Aarno Palotie

List of Publications by Year in descending order

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216 papers	51,301 citations	10979 71 h-index	2125 203 g-index
241 all docs	241 docs citations	241 times ranked	69807 citing authors

#	Article	IF	Citations
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
2	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
5	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
6	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
7	A mutation in APP protects against Alzheimerâ€™s disease and age-related cognitive decline. Nature, 2012, 488, 96-99.	13.7	1,442
8	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
9	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
10	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
11	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	9.4	943
12	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
13	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
14	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
15	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
16	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
17	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
18	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520

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19	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	9.4	516
20	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
21	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.	9.4	426
22	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
23	Genome-wide association study reveals three susceptibility loci for common migraine in the general population. Nature Genetics, 2011, 43, 695-698.	9.4	355
24	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
25	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
26	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
27	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
28	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
29	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
30	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	9.4	294
31	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
32	Genetic and Environmental Influences on Migraine: A Twin Study Across Six Countries. Twin Research and Human Genetics, 2003, 6, 422-431.	1.3	285
33	Biomarker Profiling by Nuclear Magnetic Resonance Spectroscopy for the Prediction of All-Cause Mortality: An Observational Study of 17,345 Persons. PLoS Medicine, 2014, 11, e1001606.	3.9	281
34	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.	15.2	281
35	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	1.0	277
36	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261

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37	A recurrent de novo mutation in KCNC1 causes progressive myoclonus epilepsy. Nature Genetics, 2015, 47, 39-46.	9.4	245
38	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
39	De novo variants in neurodevelopmental disorders with epilepsy. Nature Genetics, 2018, 50, 1048-1053.	9.4	230
40	De novo loss- or gain-of-function mutations in KCNA2 cause epileptic encephalopathy. Nature Genetics, 2015, 47, 393-399.	9.4	224
41	The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. Nature Genetics, 2017, 49, 1167-1173.	9.4	200
42	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
43	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
44	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.	1.4	181
45	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
46	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
47	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
48	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
49	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	1.5	150
50	A Genome-Wide Association Study of Depressive Symptoms. Biological Psychiatry, 2013, 73, 667-678.	0.7	149
51	Genetic Risk Prediction and a 2-Stage Risk Screening Strategy for Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2261-2266.	1.1	147
52	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
53	A Susceptibility Locus for Migraine with Aura, on Chromosome 4q24. American Journal of Human Genetics, 2002, 70, 652-662.	2.6	146
54	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	7.1	144

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55	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	9.4	135
56	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	5.8	134
57	The Genome-wide Patterns of Variation Expose Significant Substructure in a Founder Population. American Journal of Human Genetics, 2008, 83, 787-794.	2.6	132
58	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
59	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
60	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
61	CHD2variants are a risk factor for photosensitivity in epilepsy. Brain, 2015, 138, 1198-1208.	3.7	112
62	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
63	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
64	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	1.5	105
65	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613.	2.9	103
66	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102
67	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. Nature Communications, 2020, 11, 6383.	5.8	101
68	Sleep apnoea is a risk factor for severe COVID-19. BMJ Open Respiratory Research, 2021, 8, e000845.	1.2	92
69	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
70	A high-density association screen of 155 ion transport genes for involvement with common migraine. Human Molecular Genetics, 2008, 17, 3318-3331.	1.4	90
71	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
72	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. American Journal of Human Genetics, 2019, 104, 1169-1181.	2.6	90

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73	Describing the genetic architecture of epilepsy through heritability analysis. Brain, 2014, 137, 2680-2689.	3.7	87
74	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232.	1.6	87
75	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	0.8	86
76	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.	2.6	86
77	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. Nature Communications, 2020, 11, 3981.	5.8	86
78	Towards a European consensus for reporting incidental findings during clinical NGS testing. European Journal of Human Genetics, 2015, 23, 1601-1606.	1.4	85
79	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. European Respiratory Journal, 2021, 57, 2003091.	3.1	85
80	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	1.3	81
81	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	15.2	79
82	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
83	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	2.3	76
84	Genome-wide Polygenic Burden of Rare Deleterious Variants in Sudden Unexpected Death in Epilepsy. EBioMedicine, 2015, 2, 1063-1070.	2.7	74
85	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
86	Biallelic Variants in UBA5 Link Dysfunctional UFM1ÂUbiquitin-like Modifier Pathway to Severe Infantile-Onset Encephalopathy. American Journal of Human Genetics, 2016, 99, 683-694.	2.6	72
87	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
88	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, 749-763.	0.7	67
89	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. Nature Communications, 2019, 10, 1252.	5.8	67
90	Genetic associations of protein-coding variants in human disease. Nature, 2022, 603, 95-102.	13.7	67

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91	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
92	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
93	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
94	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
95	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
96	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
97	Diagnostic implications of genetic copy number variation in epilepsy plus. Epilepsia, 2019, 60, 689-706.	2.6	61
98	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
99	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.	1.4	60
100	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	1.6	60
101	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	2.9	57
102	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	2.6	57
103	Analysis of Tie receptor tyrosine kinase in haemopoietic progenitor and leukaemia cells. British Journal of Haematology, 1997, 98, 195-203.	1.2	55
104	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	1.5	55
105	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.	0.8	54
106	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: TableÂ1. BMJ Open, 2015, 5, e008808.	0.8	53
107	How Communicating Polygenic and Clinical Risk for Atherosclerotic Cardiovascular Disease Impacts Health Behavior: an Observational Follow-up Study. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003459.	1.6	53
108	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. Genome Research, 2010, 20, 1344-1351.	2.4	52

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109	Genome-Wide Association Study of Intracranial Aneurysm Identifies a New Association on Chromosome 7. Stroke, 2014, 45, 3194-3199.	1.0	52
110	Apolipoprotein E4 Polymorphism and Outcomes from Traumatic Brain Injury: A Living Systematic Review and Meta-Analysis. Journal of Neurotrauma, 2021, 38, 1124-1136.	1.7	51
111	Gain-of-Function Mutation of the SCN5A Gene Causes Exercise-Induced Polymorphic Ventricular Arrhythmias. Circulation: Cardiovascular Genetics, 2014, 7, 771-781.	5.1	49
112	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
113	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	1.5	48
114	CTCF variants in 39 individuals with a variable neurodevelopmental disorder broaden the mutational and clinical spectrum. Genetics in Medicine, 2019, 21, 2723-2733.	1.1	48
115	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
116	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
117	Identification of pathogenic variant enriched regions across genes and gene families. Genome Research, 2020, 30, 62-71.	2.4	47
118	Clinical and morphological correlations for transglutaminase 1 gene mutations in autosomal recessive congenital ichthyosis. European Journal of Human Genetics, 1999, 7, 625-632.	1.4	46
119	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. Genome Biology, 2017, 18, 146.	3.8	46
120	Stratification by Smoking Status Reveals an Association of CHRNA5-A3-B4 Genotype with Body Mass Index in Never Smokers. PLoS Genetics, 2014, 10, e1004799.	1.5	45
121	Genomeâ€wide association study of sleep duration in the <scp>F</scp>innish population. Journal of Sleep Research, 2014, 23, 609-618.	1.7	44
122	Investigation of GRIN2A in common epilepsy phenotypes. Epilepsy Research, 2015, 115, 95-99.	0.8	44
123	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.	1.7	43
124	N-ras gene mutations in acute myeloid leukemia: Accurate detection by solid-phase minisequencing. International Journal of Cancer, 1992, 50, 713-718.	2.3	42
125	Systematic re-evaluation of genes from candidate gene association studies in migraine using a large genome-wide association data set. Cephalalgia, 2016, 36, 604-614.	1.8	41
126	Progressive myoclonus epilepsiesâ€”Residual unsolved cases have marked genetic heterogeneity including dolichol-dependent protein glycosylation pathway genes. American Journal of Human Genetics, 2021, 108, 722-738.	2.6	41

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127	Consistently Replicating Locus Linked to Migraine on 10q22-q23. American Journal of Human Genetics, 2008, 82, 1051-1063.	2.6	40
128	Simultaneous impairment of neuronal and metabolic function of mutated gephyrin in a patient with epileptic encephalopathy. EMBO Molecular Medicine, 2015, 7, 1580-1594.	3.3	39
129	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.	1.8	38
130	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
131	Effects of TM6SF2 E167K on hepatic lipid and very low-density lipoprotein metabolism in humans. JCI Insight, 2020, 5, .	2.3	38
132	Variation at 2q35 (PNKDandTMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. Human Molecular Genetics, 2016, 25, 2349-2359.	1.4	37
133	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
134	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	3.0	34
135	Dysfunctional ADAM22 implicated in progressive encephalopathy with cortical atrophy and epilepsy. Neurology: Genetics, 2016, 2, e46.	0.9	33
136	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
137	Contribution of rare and common variants to intellectual disability in a sub-isolate of Northern Finland. Nature Communications, 2019, 10, 410.	5.8	32
138	Mitochondrial EFTs defects in juvenile-onset Leigh disease, ataxia, neuropathy, and optic atrophy. Neurology, 2014, 83, 743-751.	1.5	31
139	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. American Journal of Human Genetics, 2019, 105, 1076-1090.	2.6	31
140	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. PLoS Genetics, 2020, 16, e1008682.	1.5	31
141	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. Nature Genetics, 2022, 54, 772-782.	9.4	29
142	Shared genetic risk between eating disorderâ€•and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
143	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. PLoS Genetics, 2021, 17, e1009501.	1.5	28
144	Combined effects of genotype and childhood adversity shape variability of DNA methylation across age. Translational Psychiatry, 2021, 11, 88.	2.4	27

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145	CXCR3 Polymorphism and Expression Associate with Spontaneous Preterm Birth. Journal of Immunology, 2015, 195, 2187-2198.	0.4	26
146	Serum calcium and risk of migraine: a Mendelian randomization study. Human Molecular Genetics, 2017, 26, ddw416.	1.4	26
147	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	2.3	26
148	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, 168, 363-373.	1.1	25
149	Epigenetic DNA methylation changes associated with headache chronification: A retrospective case-control study. Cephalalgia, 2018, 38, 312-322.	1.8	25
150	Genetics of migraine. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 148, 493-503.	1.0	25
151	Lifetime risk of rheumatoid arthritis-associated interstitial lung disease in MUC5B mutation carriers. Annals of the Rheumatic Diseases, 2021, 80, 1530-1536.	0.5	25
152	From genetic discovery to future personalized health research. New Biotechnology, 2013, 30, 291-295.	2.4	24
153	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Populationâ€Ascertained Hyperlipidemias. Journal of the American Heart Association, 2019, 8, e012415.	1.6	24
154	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. PLoS ONE, 2016, 11, e0163877.	1.1	23
155	Idiopathic macrocytic anaemia in the aged: molecular and cytogenetic findings. British Journal of Haematology, 1995, 90, 797-803.	1.2	22
156	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, 1473-1478.	1.4	22
157	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	9.4	22
158	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	2.6	22
159	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. Nature Communications, 2022, 13, .	5.8	22
160	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.	1.1	19
161	Genomic prediction of alcohol-related morbidity and mortality. Translational Psychiatry, 2020, 10, 23.	2.4	19
162	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. European Journal of Human Genetics, 2021, 29, 309-324.	1.4	19

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163	Genome-wide association study of bronchopulmonary dysplasia: a potential role for variants near the CRP gene. Scientific Reports, 2017, 7, 9271.	1.6	18
164	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. PLoS ONE, 2017, 12, e0186456.	1.1	18
165	Chromosome 19p13 loci in Finnish migraine with aura families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 132B, 85-89.	1.1	17
166	The relation of severe malocclusion to patientsâ€™ mental and behavioral disorders, growth, and speech problems. European Journal of Orthodontics, 2021, 43, 159-164.	1.1	17
167	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. European Journal of Human Genetics, 2021, 29, 615-624.	1.4	17
168	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
169	A genome-wide association study of outcome from traumatic brain injury. EBioMedicine, 2022, 77, 103933.	2.7	17
170	Solid-phase minisequencing confirmed by FISH analysis in determination of gene copy number. Human Genetics, 1995, 96, 275-80.	1.8	15
171	Involvement of astrocyte and oligodendrocyte gene sets in migraine. Cephalalgia, 2016, 36, 640-647.	1.8	15
172	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.	1.4	14
173	Phenotype mining in CNV carriers from a population cohort â€. Human Molecular Genetics, 2011, 20, 2686-2695.	1.4	13
174	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12
175	High-resolution FluorescenceIn SituHybridization: A New Approach in Genome Mapping. Annals of Medicine, 1996, 28, 101-106.	1.5	11
176	Independent and cumulative coeliac disease-susceptibility loci are associated with distinct disease phenotypes. Journal of Human Genetics, 2021, 66, 613-623.	1.1	11
177	A Colorimetric Minisequencing Assay for the Mutation in Codon 506 of the Coagulation Factor V Gene. Thrombosis and Haemostasis, 1997, 77, 701-703.	1.8	10
178	Targeted Resequencing of the Pericentromere of Chromosome 2 Linked to Constitutional Delay of Growth and Puberty. PLoS ONE, 2015, 10, e0128524.	1.1	10
179	Comprehensive genome-wide association study of different forms of hernia identifies more than 80 associated loci. Nature Communications, 2022, 13, .	5.8	9
180	Development of molecular genetic methods for monitoring myeloid malignancies. Scandinavian Journal of Clinical and Laboratory Investigation, 1993, 53, 29-38.	0.6	8

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181	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, 217-223.	1.1	8
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183	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.	0.6	8
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