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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.

39 papers	2,459 citations	22 h-index	48 g-index
48 ext. papers	3,119 ext. citations	12.2 avg, IF	2.95 L-index

#	Paper	IF	Citations
39	Significant sparse polygenic risk scores across 813 traits in UK Biobank.. <i>PLoS Genetics</i> , 2022 , 18, e1010105	10.5	0
38	Cannabinoid receptor 1 antagonist genistein attenuates marijuana-induced vascular inflammation.. <i>Cell</i> , 2022 ,	56.2	5
37	Combining Clinical and Polygenic Risk Improves Stroke Prediction Among Individuals With Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003168	5.2	3
36	Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. <i>Biostatistics</i> , 2020 ,	3.7	7
35	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. <i>Nature Communications</i> , 2019 , 10, 4064	17.4	26
34	Pro12Ala Ala carriers exhibit greater improvements in peripheral insulin sensitivity in response to 12 weeks of aerobic exercise training. <i>Physiological Genomics</i> , 2019 , 51, 254-260	3.6	2
33	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
32	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018 , 3, 4	4.8	16
31	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105
30	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
29	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.6	310
28	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
27	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
26	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
25	Increasing insulin resistance accentuates the effect of triglyceride-associated loci on serum triglycerides during 5 years. <i>Journal of Lipid Research</i> , 2016 , 57, 2193-2199	6.3	2
24	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
23	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76

22	A genetic risk score of 45 coronary artery disease risk variants associates with increased risk of myocardial infarction in 6041 Danish individuals. <i>Atherosclerosis</i> , 2015 , 240, 305-10	3.1	50
21	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
20	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 465-72		25
19	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. <i>Nature Genetics</i> , 2014 , 46, 294-8	36.3	241
18	The effect of GWAS identified BMI loci on changes in body weight among middle-aged Danes during a five-year period. <i>Obesity</i> , 2014 , 22, 901-8	8	24
17	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013 , 56, 298-310	10.3	102
16	The frequent UCP2 -866G>A polymorphism protects against insulin resistance and is associated with obesity: a study of obesity and related metabolic traits among 17 636 Danes. <i>International Journal of Obesity</i> , 2013 , 37, 175-81	5.5	31
15	Type 2 diabetes risk alleles near BCAR1 and in ANK1 associate with decreased β cell function whereas risk alleles near ANKRD55 and GRB14 associate with decreased insulin sensitivity in the Danish Inter99 cohort. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013 , 98, E801-6	5.6	46
14	Genetic risk score of 46 type 2 diabetes risk variants associates with changes in plasma glucose and estimates of pancreatic β cell function over 5 years of follow-up. <i>Diabetes</i> , 2013 , 62, 3610-7	0.9	36
13	Solute carrier family 2 member 1 is involved in the development of nonalcoholic fatty liver disease. <i>Hepatology</i> , 2013 , 57, 505-14	11.2	18
12	Association studies of novel obesity-related gene variants with quantitative metabolic phenotypes in a population-based sample of 6,039 Danish individuals. <i>Diabetologia</i> , 2012 , 55, 105-13	10.3	31
11	Bioinformatics-driven identification and examination of candidate genes for non-alcoholic fatty liver disease. <i>PLoS ONE</i> , 2011 , 6, e16542	3.7	19
10	The minor C-allele of rs2014355 in ACADS is associated with reduced insulin release following an oral glucose load. <i>BMC Medical Genetics</i> , 2011 , 12, 4	2.1	10
9	Studies of the association of Arg72Pro of tumor suppressor protein p53 with type 2 diabetes in a combined analysis of 55,521 Europeans. <i>PLoS ONE</i> , 2011 , 6, e15813	3.7	41
8	Implications of central obesity-related variants in LYPLAL1, NRXN3, MSRA, and TFAP2B on quantitative metabolic traits in adult Danes. <i>PLoS ONE</i> , 2011 , 6, e20640	3.7	36
7	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2011 , 3, 4	4.8	6
6	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2011 , 3, 4	4.8	1
5	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight novel adipocyte biology		2

4	Fast Lasso method for Large-scale and Ultrahigh-dimensional Cox Model with applications to UK Biobank	2
3	Pervasive additive and non-additive effects within the HLA region contribute to disease risk in the UK Biobank	2
2	Combining clinical and polygenic risk improves stroke prediction among individuals with atrial fibrillation	2
1	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1