Reedik MÃ¤gi

List of Publications by Year
in descending order

32 papers	15,808 citations	236925 25 h-index	414414 32 g-index
38 all docs	38 docs citations	38 times ranked	24036 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
4	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
5	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
6	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
7	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
8	GWAMA: software for genome-wide association meta-analysis. BMC Bioinformatics, 2010, 11, 288.	2.6	456
9	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
10	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	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.	3.5	331
13	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. International Journal of Epidemiology, 2015, 44, 1137-1147.	1.9	314
14	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
15	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
16	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.	2.8	181
17	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
18	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. Human Molecular Genetics, 2017, 26, 3639-3650.	2.9	170

#	Article	IF	Citations
19	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
20	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
21	Metaâ€analysis of sexâ€specific genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 846-853.	1.3	96
22	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. Science Translational Medicine, 2020, 12, .	12.4	68
23	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
24	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	2.9	47
25	Contribution of 32 GWAS-Identified Common Variants to Severe Obesity in European Adults Referred for Bariatric Surgery. PLoS ONE, 2013, 8, e70735.	2.5	39
26	Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002932.	3.6	30
27	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. European Journal of Human Genetics, 2019, 27, 442-454.	2.8	29
28	Genomic architecture and prediction of censored time-to-event phenotypes with a Bayesian genome-wide analysis. Nature Communications, 2021, 12, 2337.	12.8	11
29	Assessing the impact of missing genotype data in rare variant association analysis. BMC Proceedings, 2011, 5, S107.	1.6	8
30	Advancing our understanding of genetic risk factors and potential personalized strategies for pelvic organ prolapse. Nature Communications, 2022, 13, .	12.8	7
31	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
32	Response to comment on â€œEvaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human geneticsâ€. Science Translational Medicine, 2021, 13, eabf4530.	12.4	1