Samuli Ripatti

List of Publications by Citations

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	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
278	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
277	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
276	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
275	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
274	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
273	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
272	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
271	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
270	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
269	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
268	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
267	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
266	Prostate cancer and supplementation with alpha-tocopherol and beta-carotene: incidence and mortality in a controlled trial. *Journal of the National Cancer Institute*, **1998**, 90, 440-6	9.7	744
265	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, 949-60	36.3	724
264	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708
263	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666

262	Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2	36.3	624
261	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
260	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
259	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. *Nature Genetics*, **2009**, 41, 35-46	36.3	588
258	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
257	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
256	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
255	Randomised trial of alpha-tocopherol and beta-carotene supplements on incidence of major coronary events in men with previous myocardial infarction. *Lancet, The*, **1997**, 349, 1715-20	40	480
254	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. *Nature Genetics*, **2012**, 44, 269-76	36.3	441
253	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
252	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
251	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
250	A multilocus genetic risk score for coronary heart disease: case-control and prospective cohort analyses. *Lancet, The*, **2010**, 376, 1393-400	40	411
249	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
248	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
247	Metabolite profiling and cardiovascular event risk: a prospective study of 3 population-based cohorts. *Circulation*, **2015**, 131, 774-85	16.7	367
246	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
245	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. *Nature Communications*, **2016**, 7, 11122	17.4	335

244	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 2264-76	9.4	318
243	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
242	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
241	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
240	FINEMAP: efficient variable selection using summary data from genome-wide association studies. *Bioinformatics*, **2016**, 32, 1493-501	7.2	303
239	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. *Nature Genetics*, **2019**, 51, 1207-1214	36.3	303
238	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
237	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
236	Forty-three loci associated with plasma lipoprotein size, concentration, and cholesterol content in genome-wide analysis. *PLoS Genetics*, **2009**, 5, e1000730	6	265
235	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nature Neuroscience*, **2018**, 21, 1656-1669	25.5	257
234	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 719-29	18.1	250
233	Estimation of multivariate frailty models using penalized partial likelihood. *Biometrics*, **2000**, 56, 1016-22	1.8	244
232	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243
231	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
230	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
229	Metabolic signatures of insulin resistance in 7,098 young adults. *Diabetes*, **2012**, 61, 1372-80	0.9	224
228	Childhood adversities are associated with shorter telomere length at adult age both in individuals with an anxiety disorder and controls. *PLoS ONE*, **2010**, 5, e10826	3.7	212
227	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	11.6	206

226	Effect of vitamin E and beta carotene on the incidence of primary nonfatal myocardial infarction and fatal coronary heart disease. *Archives of Internal Medicine*, **1998**, 158, 668-75		204
225	Metabolic signatures of adiposity in young adults: Mendelian randomization analysis and effects of weight change. *PLoS Medicine*, **2014**, 11, e1001765	11.6	193
224	Metabonomic, transcriptomic, and genomic variation of a population cohort. *Molecular Systems Biology*, **2010**, 6, 441	12.2	187
223	Genomic prediction of coronary heart disease. *European Heart Journal*, **2016**, 37, 3267-3278	9.5	184
222	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
221	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
220	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
219	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
218	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. *Circulation: Cardiovascular Genetics*, **2012**, 5, 242-9		153
217	Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18	59.2	152
216	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
215	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. *Human Molecular Genetics*, **2013**, 22, 2735-47	5.6	138
214	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*, **2017**, 49, 1450-1457	36.3	136
213	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, 4007-12	5.6	134
212	Genome-wide Association Study Identifies 27 Loci Influencing Concentrations of Circulating Cytokines and Growth Factors. *American Journal of Human Genetics*, **2017**, 100, 40-50	11	133
211	Novel Loci for metabolic networks and multi-tissue expression studies reveal genes for atherosclerosis. *PLoS Genetics*, **2012**, 8, e1002907	6	125
210	The genome-wide patterns of variation expose significant substructure in a founder population. *American Journal of Human Genetics*, **2008**, 83, 787-94	11	116
209	The Biomarker GlycA Is Associated with Chronic Inflammation and Predicts Long-Term Risk of Severe Infection. *Cell Systems*, **2015**, 1, 293-301	10.6	113

208	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung disease, and their joint effects on lung function. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 184, 786-95	10.2	112
207	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. *American Journal of Human Genetics*, **2017**, 101, 539-551	11	111
206	Deletion of TOP3β, a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. *Nature Neuroscience*, **2013**, 16, 1228-1237	25.5	110
205	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. *Nature Medicine*, **2020**, 26, 549-557	50.5	109
204	Coding haplotype analysis supports HCR as the putative susceptibility gene for psoriasis at the MHC PSORS1 locus. *Human Molecular Genetics*, **2002**, 11, 589-97	5.6	106
203	Genetic risk prediction and a 2-stage risk screening strategy for coronary heart disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 2261-6	9.4	105
202	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
201	Determinants of the progression in lumbar degeneration: a 5-year follow-up study of adult male monozygotic twins. *Spine*, **2006**, 31, 671-8	3.3	103
200	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. *International Journal of Epidemiology*, **2015**, 44, 578-86	7.8	97
199	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
198	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
197	An immune response network associated with blood lipid levels. *PLoS Genetics*, **2010**, 6, e1001113	6	87
196	Regularized machine learning in the genetic prediction of complex traits. *PLoS Genetics*, **2014**, 10, e1004754	7	86
195	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
194	Pubertal timing and growth influences cardiometabolic risk factors in adult males and females. *Diabetes Care*, **2012**, 35, 850-6	14.6	85
193	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. *European Journal of Human Genetics*, **2017**, 25, 869-876	5.3	82
192	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81
191	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81

190	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. *PLoS Genetics*, **2015**, 11, e1005498	6	80
189	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
188	Genomic association analysis of common variants influencing antihypertensive response to hydrochlorothiazide. *Hypertension*, **2013**, 62, 391-7	8.5	79
187	Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, **2021**, 53, 185-194	36.3	78
186	metaCCA: summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis. *Bioinformatics*, **2016**, 32, 1981-9	7.2	76
185	Phenome-wide association studies across large population cohorts support drug target validation. *Nature Communications*, **2018**, 9, 4285	17.4	76
184	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. *Human Molecular Genetics*, **2012**, 21, 1444-55	5.6	74
183	Exome sequencing of Finnish isolates enhances rare-variant association power. *Nature*, **2019**, 572, 323-328	38.4	69
182	Pain in 1,000 women treated for breast cancer: a prospective study of pain sensitivity and postoperative pain. *Anesthesiology*, **2013**, 119, 1410-21	4.3	69
181	Geographical structure and differential natural selection among North European populations. *Genome Research*, **2009**, 19, 804-14	9.7	68
180	Distinct variants at LIN28B influence growth in height from birth to adulthood. *American Journal of Human Genetics*, **2010**, 86, 773-82	11	68
179	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. *Human Molecular Genetics*, **2014**, 23, 4452-64	5.6	66
178	Gender differences in genetic risk profiles for cardiovascular disease. *PLoS ONE*, **2008**, 3, e3615	3.7	66
177	Increased genetic vulnerability to smoking at CHRNA5 in early-onset smokers. *Archives of General Psychiatry*, **2012**, 69, 854-60		65
176	Work-related exhaustion and telomere length: a population-based study. *PLoS ONE*, **2012**, 7, e40186	3.7	61
175	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. *Nature Genetics*, **2021**, 53, 1300-1310	36.3	60
174	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
173	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. *American Journal of Human Genetics*, **2018**, 102, 1204-1211	11	59

172	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. *Nature Communications*, **2019**, 10, 4329	17.4	58
171	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. *BMC Genomics*, **2016**, 17, 874	4.5	56
170	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. *European Journal of Cancer*, **2017**, 84, 228-238	7.5	56
169	Mondo-Mlx Mediates Organismal Sugar Sensing through the Gli-Similar Transcription Factor Sugarbabe. *Cell Reports*, **2015**, 13, 350-64	10.6	56
168	Use of genome-wide expression data to mine the "Gray Zone" of GWA studies leads to novel candidate obesity genes. *PLoS Genetics*, **2010**, 6, e1000976	6	56
167	Clinical Prediction Model and Tool for Assessing Risk of Persistent Pain After Breast Cancer Surgery. *Journal of Clinical Oncology*, **2017**, 35, 1660-1667	2.2	54
166	Pharmacogenomics of hypertension: a genome-wide, placebo-controlled cross-over study, using four classes of antihypertensive drugs. *Journal of the American Heart Association*, **2015**, 4, e001521	6	54
165	Evaluating drug targets through human loss-of-function genetic variation. *Nature*, **2020**, 581, 459-464	50.4	53
164	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nature Communications*, **2018**, 9, 2606	17.4	53
163	Adipose tissue gene expression analysis reveals changes in inflammatory, mitochondrial respiratory and lipid metabolic pathways in obese insulin-resistant subjects. *BMC Medical Genomics*, **2012**, 5, 9	3.7	53
162	The genetic structure of the Swedish population. *PLoS ONE*, **2011**, 6, e22547	3.7	53
161	Partial sleep restriction activates immune response-related gene expression pathways: experimental and epidemiological studies in humans. *PLoS ONE*, **2013**, 8, e77184	3.7	53
160	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. *International Journal of Cancer*, **2017**, 140, 2701-2708	7.5	50
159	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. *American Journal of Human Genetics*, **2019**, 104, 1169-1181	11	50
158	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. *Diabetes*, **2015**, 64, 1841-52	9	50
157	Fine-Scale Genetic Structure in Finland. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3459-3468	3.2	50
156	European lactase persistence genotype shows evidence of association with increase in body mass index. *Human Molecular Genetics*, **2010**, 19, 1129-36	5.6	50
155	Association of variants in DISC1 with psychosis-related traits in a large population cohort. *Archives of General Psychiatry*, **2009**, 66, 134-41		49

154	Analysis of detailed phenotype profiles reveals CHRNA5-CHRNA3-CHRNB4 gene cluster association with several nicotine dependence traits. *Nicotine and Tobacco Research*, **2012**, 14, 720-33	4.9	48
153	Effect of catechol-o-methyltransferase-gene (COMT) variants on experimental and acute postoperative pain in 1,000 women undergoing surgery for breast cancer. *Anesthesiology*, **2013**, 119, 1422-33	4.3	47
152	USF1 deficiency activates brown adipose tissue and improves cardiometabolic health. *Science Translational Medicine*, **2016**, 8, 323ra13	17.5	46
151	Chromosome X-wide association study identifies Loci for fasting insulin and height and evidence for incomplete dosage compensation. *PLoS Genetics*, **2014**, 10, e1004127	6	46
150	High risk population isolate reveals low frequency variants predisposing to intracranial aneurysms. *PLoS Genetics*, **2014**, 10, e1004134	6	43
149	Genetic variants and blood pressure in a population-based cohort: the Cardiovascular Risk in Young Finns study. *Hypertension*, **2011**, 58, 1079-85	8.5	43
148	A large-scale genome-wide association study meta-analysis of cannabis use disorder. *Lancet Psychiatry,the*, **2020**, 7, 1032-1045	23.3	43
147	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. *Neuron*, **2018**, 98, 743-753.e4	13.9	42
146	Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. *PLoS Genetics*, **2014**, 10, e1004147	6	42
145	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. *European Journal of Human Genetics*, **2017**, 25, 477-484	5.3	41
144	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. *Genome Research*, **2010**, 20, 1344-51	9.7	40
143	Genetic loci associated with coronary artery disease harbor evidence of selection and antagonistic pleiotropy. *PLoS Genetics*, **2017**, 13, e1006328	6	39
142	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. *British Journal of Cancer*, **2016**, 115, 266-72	8.7	39
141	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. *PLoS Genetics*, **2016**, 12, e1006327	6	38
140	The Contribution of GWAS Loci in Familial Dyslipidemias. *PLoS Genetics*, **2016**, 12, e1006078	6	38
139	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nature Communications*, **2017**, 8, 15927	17.4	37
138	Sleep apnoea is a risk factor for severe COVID-19. *BMJ Open Respiratory Research*, **2021**, 8,	5.6	37
137	A longitudinal Swedish study on screening for squamous cell carcinoma and adenocarcinoma: evidence of effectiveness and overtreatment. *Cancer Epidemiology Biomarkers and Prevention*, **2007**, 16, 2641-8	4	35

136	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. *American Journal of Human Genetics*, **2018**, 102, 760-775	11	34
135	Genetic association and interaction analysis of USF1 and APOA5 on lipid levels and atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 346-52	9.4	34
134	Genomic, transcriptomic, and lipidomic profiling highlights the role of inflammation in individuals with low high-density lipoprotein cholesterol. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 847-57	9.4	33
133	Association of known loci with lipid levels among children and prediction of dyslipidemia in adults. *Circulation: Cardiovascular Genetics*, **2011**, 4, 673-80		33
132	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
131	Does expecting more pain make it more intense? Factors associated with the first week pain trajectories after breast cancer surgery. *Pain*, **2017**, 158, 922-930	8	32
130	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
129	Support for involvement of glutamate decarboxylase 1 and neuropeptide Y in anxiety susceptibility. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 316-27	3.5	30
128	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
127	A random change point model for assessing variability in repeated measures of cognitive function. *Statistics in Medicine*, **2008**, 27, 5786-98	2.3	29
126	The molecular genetic architecture of self-employment. *PLoS ONE*, **2013**, 8, e60542	3.7	28
125	Maximum likelihood inference for multivariate frailty models using an automated Monte Carlo EM algorithm. *Lifetime Data Analysis*, **2002**, 8, 349-60	1.3	28
124	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. *Genome Biology*, **2017**, 18, 146	18.3	27
123	Variation at 2q35 (PNKD and TMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. *Human Molecular Genetics*, **2016**, 25, 2349-2359	5.6	27
122	Missing value imputation in longitudinal measures of alcohol consumption. *International Journal of Methods in Psychiatric Research*, **2011**, 20, 50-61	4.3	27
121	Educational differences in lung cancer mortality in male smokers. *International Journal of Epidemiology*, **2001**, 30, 264-7	7.8	27
120	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
119	Obstructive sleep apnoea and the risk for coronary heart disease and type 2 diabetes: a longitudinal population-based study in Finland. *BMJ Open*, **2018**, 8, e022752	3	27

118	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002725	5.2	26
117	Psychiatric comorbidity in couples: a longitudinal study of 202,959 married and cohabiting individuals. *Social Psychiatry and Psychiatric Epidemiology*, **2011**, 46, 623-33	4.5	26
116	Impact of common variation in bone-related genes on type 2 diabetes and related traits. *Diabetes*, **2012**, 61, 2176-86	0.9	25
115	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. *PLoS ONE*, **2012**, 7, e28931	3.7	25
114	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	6	25
113	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, 691-9	2.2	25
112	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. *Nature Medicine*, **2021**, 27, 1876-1884	50.5	25
111	Genetics of 38 blood and urine biomarkers in the UK Biobank		25
110	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
109	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
108	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
107	A genome-wide analysis of populations from European Russia reveals a new pole of genetic diversity in northern Europe. *PLoS ONE*, **2013**, 8, e58552	3.7	24
106	Genetic Influences on Patient-Oriented Outcomes in Traumatic Brain Injury: A Living Systematic Review of Non-Apolipoprotein E Single-Nucleotide Polymorphisms. *Journal of Neurotrauma*, **2021**, 38, 1107-1123	5.4	24
105	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. *Nature Communications*, **2020**, 11, 6383	17.4	23
104	Genome-wide association meta-analysis of nicotine metabolism and cigarette consumption measures in smokers of European descent. *Molecular Psychiatry*, **2021**, 26, 2212-2223	15.1	22
103	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. *International Journal of Cancer*, **2018**, 142, 540-546	7.5	21
102	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. *European Journal of Human Genetics*, **2016**, 24, 521-8	5.3	19
101	From genetic discovery to future personalized health research. *New Biotechnology*, **2013**, 30, 291-5	6.4	19

100	Genetic architecture of circulating lipid levels. *European Journal of Human Genetics*, **2011**, 19, 813-9	5.3	19
99	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
98	Assessing multivariate gene-metabolome associations with rare variants using Bayesian reduced rank regression. *Bioinformatics*, **2014**, 30, 2026-34	7.2	18
97	Refining fine-mapping: effect sizes and regional heritability		17
96	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. *European Respiratory Journal*, **2021**, 57,	13.6	17
95	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	11	16
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