Aarno Palotie

List of Publications by Citations

213 papers	31,953 citations	63 h-index	178 g-index
241 ext. papers	43,517 ext. citations	14.2 avg, IF	5.65 L-index

#	Paper	IF	Citations
213	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
212	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
211	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
210	Synaptic, transcriptional and chromatin genes disrupted in autism. *Nature*, **2014**, 515, 209-15	50.4	1581
209	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
208	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. *Nature*, **2012**, 488, 96-9	50.4	1194
207	De novo mutations in schizophrenia implicate synaptic networks. *Nature*, **2014**, 506, 179-84	50.4	1163
206	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
205	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
204	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
203	A framework for the interpretation of de novo mutation in human disease. *Nature Genetics*, **2014**, 46, 944-50	36.3	656
202	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530
201	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nature Genetics*, **2018**, 50, 912-919	36.3	475
200	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. *Nature Genetics*, **2012**, 44, 269-76	36.3	441
199	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
198	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
197	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355

196	Genome-wide association study reveals three susceptibility loci for common migraine in the general population. *Nature Genetics*, **2011**, 43, 695-8	36.3	295
195	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. *Nature Genetics*, **2010**, 42, 869-73	36.3	277
194	Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nature Genetics*, **2013**, 45, 912-917	36.3	276
193	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
192	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
191	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
190	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243
189	Genome-wide association analysis identifies susceptibility loci for migraine without aura. *Nature Genetics*, **2012**, 44, 777-82	36.3	243
188	Genetic and environmental influences on migraine: a twin study across six countries. *Twin Research and Human Genetics*, **2003**, 6, 422-31		231
187	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
186	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
185	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
184	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
183	Genomic prediction of coronary heart disease. *European Heart Journal*, **2016**, 37, 3267-3278	9.5	184
182	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
181	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
180	A recurrent de novo mutation in KCNC1 causes progressive myoclonus epilepsy. *Nature Genetics*, **2015**, 47, 39-46	36.3	177
179	De novo loss- or gain-of-function mutations in KCNA2 cause epileptic encephalopathy. *Nature Genetics*, **2015**, 47, 393-399	36.3	162

178	De novo variants in neurodevelopmental disorders with epilepsy. *Nature Genetics*, **2018**, 50, 1048-1053	36.3	139
177	A genome-wide association study of depressive symptoms. *Biological Psychiatry*, **2013**, 73, 667-78	7.9	135
176	The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. *Nature Genetics*, **2017**, 49, 1167-1173	36.3	132
175	A susceptibility locus for migraine with aura, on chromosome 4q24. *American Journal of Human Genetics*, **2002**, 70, 652-62	11	129
174	A central role for GRB10 in regulation of islet function in man. *PLoS Genetics*, **2014**, 10, e1004235	6	124
173	Identification of novel genetic Loci associated with thyroid peroxidase antibodies and clinical thyroid disease. *PLoS Genetics*, **2014**, 10, e1004123	6	122
172	The genome-wide patterns of variation expose significant substructure in a founder population. *American Journal of Human Genetics*, **2008**, 83, 787-94	11	116
171	Deletion of TOP3β, a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. *Nature Neuroscience*, **2013**, 16, 1228-1237	25.5	110
170	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
169	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
168	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. *Molecular Psychiatry*, **2020**, 25, 1859-1875	15.1	106
167	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
166	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. *Nature Neuroscience*, **2017**, 20, 1661-1668	25.5	95
165	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
164	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
163	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
162	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
161	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81

160	CHD2 variants are a risk factor for photosensitivity in epilepsy. *Brain*, **2015**, 138, 1198-207	11.2	81
159	O5.5. SLEEP IN MAJOR PSYCHIATRIC DISORDERS: RESULTS FROM NATIONWIDE SUPER FINLAND STUDY. *Schizophrenia Bulletin*, **2018**, 44, S88-S88	1.3	78
158	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
157	Phenome-wide association studies across large population cohorts support drug target validation. *Nature Communications*, **2018**, 9, 4285	17.4	76
156	A high-density association screen of 155 ion transport genes for involvement with common migraine. *Human Molecular Genetics*, **2008**, 17, 3318-31	5.6	73
155	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. *Cell Reports*, **2017**, 21, 2597-2613	10.6	71
154	Shared genetic basis for migraine and ischemic stroke: A genome-wide analysis of common variants. *Neurology*, **2015**, 84, 2132-45	6.5	71
153	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
152	Exome sequencing of Finnish isolates enhances rare-variant association power. *Nature*, **2019**, 572, 323-328	38.4	69
151	Towards a European consensus for reporting incidental findings during clinical NGS testing. *European Journal of Human Genetics*, **2015**, 23, 1601-6	5.3	69
150	Describing the genetic architecture of epilepsy through heritability analysis. *Brain*, **2014**, 137, 2680-9	11.2	63
149	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. *Nature Neuroscience*, **2016**, 19, 1563-1565	25.5	63
148	Genome-wide Polygenic Burden of Rare Deleterious Variants in Sudden Unexpected Death in Epilepsy. *EBioMedicine*, **2015**, 2, 1063-70	8.8	61
147	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
146	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. *Nature Communications*, **2019**, 10, 4329	17.4	58
145	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. *European Journal of Cancer*, **2017**, 84, 228-238	7.5	56
144	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. *Circulation*, **2018**, 137, 222-232	16.7	53
143	Analysis of Tie receptor tyrosine kinase in haemopoietic progenitor and leukaemia cells. *British Journal of Haematology*, **1997**, 98, 195-203	4.5	53

142	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. *International Journal of Cancer*, **2017**, 140, 2701-2708	7.5	50
141	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
140	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. *Diabetes*, **2015**, 64, 1841-52	7.9	50
139	Fine-Scale Genetic Structure in Finland. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3459-3468	3.2	50
138	Genome-wide studies of verbal declarative memory in nondemented older people: the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. *Biological Psychiatry*, **2015**, 77, 749-63	7.9	48
137	The effect of LRRK2 loss-of-function variants in humans. *Nature Medicine*, **2020**, 26, 869-877	50.5	47
136	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. *Nature Communications*, **2021**, 12, 1258	17.4	47
135	Genetic analysis for a shared biological basis between migraine and coronary artery disease. *Neurology: Genetics*, **2015**, 1, e10	3.8	46
134	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
133	Biallelic Variants in UBA5 Link Dysfunctional UFM1 Ubiquitin-like Modifier Pathway to Severe Infantile-Onset Encephalopathy. *American Journal of Human Genetics*, **2016**, 99, 683-694	11	43
132	High risk population isolate reveals low frequency variants predisposing to intracranial aneurysms. *PLoS Genetics*, **2014**, 10, e1004134	6	43
131	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. *Neuron*, **2018**, 98, 743-753.e4	13.9	42
130	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
129	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. *PLoS Genetics*, **2018**, 14, e1007329	6	41
128	Genome-wide association study of intracranial aneurysm identifies a new association on chromosome 7. *Stroke*, **2014**, 45, 3194-9	6.7	41
127	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. *Nature Communications*, **2019**, 10, 1252	17.4	40
126	Stratification by smoking status reveals an association of CHRNA5-A3-B4 genotype with body mass index in never smokers. *PLoS Genetics*, **2014**, 10, e1004799	6	40
125	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

124	A cross-population atlas of genetic associations for 220 human phenotypes. *Nature Genetics*, **2021**, 53, 1415-1424	36.3	40
123	Gain-of-function mutation of the SCN5A gene causes exercise-induced polymorphic ventricular arrhythmias. *Circulation: Cardiovascular Genetics*, **2014**, 7, 771-81		39
122	Heavier smoking may lead to a relative increase in waist circumference: evidence for a causal relationship from a Mendelian randomisation meta-analysis. The CARTA consortium. *BMJ Open*, **2015**, 5, e008808	3	39
121	Clinical and morphological correlations for transglutaminase 1 gene mutations in autosomal recessive congenital ichthyosis. *European Journal of Human Genetics*, **1999**, 7, 625-32	5.3	39
120	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. *British Journal of Cancer*, **2016**, 115, 266-72	8.7	39
119	The Contribution of GWAS Loci in Familial Dyslipidemias. *PLoS Genetics*, **2016**, 12, e1006078	6	38
118	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
117	Diagnostic implications of genetic copy number variation in epilepsy plus. *Epilepsia*, **2019**, 60, 689-706	6.4	37
116	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. *American Journal of Human Genetics*, **2019**, 105, 334-350	11	37
115	Genome-wide association study of sleep duration in the Finnish population. *Journal of Sleep Research*, **2014**, 23, 609-618	5.8	37
114	Investigation of GRIN2A in common epilepsy phenotypes. *Epilepsy Research*, **2015**, 115, 95-9	3	37
113	Sleep apnoea is a risk factor for severe COVID-19. *BMJ Open Respiratory Research*, **2021**, 8,	5.6	37
112	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
111	Consistently replicating locus linked to migraine on 10q22-q23. *American Journal of Human Genetics* , **2008**, 82, 1051-63	11	36
110	N-ras gene mutations in acute myeloid leukemia: accurate detection by solid-phase minisequencing. *International Journal of Cancer*, **1992**, 50, 713-8	7.5	36
109	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
108	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. *American Journal of Human Genetics*, **2018**, 102, 760-775	11	34
107	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33

106	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. *Cephalalgia*, **2016**, 36, 648-57	6.1	31
105	Mitochondrial EFTs defects in juvenile-onset Leigh disease, ataxia, neuropathy, and optic atrophy. *Neurology*, **2014**, 83, 743-51	6.5	30
104	Systematic re-evaluation of genes from candidate gene association studies in migraine using a large genome-wide association data set. *Cephalalgia*, **2016**, 36, 604-14	6.1	29
103	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
102	Dysfunctional ADAM22 implicated in progressive encephalopathy with cortical atrophy and epilepsy. *Neurology: Genetics*, **2016**, 2, e46	3.8	28
101	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. *Genome Biology*, **2017**, 18, 146	18.3	27
100	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
99	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
98	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002725	5.2	26
97	Simultaneous impairment of neuronal and metabolic function of mutated gephyrin in a patient with epileptic encephalopathy. *EMBO Molecular Medicine*, **2015**, 7, 1580-94	12	26
96	Apolipoprotein E4 Polymorphism and Outcomes from Traumatic Brain Injury: A Living Systematic Review and Meta-Analysis. *Journal of Neurotrauma*, **2021**, 38, 1124-1136	5.4	26
95	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. *Cephalalgia*, **2015**, 35, 489-99	6.1	25
94	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
93	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
92	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. *Nature Communications*, **2020**, 11, 6383	17.4	23
91	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. *Nature Communications*, **2020**, 11, 3368	17.4	22
90	The contribution of CACNA1A, ATP1A2 and SCN1A mutations in hemiplegic migraine: A clinical and genetic study in Finnish migraine families. *Cephalalgia*, **2018**, 38, 1849-1863	6.1	22
89	Genetics of migraine. *Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn*, **2018**, 148, 493-503	3	22

88	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
87	Independent evidence for an association between general cognitive ability and a genetic locus for educational attainment. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2015**, 168B, 363-73	3.5	21
86	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. *Nature Communications*, **2020**, 11, 3981	17.4	21
85	CXCR3 Polymorphism and Expression Associate with Spontaneous Preterm Birth. *Journal of Immunology*, **2015**, 195, 2187-98	5.3	20
84	Contribution of rare and common variants to intellectual disability in a sub-isolate of Northern Finland. *Nature Communications*, **2019**, 10, 410	17.4	19
83	From genetic discovery to future personalized health research. *New Biotechnology*, **2013**, 30, 291-5	6.4	19
82	Idiopathic macrocytic anaemia in the aged: molecular and cytogenetic findings. *British Journal of Haematology*, **1995**, 90, 797-803	4.5	19
81	CTCF variants in 39 individuals with a variable neurodevelopmental disorder broaden the mutational and clinical spectrum. *Genetics in Medicine*, **2019**, 21, 2723-2733	8.1	18
80	Enrichment of rare variants in population isolates: single AICDA mutation responsible for hyper-IgM syndrome type 2 in Finland. *European Journal of Human Genetics*, **2016**, 24, 1473-8	5.3	17
79	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. *European Respiratory Journal*, **2021**, 57,	13.6	17
78	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
77	Chromosome 19p13 loci in Finnish migraine with aura families. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2005**, 132B, 85-9	3.5	16
76	Rare coding variants in ten genes confer substantial risk for schizophrenia.. *Nature*, **2022**,	50.4	16
75	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. *PLoS ONE*, **2017**, 12, e0186456	3.7	15
74	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. *PLoS ONE*, **2016**, 11, e0163877	3.7	15
73	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. *International Journal of Epidemiology*, **2020**, 49, 1022-1031	7.8	15
72	Identification of pathogenic variant enriched regions across genes and gene families. *Genome Research*, **2020**, 30, 62-71	9.7	14
71	Epigenetic DNA methylation changes associated with headache chronification: A retrospective case-control study. *Cephalalgia*, **2018**, 38, 312-322	6.1	13

70	Phenotype mining in CNV carriers from a population cohort. *Human Molecular Genetics*, **2011**, 20, 2686-95	5.6	13
69	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles.. *Nature Genetics*, **2022**, 54, 152-160	36.3	13
68	Effects of TM6SF2 E167K on hepatic lipid and very low-density lipoprotein metabolism in humans. *JCI Insight*, **2020**, 5,	9.9	13
67	Roadmap for a precision-medicine initiative in the Nordic region. *Nature Genetics*, **2019**, 51, 924-930	36.3	12
66	Solid-phase minisequencing confirmed by FISH analysis in determination of gene copy number. *Human Genetics*, **1995**, 96, 275-80	6.3	12
65	Shared genetic risk between eating disorder- and substance-use-related phenotypes: Evidence from genome-wide association studies. *Addiction Biology*, **2021**, 26, e12880	4.6	12
64	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. *PLoS Genetics*, **2020**, 16, e1008682	6	11
63	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Population-Ascertained Hyperlipidemias. *Journal of the American Heart Association*, **2019**, 8, e012415	6	11
62	Genome-wide association study of bronchopulmonary dysplasia: a potential role for variants near the CRP gene. *Scientific Reports*, **2017**, 7, 9271	4.9	11
61	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. *Biological Psychiatry*, **2022**, 91, 102-117	7.9	11
60	Serum calcium and risk of migraine: a Mendelian randomization study. *Human Molecular Genetics*, **2017**, 26, 820-828	5.6	11
59	FinnGen: Unique genetic insights from combining isolated population and national health register data		11
58	Involvement of astrocyte and oligodendrocyte gene sets in migraine. *Cephalalgia*, **2016**, 36, 640-7	6.1	10
57	High-resolution fluorescence in situ hybridization: a new approach in genome mapping. *Annals of Medicine*, **1996**, 28, 101-6	1.5	10
56	Progressive myoclonus epilepsies-Residual unsolved cases have marked genetic heterogeneity including dolichol-dependent protein glycosylation pathway genes. *American Journal of Human Genetics*, **2021**, 108, 722-738	11	10
55	A Colorimetric Minisequencing Assay for the Mutation in Codon 506 of the Coagulation Factor V Gene. *Thrombosis and Haemostasis*, **1997**, 77, 701-703	7	9
54	Combined effects of genotype and childhood adversity shape variability of DNA methylation across age. *Translational Psychiatry*, **2021**, 11, 88	8.6	9
53	Phenotypic spectrum associated with a CRADD founder variant underlying frontotemporal predominant pachygyria in the Finnish population. *European Journal of Human Genetics*, **2019**, 27, 1235-1243	5.3	8

52	Screening for mutations in the exon 26 of the apolipoprotein B gene in hypercholesterolemic Finnish families by the single-strand conformation polymorphism method. *Human Mutation*, **1994**, 4, 217-23	4.7	8
51	Targeted resequencing of the pericentromere of chromosome 2 linked to constitutional delay of growth and puberty. *PLoS ONE*, **2015**, 10, e0128524	3.7	8
50	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. *PLoS Genetics*, **2021**, 17, e1009501	6	8
49	Genomic prediction of alcohol-related morbidity and mortality. *Translational Psychiatry*, **2020**, 10, 23	8.6	7
48	Trans-ancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders		7
47	Biallelic loss-of-function P4HTM gene variants cause hypotonia, hypoventilation, intellectual disability, dysautonomia, epilepsy, and eye abnormalities (HIDEA syndrome). *Genetics in Medicine*, **2019**, 21, 2355-2363	8.1	6
46	Antenatal gene tests in low-risk pregnancies: molecular screening for aspartylglucosaminuria (AGU) and infantile neuronal ceroid lipofuscinosis (INCL) in Finland. *Prenatal Diagnosis*, **2001**, 21, 409-12	3.2	6
45	Development of molecular genetic methods for monitoring myeloid malignancies. *Scandinavian Journal of Clinical and Laboratory Investigation*, **1993**, 213, 29-38	2	6
44	Polygenic and clinical risk scores and their impact on age at onset of cardiometabolic diseases and common cancers		6
43	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. *European Journal of Human Genetics*, **2021**, 29, 309-324	5.3	6
42	Guideline-based and bioinformatic reassessment of lesion-associated gene and variant pathogenicity in focal human epilepsies. *Epilepsia*, **2018**, 59, 2145-2152	6.4	6
41	Breakpoint mapping and haplotype analysis of translocation t(1;12)(q43;q21.1) in two apparently independent families with vascular phenotypes. *Molecular Genetics & Genomic Medicine*, **2018**, 6, 56-68	2.3	5
40	Family-specific aggregation of lipid GWAS variants confers the susceptibility to familial hypercholesterolemia in a large Austrian family. *Atherosclerosis*, **2017**, 264, 58-66	3.1	5
39	Genetic Variants on Chromosome 1p13.3 Are Associated with Non-ST Elevation Myocardial Infarction and the Expression of DRAM2 in the Finnish Population. *PLoS ONE*, **2015**, 10, e0140576	3.7	5
38	No evidence for genome-wide interactions on plasma fibrinogen by smoking, alcohol consumption and body mass index: results from meta-analyses of 80,607 subjects. *PLoS ONE*, **2014**, 9, e111156	3.7	5
37	Advantages of genotype imputation with ethnically matched reference panel for rare variant association analyses		5
36	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
35	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. *European Journal of Human Genetics*, **2021**, 29, 615-624	5.3	5

34	Genetic associations of protein-coding variants in human disease.. *Nature*, **2022**, 603, 95-102	50.4	5
33	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci.. *Nature Communications*, **2022**, 13, 1644	17.4	5
32	How Communicating Polygenic and Clinical Risk for Atherosclerotic Cardiovascular Disease Impacts Health Behavior: an Observational Follow-up Study.. *Circulation Genomic and Precision Medicine*, **2022**, CIRCGEN121003459	5.2	4
31	The relation of severe malocclusion to patients?mental and behavioral disorders, growth, and speech problems. *European Journal of Orthodontics*, **2021**, 43, 159-164	3.3	4
30	Independent and cumulative coeliac disease-susceptibility loci are associated with distinct disease phenotypes. *Journal of Human Genetics*, **2021**, 66, 613-623	4.3	4
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