

Juha Karjalainen

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

17,595
citations

108046

37
h-index

242451

47
g-index

64
all docs

64
docs citations

64
times ranked

32554
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
3	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	9.4	1,544
4	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
5	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
6	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
7	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
8	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	13.5	623
9	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	2.6	569
10	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	9.4	560
11	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
12	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
13	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	9.4	310
14	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. <i>Nature Medicine</i> , 2020, 26, 549-557.	15.2	281
15	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. <i>PLoS Genetics</i> , 2013, 9, e1003201.	1.5	247
16	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
17	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13790-13794.	3.3	244
18	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235

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19	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , 2021, 12, 1258.	5.8	196
20	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	13.7	142
21	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021, 53, 663-671.	9.4	124
22	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4329.	5.8	120
23	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	2.6	119
24	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	1.5	115
25	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020, 586, 769-775.	13.7	101
26	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020, 16, e1008629.	1.5	101
27	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013, 45, 542-545.	9.4	96
28	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. <i>Genome Medicine</i> , 2014, 6, 88.	3.6	95
29	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. <i>Genome Medicine</i> , 2015, 7, 30.	3.6	91
30	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. <i>Thorax</i> , 2015, 70, 21-32.	2.7	89
31	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. <i>Nature Communications</i> , 2020, 11, 3981.	5.8	86
32	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. <i>European Respiratory Journal</i> , 2021, 57, 2003091.	3.1	85
33	ImmunoChip SNP array identifies novel genetic variants conferring susceptibility to candidaemia. <i>Nature Communications</i> , 2014, 5, 4675.	5.8	76
34	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. <i>Nature Medicine</i> , 2020, 26, 542-548.	15.2	74
35	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016, 68, 62-74.	3.0	64
36	Shared genetic etiology between idiopathic pulmonary fibrosis and COVID-19 severity. <i>EBioMedicine</i> , 2021, 65, 103277.	2.7	63

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37	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. <i>Human Molecular Genetics</i> , 2015, 24, 397-409.	1.4	54
38	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. <i>PLoS Genetics</i> , 2020, 16, e1008682.	1.5	31
39	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. <i>PLoS Genetics</i> , 2021, 17, e1009501.	1.5	28
40	Mendelian randomization highlights insomnia as a risk factor for pain diagnoses. <i>Sleep</i> , 2021, 44, .	0.6	21
41	Integration of questionnaire-based risk factors improves polygenic risk scores for human coronary heart disease and type 2 diabetes. <i>Communications Biology</i> , 2022, 5, 158.	2.0	18
42	Association of the <i>MYOC</i> p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. <i>JAMA Ophthalmology</i> , 2021, 139, 762.	1.4	7
43	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. <i>PLoS ONE</i> , 2021, 16, e0255402.	1.1	6
44	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.1	2
45	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
46	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
47	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
48	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0