

Reedik Mgi

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

33
papers

11,057
citations

24
h-index

38
g-index

38
ext. papers

14,016
ext. citations

17
avg, IF

4.37
L-index

#	Paper	IF	Citations
33	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	17.5	
32	Genomic architecture and prediction of censored time-to-event phenotypes with a Bayesian genome-wide analysis. <i>Nature Communications</i> , 2021 , 12, 2337	17.4	2
31	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
30	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,	17.5	27
29	Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002932	5.2	9
28	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
27	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	5.3	13
26	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	36.3	675
25	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	5.3	82
24	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017 , 8, 744	17.4	37
23	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	5.6	67
22	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
21	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
20	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	6	220
19	Copy number variations and cognitive phenotypes in unselected populations. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 2044-54	27.4	96
18	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
17	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687

16	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. <i>International Journal of Epidemiology</i> , 2015 , 44, 1137-47	7.8	175
15	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
14	Impact of type 2 diabetes susceptibility variants on quantitative glycemetic traits reveals mechanistic heterogeneity. <i>Diabetes</i> , 2014 , 63, 2158-71	0.9	235
13	A central role for GRB10 in regulation of islet function in man. <i>PLoS Genetics</i> , 2014 , 10, e1004235	6	124
12	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. <i>PLoS Medicine</i> , 2013 , 10, e1001474	11.6	144
11	Contribution of 32 GWAS-identified common variants to severe obesity in European adults referred for bariatric surgery. <i>PLoS ONE</i> , 2013 , 8, e70735	3.7	34
10	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemetic traits and insulin resistance. <i>Nature Genetics</i> , 2012 , 44, 659-69	36.3	615
9	Large-scale association analyses identify new loci influencing glycemetic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
8	Assessing the impact of missing genotype data in rare variant association analysis. <i>BMC Proceedings</i> , 2011 , 5 Suppl 9, S107	2.3	7
7	Common variants at 10 genomic loci influence hemoglobin A _{1c} levels via glycemetic and nonglycemetic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314
6	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
5	GWAMA: software for genome-wide association meta-analysis. <i>BMC Bioinformatics</i> , 2010 , 11, 288	3.6	342
4	Meta-analysis of sex-specific genome-wide association studies. <i>Genetic Epidemiology</i> , 2010 , 34, 846-53	2.6	69
3	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
2	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3
1	Advantages of genotype imputation with ethnically matched reference panel for rare variant association analyses		5