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List of Publications by Year in Descending Order

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	Assortative mating biases marker-based heritability estimators.. *Nature Communications*, **2022**, 13, 660	17.4	2
124	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. *Nature Genetics*, **2022**,	36.3	6
123	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
122	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
121	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	
120	Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes. *Scientific Reports*, **2021**, 11, 6197	4.9	6
119	Quantifying genetic heterogeneity between continental populations for human height and body mass index. *Scientific Reports*, **2021**, 11, 5240	4.9	6
118	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
117	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
116	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. *Biological Psychiatry*, **2021**, 89, 11-19	7.9	20
115	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
114	Widespread signatures of natural selection across human complex traits and functional genomic categories. *Nature Communications*, **2021**, 12, 1164	17.4	12
113	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. *Nature Communications*, **2021**, 12, 1050	17.4	7
112	Genomic partitioning of inbreeding depression in humans. *American Journal of Human Genetics*, **2021**, 108, 1488-1501	11	3
111	Discovery and implications of polygenicity of common diseases. *Science*, **2021**, 373, 1468-1473	33.3	13
110	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
109	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. *Nature Metabolism*, **2020**, 2, 1126-1134	14.6	9

108	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
107	A unified framework for association and prediction from vertex-wise grey-matter structure. *Human Brain Mapping*, **2020**, 41, 4062-4076	5.9	3
106	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. *Nature Communications*, **2020**, 11, 3865	17.4	42
105	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. *Nature Communications*, **2020**, 11, 4799	17.4	41
104	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. *PLoS Genetics*, **2020**, 16, e1008780	6	3
103	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
102	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
101	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
100	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock **2020**, 16, e1008780		
99	Extreme inbreeding in a European ancestry sample from the contemporary UK population. *Nature Communications*, **2019**, 10, 3719	17.4	14
98	Genome-wide association study of medication-use and associated disease in the UK Biobank. *Nature Communications*, **2019**, 10, 1891	17.4	48
97	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
96	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
95	Genetic correlates of social stratification in Great Britain. *Nature Human Behaviour*, **2019**, 3, 1332-1342	12.8	83
94	Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature Communications*, **2019**, 10, 5086	17.4	114
93	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
92	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
91	Signatures of negative selection in the genetic architecture of human complex traits. *Nature Genetics*, **2018**, 50, 746-753	36.3	178

90	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
89	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. *Diabetes*, **2018**, 67, 1310-1321	0.9	42
88	Association Between Population Density and Genetic Risk for Schizophrenia. *JAMA Psychiatry*, **2018** , 75, 901-910	14.5	35
87	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
86	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nature Communications*, **2018**, 9, 2941	17.4	262
85	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
84	Imprint of assortative mating on the human genome. *Nature Human Behaviour*, **2018**, 2, 948-954	12.8	45
83	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
82	Assortative mating on complex traits revisited: Double first cousins and the X-chromosome. *Theoretical Population Biology*, **2018**, 124, 51-60	1.2	2
81	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
80	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
79	Misestimation of heritability and prediction accuracy of male-pattern baldness. *Nature Communications*, **2018**, 9, 2537	17.4	14
78	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
77	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. *Diabetologia*, **2017**, 60, 1740-1750	10.3	62
76	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
75	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
74	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
73	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. *BMC Medicine*, **2017**, 15, 37	11.4	35

72	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
71	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
70	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
69	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
68	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
67	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
66	Genomic insights into the origin of farming in the ancient Near East. *Nature*, **2016**, 536, 419-24	50.4	485
65	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
64	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
63	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
62	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
61	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
60	Post-Bariatric Surgery Changes in Quinolinic and Xanthurenic Acid Concentrations Are Associated with Glucose Homeostasis. *PLoS ONE*, **2016**, 11, e0158051	3.7	16
59	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
58	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
57	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
56	Detection of human adaptation during the past 2000 years. *Science*, **2016**, 354, 760-764	33.3	224
55	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119

54	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
53	The loss-of-function PCSK9 p.R46L genetic variant does not alter glucose homeostasis. *Diabetologia* , **2015**, 58, 2051-5	10.3	36
52	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
51	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
50	The kynurenine pathway is activated in human obesity and shifted toward kynurenine monooxygenase activation. *Obesity*, **2015**, 23, 2066-74	8	131
49	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
48	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
47	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
46	Association of gene variants with susceptibility to type 2 diabetes among Omanis. *World Journal of Diabetes*, **2015**, 6, 358-66	4.7	31
45	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
44	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
43	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
42	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
41	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
40	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
39	Association between large detectable clonal mosaicism and type 2 diabetes with vascular complications. *Nature Genetics*, **2013**, 45, 1040-3	36.3	72
38	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
37	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

36	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. *Diabetologia*, **2013**, 56, 298-310	10.3	102
35	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
34	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
33	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
32	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
31	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
30	GUESS-ing polygenic associations with multiple phenotypes using a GPU-based evolutionary stochastic search algorithm. *PLoS Genetics*, **2013**, 9, e1003657	6	45
29	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
28	Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human. *Nature*, **2012**, 483, 350-4	50.4	484
27	European genetic variants associated with type 2 diabetes in North African Arabs. *Diabetes and Metabolism*, **2012**, 38, 316-23	5.4	55
26	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. *Nature Genetics*, **2012**, 44, 297-301	36.3	279
25	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
24	Heterozygous mutations causing partial prohormone convertase 1 deficiency contribute to human obesity. *Diabetes*, **2012**, 61, 383-90	0.9	82
23	Low-frequency variants in HMGA1 are not associated with type 2 diabetes risk. *Diabetes*, **2012**, 61, 524-30	0.9	13
22	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
21	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
20	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		
19	Recovery of trait heritability from whole genome sequence data. *Yearbook of Paediatric Endocrinology*,		21

18	Improved polygenic prediction by Bayesian multiple regression on summary statistics	2
17	Detection of human adaptation during the past 2,000 years	5
16	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes	4
15	Widespread signatures of negative selection in the genetic architecture of human complex traits	7
14	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations	4
13	Trans-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation	10
12	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals	3
11	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
10	Meta-analysis of genome-wide association studies for height and body mass index in ~700,000 individuals of European ancestry	29
9	Imprint of Assortative Mating on the Human Genome	2
8	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry	1
7	Expectation of the intercept from bivariate LD score regression in the presence of population stratification	13
6	Machine Learning in Multi-Omics Data to Assess Longitudinal Predictors of Glycaemic Health	2
5	Genetic Consequences of Social Stratification in Great Britain	10
4	Recovery of trait heritability from whole genome sequence data	83
3	Bayesian analysis of GWAS summary data reveals differential signatures of natural selection across human complex traits and functional genomic categories	8
2	Quantifying genetic heterogeneity between continental populations for human height and body mass index	4
1	Assortative Mating Biases Marker-based Heritability Estimators	4