter telomere length at adult age both in individuals with an anxiety disorder and controls. <i>PLoS ONE</i> , 2010 , 5, e10826	3.7	212
62	Genetic association and interaction analysis of USF1 and APOA5 on lipid levels and atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 346-52	9.4	34
61	European lactase persistence genotype shows evidence of association with increase in body mass index. <i>Human Molecular Genetics</i> , 2010 , 19, 1129-36	5.6	50
60	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. <i>Genome Research</i> , 2010 , 20, 1344-51	9.7	40
59	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 2264-76	9.4	318
58	Common variants at 10 genomic loci influence hemoglobin A _{1c} levels via glycemic and nonglycemic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314
57	An immune response network associated with blood lipid levels. <i>PLoS Genetics</i> , 2010 , 6, e1001113	6	87
56	Use of genome-wide expression data to mine the "Gray Zone" of GWA studies leads to novel candidate obesity genes. <i>PLoS Genetics</i> , 2010 , 6, e1000976	6	56
55	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
54	A multilocus genetic risk score for coronary heart disease: case-control and prospective cohort analyses. <i>Lancet, The</i> , 2010 , 376, 1393-400	40	411
53	Metabonomic, transcriptomic, and genomic variation of a population cohort. <i>Molecular Systems Biology</i> , 2010 , 6, 441	12.2	187
52	Distinct variants at LIN28B influence growth in height from birth to adulthood. <i>American Journal of Human Genetics</i> , 2010 , 86, 773-82	11	68
51	Geographical structure and differential natural selection among North European populations. <i>Genome Research</i> , 2009 , 19, 804-14	9.7	68
50	Association of serum cotinine level with a cluster of three nicotinic acetylcholine receptor genes (CHRNA3/CHRNA5/CHRNA4) on chromosome 15. <i>Human Molecular Genetics</i> , 2009 , 18, 4007-12	5.6	134
49	GENESTAT: an information portal for design and analysis of genetic association studies. <i>European Journal of Human Genetics</i> , 2009 , 17, 533-6	5.3	5
48	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. <i>Nature Genetics</i> , 2009 , 41, 47-55	36.3	708
47	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009 , 41, 35-46	36.3	588

46	Association of variants in DISC1 with psychosis-related traits in a large population cohort. <i>Archives of General Psychiatry</i> , 2009 , 66, 134-41		49
45	Forty-three loci associated with plasma lipoprotein size, concentration, and cholesterol content in genome-wide analysis. <i>PLoS Genetics</i> , 2009 , 5, e1000730	6	265
44	Further evidence for the role of ENPP1 in obesity: association with morbid obesity in Finns. <i>Obesity</i> , 2008 , 16, 2113-9	8	13
43	Gender differences in genetic risk profiles for cardiovascular disease. <i>PLoS ONE</i> , 2008 , 3, e3615	3.7	66
42	A random change point model for assessing variability in repeated measures of cognitive function. <i>Statistics in Medicine</i> , 2008 , 27, 5786-98	2.3	29
41	Conditional models accounting for regression to the mean in observational multi-wave panel studies on alcohol consumption. <i>Addiction</i> , 2008 , 103, 24-31	4.6	8
40	The genome-wide patterns of variation expose significant substructure in a founder population. <i>American Journal of Human Genetics</i> , 2008 , 83, 787-94	11	116
39	A longitudinal Swedish study on screening for squamous cell carcinoma and adenocarcinoma: evidence of effectiveness and overtreatment. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007 , 16, 2641-8	4	35
38	Determinants of changes in bone density: a 5-year follow-up study of adult male monozygotic twins. <i>Journal of Clinical Densitometry</i> , 2007 , 10, 408-14	3.5	1
37	Determinants of the progression in lumbar degeneration: a 5-year follow-up study of adult male monozygotic twins. <i>Spine</i> , 2006 , 31, 671-8	3.3	103
36	Three-state frailty model for age at onset of dementia and death in Swedish twins. <i>Genetic Epidemiology</i> , 2003 , 24, 139-49	2.6	12
35	The influence of mortality on twin models of change: addressing missingness through multiple imputation. <i>Behavior Genetics</i> , 2003 , 33, 161-9	3.2	16
34	Maximum likelihood inference for multivariate frailty models using an automated Monte Carlo EM algorithm. <i>Lifetime Data Analysis</i> , 2002 , 8, 349-60	1.3	28
33	Coding haplotype analysis supports HCR as the putative susceptibility gene for psoriasis at the MHC PSORS1 locus. <i>Human Molecular Genetics</i> , 2002 , 11, 589-97	5.6	106
32	Fitting exponential family mixed models. <i>Statistical Modelling</i> , 2002 , 2, 23-38	0.7	1
31	Bayesian association mapping for quantitative traits in a mixture of two populations. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S692-9	2.6	16
30	Joint modeling of genetic association and population stratification using latent class models. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S409-14	2.6	8
29	Educational differences in lung cancer mortality in male smokers. <i>International Journal of Epidemiology</i> , 2001 , 30, 264-7	7.8	27

28	Estimation of multivariate frailty models using penalized partial likelihood. <i>Biometrics</i> , 2000 , 56, 1016-22.	18	244
27	Effect of vitamin E and beta carotene on the incidence of primary nonfatal myocardial infarction and fatal coronary heart disease. <i>Archives of Internal Medicine</i> , 1998 , 158, 668-75		204
26	Prostate cancer and supplementation with alpha-tocopherol and beta-carotene: incidence and mortality in a controlled trial. <i>Journal of the National Cancer Institute</i> , 1998 , 90, 440-6	9.7	744
25	Randomised trial of alpha-tocopherol and beta-carotene supplements on incidence of major coronary events in men with previous myocardial infarction. <i>Lancet, The</i> , 1997 , 349, 1715-20	40	480
24	Polygenic risk, susceptibility genes, and breast cancer over the life course		1
23	Haplotype sharing provides insights into fine-scale population history and disease in Finland		2
22	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals		4
21	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries		1
20	Coronary artery disease risk and lipidomic profiles are similar in familial and population-ascertained hyperlipidemias		
19	ANGPTL8 protein-truncating variant and the risk of coronary disease, type 2 diabetes and adverse effects		2
18	Whole genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom		2
17	The rate of false polymorphisms introduced when imputing genotypes from global imputation panels		6
16	Communicating polygenic and non-genetic risk for atherosclerotic cardiovascular disease - An observational follow-up study		8
15	Genome-wide Screen of Otosclerosis in Population Biobanks: 18 Loci and Shared Heritability with Skeletal Structure		3
14	Phenome-wide association studies (PheWAS) across large real-world data population cohorts support drug target validation		5
13	Trans-ancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders		7
12	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation		1
11	Refining fine-mapping: effect sizes and regional heritability		17

10	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis	175
9	Genetics of human plasma lipidome: Understanding lipid metabolism and its link to diseases beyond traditional lipids	5
8	Geographic variation and bias in polygenic scores of complex diseases and traits in Finland	5
7	Advantages of genotype imputation with ethnically matched reference panel for rare variant association analyses	5
6	Genetics of 38 blood and urine biomarkers in the UK Biobank	25
5	Polygenic and clinical risk scores and their impact on age at onset of cardiometabolic diseases and common cancers	6
4	CCR5-del32 is not deleterious in the homozygous state in humans	2
3	Quantifying the impact of rare and ultra-rare coding variation across the phenotypic spectrum	1
2	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles	2
1	FinnGen: Unique genetic insights from combining isolated population and national health register data	11