Juha Karjalainen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11460822/publications.pdf

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48	17,595	108046	242451
papers	citations	37 h-index	47 g-index

64	64	64	32554
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. European Respiratory Journal, 2021, 57, 2003091.	3.1	85
3	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
4	Mendelian randomization highlights insomnia as a risk factor for pain diagnoses. Sleep, 2021, 44, .	0.6	21
5	Shared genetic etiology between idiopathic pulmonary fibrosis and COVID-19 severity. EBioMedicine, 2021, 65, 103277.	2.7	63
6	ANGPTL8 protein-truncating variant associated with lower serum triglycerides and risk of coronary disease. PLoS Genetics, 2021, 17, e1009501.	1.5	28
7	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
8	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. JAMA Ophthalmology, 2021, 139, 762.	1.4	7
9	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	1.1	6
10	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
11	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
12	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. Nature Communications, 2020, 11, 3981.	5.8	86
13	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. PLoS Genetics, 2020, 16, e1008682.	1.5	31
14	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	13.7	142
15	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. Nature Medicine, 2020, 26, 542-548.	15.2	74
16	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
17	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	1.5	101
18	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0

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19	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
20	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
21	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
22	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
23	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
24	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
25	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
26	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
27	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
28	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
29	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	3.0	64
30	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. Genome Medicine, 2015, 7, 30.	3.6	91
31	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
32	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
33	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
34	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. Thorax, 2015, 70, 21-32.	2.7	89
35	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
36	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310

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37	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
38	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. Human Molecular Genetics, 2015, 24, 397-409.	1.4	54
39	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
40	Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia. Nature Communications, 2014, 5, 4675.	5.8	76
41	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
42	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. Genome Medicine, 2014, 6, 88.	3.6	95
43	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
44	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
45	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
46	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96
47	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
48	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247