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List of Publications by Citations

125 papers	19,489 citations	48 h-index	137 g-index
137 ext. papers	26,082 ext. citations	16.6 avg, IF	5.39 L-index

#	Paper	IF	Citations
125	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
124	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
123	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
122	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nature Genetics*, **2018**, 50, 1112-1121	36.3	950
121	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
120	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
119	Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. *Human Molecular Genetics*, **2018**, 27, 3641-3649	5.6	711
118	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
117	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	36.3	675
116	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
115	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
114	Genomic insights into the origin of farming in the ancient Near East. *Nature*, **2016**, 536, 419-24	50.4	485
113	Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human. *Nature*, **2012**, 483, 350-4	50.4	484
112	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	9.3	414
111	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
110	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
109	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. *Nature Genetics*, **2012**, 44, 297-301	36.3	279

108	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 526-534	18.1	277
107	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nature Communications*, **2018**, 9, 2941	17.4	262
106	Meta-analysis of genome-wide association studies for body fat distribution in 694 649 individuals of European ancestry. *Human Molecular Genetics*, **2019**, 28, 166-174	5.6	258
105	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
104	Detection of human adaptation during the past 2000 years. *Science*, **2016**, 354, 760-764	33.3	224
103	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
102	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
101	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	6	220
100	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
99	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
98	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
97	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
96	Signatures of negative selection in the genetic architecture of human complex traits. *Nature Genetics*, **2018**, 50, 746-753	36.3	178
95	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
94	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
93	KLB is associated with alcohol drinking, and its gene product β-Klotho is necessary for FGF21 regulation of alcohol preference. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 14372-14377	11.5	150
92	The kynurenine pathway is activated in human obesity and shifted toward kynurenine monooxygenase activation. *Obesity*, **2015**, 23, 2066-74	8	131
91	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119

90	Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature Communications*, **2019**, 10, 5086	17.4	114
89	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
88	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
87	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. *Diabetologia*, **2013**, 56, 298-310	10.3	102
86	Genetic correlates of social stratification in Great Britain. *Nature Human Behaviour*, **2019**, 3, 1332-1342	12.8	83
85	Recovery of trait heritability from whole genome sequence data		83
84	Heterozygous mutations causing partial prohormone convertase 1 deficiency contribute to human obesity. *Diabetes*, **2012**, 61, 383-90	0.9	82
83	Beneficial effect of a high number of copies of salivary amylase AMY1 gene on obesity risk in Mexican children. *Diabetologia*, **2015**, 58, 290-4	10.3	74
82	Association between large detectable clonal mosaicism and type 2 diabetes with vascular complications. *Nature Genetics*, **2013**, 45, 1040-3	36.3	72
81	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. *Diabetologia*, **2017**, 60, 1740-1750	10.3	62
80	Disruption of a novel Kruppel-like transcription factor p300-regulated pathway for insulin biosynthesis revealed by studies of the c.-331 INS mutation found in neonatal diabetes mellitus. *Journal of Biological Chemistry*, **2011**, 286, 28414-24	5.4	59
79	European genetic variants associated with type 2 diabetes in North African Arabs. *Diabetes and Metabolism*, **2012**, 38, 316-23	5.4	55
78	Low-dose exposure to bisphenols A, F and S of human primary adipocyte impacts coding and non-coding RNA profiles. *PLoS ONE*, **2017**, 12, e0179583	3.7	50
77	Genome-wide association study of medication-use and associated disease in the UK Biobank. *Nature Communications*, **2019**, 10, 1891	17.4	48
76	Analysis of the contribution of FTO, NPC1, ENPP1, NEGR1, GNPDA2 and MC4R genes to obesity in Mexican children. *BMC Medical Genetics*, **2013**, 14, 21	2.1	47
75	Contribution of 24 obesity-associated genetic variants to insulin resistance, pancreatic beta-cell function and type 2 diabetes risk in the French population. *International Journal of Obesity*, **2013**, 37, 980-5	5.5	45
74	GUESS-ing polygenic associations with multiple phenotypes using a GPU-based evolutionary stochastic search algorithm. *PLoS Genetics*, **2013**, 9, e1003657	6	45
73	Imprint of assortative mating on the human genome. *Nature Human Behaviour*, **2018**, 2, 948-954	12.8	45

72	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
71	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. *Diabetes*, **2018**, 67, 1310-1321	0.9	42
70	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. *Nature Communications*, **2020**, 11, 3865	17.4	42
69	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. *Nature Communications*, **2020**, 11, 4799	17.4	41
68	Transcription factor gene MNX1 is a novel cause of permanent neonatal diabetes in a consanguineous family. *Diabetes and Metabolism*, **2013**, 39, 276-80	5.4	38
67	The loss-of-function PCSK9 p.R46L genetic variant does not alter glucose homeostasis. *Diabetologia*, **2015**, 58, 2051-5	10.3	36
66	Association Between Population Density and Genetic Risk for Schizophrenia. *JAMA Psychiatry*, **2018**, 75, 901-910	14.5	35
65	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. *BMC Medicine*, **2017**, 15, 37	11.4	35
64	Association of gene variants with susceptibility to type 2 diabetes among Omanis. *World Journal of Diabetes*, **2015**, 6, 358-66	4.7	31
63	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
62	Type 2 diabetes-related genetic risk scores associated with variations in fasting plasma glucose and development of impaired glucose homeostasis in the prospective DESIR study. *Diabetologia*, **2014**, 57, 1601-10	10.3	29
61	Meta-analysis of genome-wide association studies for height and body mass index in ~700,000 individuals of European ancestry		29
60	Coffee and tea consumption, genotype-based CYP1A2 and NAT2 activity and colorectal cancer risk-results from the EPIC cohort study. *International Journal of Cancer*, **2014**, 135, 401-12	7.5	27
59	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
58	Reassessment of the putative role of BLK-p.A71T loss-of-function mutation in MODY and type 2 diabetes. *Diabetologia*, **2013**, 56, 492-6	10.3	24
57	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
56	Recovery of trait heritability from whole genome sequence data. *Yearbook of Paediatric Endocrinology*,		21
55	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics*, **2016**, 25, 2070-2081	5.6	20

54	Detection and quantification of inbreeding depression for complex traits from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 8602-8607	11.5	20
53	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. *Biological Psychiatry*, **2021**, 89, 11-19	7.9	20
52	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. *American Journal of Human Genetics*, **2021**, 108, 786-798	11	19
51	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18
50	Parental history of type 2 diabetes, TCF7L2 variant and lower insulin secretion are associated with incident hypertension. Data from the DESIR and RISC cohorts. *Diabetologia*, **2013**, 56, 2414-23	10.3	16
49	Post-Bariatric Surgery Changes in Quinolinic and Xanthurenic Acid Concentrations Are Associated with Glucose Homeostasis. *PLoS ONE*, **2016**, 11, e0158051	3.7	16
48	Extreme inbreeding in a European ancestry sample from the contemporary UK population. *Nature Communications*, **2019**, 10, 3719	17.4	14
47	Misestimation of heritability and prediction accuracy of male-pattern baldness. *Nature Communications*, **2018**, 9, 2537	17.4	14
46	Impact of statistical models on the prediction of type 2 diabetes using non-targeted metabolomics profiling. *Molecular Metabolism*, **2016**, 5, 918-925	8.8	13
45	Low-frequency variants in HMGA1 are not associated with type 2 diabetes risk. *Diabetes*, **2012**, 61, 524-30	9	13
44	Expectation of the intercept from bivariate LD score regression in the presence of population stratification		13
43	Discovery and implications of polygenicity of common diseases. *Science*, **2021**, 373, 1468-1473	33.3	13
42	Widespread signatures of natural selection across human complex traits and functional genomic categories. *Nature Communications*, **2021**, 12, 1164	17.4	12
41	Trans-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation		10
40	Genetic Consequences of Social Stratification in Great Britain		10
39	KAT2B Is Required for Pancreatic Beta Cell Adaptation to Metabolic Stress by Controlling the Unfolded Protein Response. *Cell Reports*, **2016**, 15, 1051-1061	10.6	10
38	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. *Nature Metabolism*, **2020**, 2, 1126-1134	14.6	9
37	Bayesian analysis of GWAS summary data reveals differential signatures of natural selection across human complex traits and functional genomic categories		8

36	Widespread signatures of negative selection in the genetic architecture of human complex traits		7
35	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. *Nature Communications*, **2021**, 12, 1050	17.4	7
34	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
33	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
32	Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes. *Scientific Reports*, **2021**, 11, 6197	4.9	6
31	Quantifying genetic heterogeneity between continental populations for human height and body mass index. *Scientific Reports*, **2021**, 11, 5240	4.9	6
30	Associations Between Type 2 Diabetes-Related Genetic Scores and Metabolic Traits, in Obese and Normal-Weight Youths. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 4244-4250	5.6	6
29	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. *Nature Genetics*, **2022**,	36.3	6
28	Detection of human adaptation during the past 2,000 years		5
27	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E2494-E2495	11.5	4
26	Common variants near BDNF and SH2B1 show nominal evidence of association with snacking behavior in European populations. *Journal of Molecular Medicine*, **2013**, 91, 1109-15	5.5	4
25	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
24	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations		4
23	Quantifying genetic heterogeneity between continental populations for human height and body mass index		4
22	No Evidence for Social Genetic Effects or Genetic Similarity Among Friends Beyond that Due to Population Stratification: A Reappraisal of Domingue et al (2018). *Behavior Genetics*, **2020**, 50, 67-71	3.2	4
21	Assortative Mating Biases Marker-based Heritability Estimators		4
20	ALDH2 Polymorphism rs671, but Not ADH1B Polymorphism rs1229984, Increases Risk for Hypo-HDL-Cholesterolemia in a/a Carriers Compared to the G/G Carriers. *Lipids*, **2018**, 53, 797-807	1.6	4
19	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. *Scientific Reports*, **2019**, 9, 9439	4.9	3

18	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals		3
17	A unified framework for association and prediction from vertex-wise grey-matter structure. *Human Brain Mapping*, **2020**, 41, 4062-4076	5.9	3
16	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. *PLoS Genetics*, **2020**, 16, e1008780	6	3
15	Genomic partitioning of inbreeding depression in humans. *American Journal of Human Genetics*, **2021**, 108, 1488-1501	11	3
14	Weight loss independent association of TCF7 L2 gene polymorphism with fasting blood glucose after Roux-en-Y gastric bypass in type 2 diabetic patients. *Surgery for Obesity and Related Diseases*, **2014**, 10, 679-83	3	2
13	Assortative mating biases marker-based heritability estimators.. *Nature Communications*, **2022**, 13, 660	17.4	2
12	Improved polygenic prediction by Bayesian multiple regression on summary statistics		2
11	Imprint of Assortative Mating on the Human Genome		2
10	Machine Learning in Multi-Omics Data to Assess Longitudinal Predictors of Glycaemic Health		2
9	Assortative mating on complex traits revisited: Double first cousins and the X-chromosome. *Theoretical Population Biology*, **2018**, 124, 51-60	1.2	2
8	Assortative Mating in Autism Spectrum Disorder: Toward an Evidence Base From DNA Data, but Not There Yet. *Biological Psychiatry*, **2019**, 86, 250-252	7.9	1
7	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry		1
6	Combined Global Sensitivity Analysis and Population PBPK Modeling for Assessing Consistency of TCDD Toxicokinetics Data in Mice. *Procedia, Social and Behavioral Sciences*, **2010**, 2, 7770-7771		
5	Polygenic burden could explain high rates of affective disorders in a community with restricted founder population. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2021**, 186, 367-375	3.5	
4	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
3	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
2	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
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