

Reedik MÃ¤gi

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

15,808
citations

236612

25
h-index

414034

32
g-index

38
all docs

38
docs citations

38
times ranked

24036
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	1.4	47
2	Advancing our understanding of genetic risk factors and potential personalized strategies for pelvic organ prolapse. <i>Nature Communications</i> , 2022, 13, .	5.8	7
3	Genomic architecture and prediction of censored time-to-event phenotypes with a Bayesian genome-wide analysis. <i>Nature Communications</i> , 2021, 12, 2337.	5.8	11
4	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
5	Response to comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". <i>Science Translational Medicine</i> , 2021, 13, eabf4530.	5.8	1
6	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002769.	1.6	5
7	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	68
8	Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002932.	1.6	30
9	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. <i>European Journal of Human Genetics</i> , 2019, 27, 442-454.	1.4	29
10	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	9.4	1,331
11	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. <i>European Journal of Human Genetics</i> , 2017, 25, 869-876.	1.4	181
12	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017, 8, 744.	5.8	64
13	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. <i>Human Molecular Genetics</i> , 2017, 26, 3639-3650.	1.4	170
14	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
15	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
16	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 2044.	3.8	143
17	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
18	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823

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19	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. <i>International Journal of Epidemiology</i> , 2015, 44, 1137-1147.	0.9	314
20	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	9.4	365
21	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.3	297
22	A Central Role for GRB10 in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	1.5	164
23	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
24	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	3.9	178
25	Contribution of 32 GWAS-Identified Common Variants to Severe Obesity in European Adults Referred for Bariatric Surgery. <i>PLoS ONE</i> , 2013, 8, e70735.	1.1	39
26	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
27	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
28	Assessing the impact of missing genotype data in rare variant association analysis. <i>BMC Proceedings</i> , 2011, 5, S107.	1.8	8
29	GWAMA: software for genome-wide association meta-analysis. <i>BMC Bioinformatics</i> , 2010, 11, 288.	1.2	456
30	Meta-analysis of sex-specific genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 846-853.	0.6	96
31	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
32	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982