Matti Pirinen

List of Publications by Year in descending order

100 papers	19,803 citations	66250 44 h-index	36203 101 g-index
126 all docs	126 docs citations	126 times ranked	35515 citing authors

#	Article	IF	Citations
1	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
2	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
3	Traumatic brain injury: integrated approaches to improve prevention, clinical care, and research. Lancet Neurology, The, 2017, 16, 987-1048.	4.9	1,571
4	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
5	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
7	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
8	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
9	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
10	FINEMAP: efficient variable selection using summary data from genome-wide association studies. Bioinformatics, 2016, 32, 1493-1501.	1.8	584
11	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576
12	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	9.4	469
13	The fine-scale genetic structure of the British population. Nature, 2015, 519, 309-314.	13.7	416
14	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	9.4	375
15	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
16	Case-mix, care pathways, and outcomes in patients with traumatic brain injury in CENTER-TBI: a European prospective, multicentre, longitudinal, cohort study. Lancet Neurology, The, 2019, 18, 923-934.	4.9	304
17	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
18	The landscape of genomic imprinting across diverse adult human tissues. Genome Research, 2015, 25, 927-936.	2.4	216

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19	Reappraisal of known malaria resistance loci in a large multicenter study. Nature Genetics, 2014, 46, 1197-1204.	9.4	206
20	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. Human Molecular Genetics, 2011, 20, 345-353.	1.4	202
21	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.	2.6	200
22	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
23	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	9.4	162
24	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
25	metaCCA: summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis. Bioinformatics, 2016, 32, 1981-1989.	1.8	138
26	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
27	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
28	Machine learning algorithms performed no better than regression models for prognostication in traumatic brain injury. Journal of Clinical Epidemiology, 2020, 122, 95-107.	2.4	117
29	Tumour budding in oral squamous cell carcinoma: a meta-analysis. British Journal of Cancer, 2018, 118, 577-586.	2.9	115
30	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. Nature Communications, 2020, 11, 6383.	5.8	101
31	Efficient computation with a linear mixed model on large-scale data sets with applications to genetic studies. Annals of Applied Statistics, 2013, 7, .	0.5	98
32	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509.	1.5	95
33	Including known covariates can reduce power to detect genetic effects in case-control studies. Nature Genetics, 2012, 44, 848-851.	9.4	94
34	Assessing allele-specific expression across multiple tissues from RNA-seq read data. Bioinformatics, 2015, 31, 2497-2504.	1.8	90
35	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology,the, 2018, 5, e333-e345.	2.2	90
36	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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37	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	9.4	86
38	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	0.8	86
39	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
40	Machine learning in oral squamous cell carcinoma: Current status, clinical concerns and prospects for futureâ€”A systematic review. Artificial Intelligence in Medicine, 2021, 115, 102060.	3.8	74
41	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	5.8	73
42	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	5.8	72
43	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
44	Chromosome X-Wide Association Study Identifies Loci for Fasting Insulin and Height and Evidence for Incomplete Dosage Compensation. PLoS Genetics, 2014, 10, e1004127.	1.5	61
45	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
46	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	1.6	60
47	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
48	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	1.5	48
49	Human genetic and metabolite variation reveals that methylthioadenosine is a prognostic biomarker and an inflammatory regulator in sepsis. Science Advances, 2017, 3, e1602096.	4.7	46
50	Genome-wide association meta-analysis of nicotine metabolism and cigarette consumption measures in smokers of European descent. Molecular Psychiatry, 2021, 26, 2212-2223.	4.1	45
51	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. Biological Psychiatry, 2014, 75, 386-397.	0.7	44
52	Comparison of nomogram with machine learning techniques for prediction of overall survival in patients with tongue cancer. International Journal of Medical Informatics, 2021, 145, 104313.	1.6	42
53	Clinical significance of tumor-stroma ratio in head and neck cancer: a systematic review and meta-analysis. BMC Cancer, 2021, 21, 480.	1.1	41
54	Fluid balance and outcome in critically ill patients with traumatic brain injury (CENTER-TBI and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 20, 627-638.	4.9	40

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55	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	2.6	39
56	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. Human Molecular Genetics, 2014, 23, 3316-3326.	1.4	37
57	Effect of frailty on 6-month outcome after traumatic brain injury: a multicentre cohort study with external validation. Lancet Neurology, The, 2022, 21, 153-162.	4.9	34
58	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	3.0	34
59	The genetic associations of acute anterior uveitis and their overlap with the genetics of ankylosing spondylitis. Genes and Immunity, 2016, 17, 46-51.	2.2	33
60	The prognostic value of immune checkpoints in oral squamous cell carcinoma. Oral Diseases, 2019, 25, 1435-1445.	1.5	33
61	Contribution of rare and common variants to intellectual disability in a sub-isolate of Northern Finland. Nature Communications, 2019, 10, 410.	5.8	32
62	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. Human Molecular Genetics, 2013, 22, 4653-4660.	1.4	29
63	Risk of nontyphoidal Salmonella bacteraemia in African children is modified by STAT4. Nature Communications, 2018, 9, 1014.	5.8	29
64	Assessing multivariate gene-metabolome associations with rare variants using Bayesian reduced rank regression. Bioinformatics, 2014, 30, 2026-2034.	1.8	28
65	Bayesian metaâ€analysis across genomeâ€wide association studies of diverse phenotypes. Genetic Epidemiology, 2019, 43, 532-547.	0.6	27
66	Does evaluation of tumour budding in diagnostic biopsies have a clinical relevance? A systematic review. Histopathology, 2019, 74, 536-544.	1.6	26
67	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
68	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. Cell Reports, 2021, 37, 110020.	2.9	25
69	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
70	Estimating genealogies from unlinked marker data: A Bayesian approach. Theoretical Population Biology, 2007, 72, 305-322.	0.5	23
71	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21
72	Tracheal intubation in traumatic brain injury: a multicentre prospective observational study. British Journal of Anaesthesia, 2020, 125, 505-517.	1.5	19

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73	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
74	Estimating population haplotype frequencies from pooled SNP data using incomplete database information. Bioinformatics, 2009, 25, 3296-3302.	1.8	18
75	Integration of questionnaire-based risk factors improves polygenic risk scores for human coronary heart disease and type 2 diabetes. Communications Biology, 2022, 5, 158.	2.0	18
76	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
77	Association of social isolation, loneliness and genetic risk with incidence of dementia: UK Biobank Cohort Study. BMJ Open, 2022, 12, e053936.	0.8	16
78	Genetic support for the causal role of insulin in coronary heart disease. Diabetologia, 2016, 59, 2369-2377.	2.9	14
79	The budding and depth of invasion model in oral cancer: A systematic review and metaâ€analysis. Oral Diseases, 2022, 28, 275-283.	1.5	14
80	Estimating Haplotype Frequencies by Combining Data from Large DNA Pools with Database Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 36-44.	1.9	12
81	Assessing association between protein truncating variants and quantitative traits. Bioinformatics, 2013, 29, 2419-2426.	1.8	12
82	Genetic variation in VAC14 is associated with bacteremia secondary to diverse pathogens in African children. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3601-E3603.	3.3	12
83	Prognostic value of blood and lymphatic vessel markers in tongue cancer: A systematic review. Cancer Science, 2019, 110, 3424-3433.	1.7	12
84	MetaPhat: Detecting and Decomposing Multivariate Associations From Univariate Genome-Wide Association Statistics. Frontiers in Genetics, 2020, 11, 431.	1.1	12
85	biMM: efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements. Bioinformatics, 2017, 33, 2405-2407.	1.8	11
86	Estimating genealogies from linked marker data: a Bayesian approach. BMC Bioinformatics, 2007, 8, 411.	1.2	9
87	Risk stratification in oral squamous cell carcinoma using staging of the eighth American Joint Committee on Cancer: Systematic review and metaâ€analysis. Head and Neck, 2020, 42, 3002-3017.	0.9	9
88	First genome-wide association study on rocuronium dose requirements shows association with SLCO1A2. British Journal of Anaesthesia, 2021, 126, 949-957.	1.5	9
89	Changes in the fine-scale genetic structure of Finland through the 20th century. PLoS Genetics, 2021, 17, e1009347.	1.5	8
90	Informed consent procedures in patients with an acute inability to provide informed consent: Policy and practice in the CENTER-TBI study. Journal of Critical Care, 2020, 59, 6-15.	1.0	8

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91	Estimating population haplotype frequencies from pooled DNA samples using PHASE algorithm. Genetical Research, 2008, 90, 509-524.	0.3	7
92	Finding Consistent Gene Transmission Patterns on Large and Complex Pedigrees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 252-262.	1.9	6
93	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.	1.1	6
94	NCOR2 is a novel candidate gene for migraine-epilepsy phenotype. Cephalalgia, 2022, 42, 631-644.	1.8	6
95	Bayesian Quantitative Trait Locus Mapping Based on Reconstruction of Recent Genetic Histories. Genetics, 2009, 183, 709-721.	1.2	5
96	Polygenic risk provides biological validity for the ICHD-3 criteria among Finnish migraine families. Cephalalgia, 2022, 42, 345-356.	1.8	5
97	Questionnaires vs Interviews for the Assessment of Global Functional Outcomes After Traumatic Brain Injury. JAMA Network Open, 2021, 4, e2134121.	2.8	5
98	Risk of pneumococcal bacteremia in Kenyan children with glucose-6-phosphate dehydrogenase deficiency. BMC Medicine, 2020, 18, 148.	2.3	4
99	Bayesian model comparison for rare-variant association studies. American Journal of Human Genetics, 2021, 108, 2354-2367.	2.6	2
100	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0