F R Day

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.

100 papers	15,151 citations	41 h-index	117 g-index
117 ext. papers	20,917 ext. citations	18.3 avg, IF	5.48 L-index

#	Paper	IF	Citations
100	Epigenome-wide association study of incident type 2 diabetes: a meta-analysis of five prospective European cohorts.. *Diabetologia*, **2022**, 65, 763	10.3	2
99	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. *PLoS Genetics*, **2022**, 18, e1010162	6	0
98	MC3R links nutritional state to childhood growth and the timing of puberty. *Nature*, **2021**, 599, 436-441	50.4	9
97	The potential shared role of inflammation in insulin resistance and schizophrenia: A bidirectional two-sample mendelian randomization study. *PLoS Medicine*, **2021**, 18, e1003455	11.6	11
96	Genetic analyses identify widespread sex-differential participation bias. *Nature Genetics*, **2021**, 53, 663-671	36.3	20
95	Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. *Nutrients*, **2021**, 13,	6.7	2
94	Positive maternal attitudes to following healthy infant feeding guidelines attenuate the associations between infant appetitive traits and both infant milk intake and weight. *Appetite*, **2021** , 161, 105124	4.5	1
93	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. *Nature Communications*, **2021**, 12, 4178	17.4	3
92	Genetic association study of childhood aggression across raters, instruments, and age. *Translational Psychiatry*, **2021**, 11, 413	8.6	7
91	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. *Diabetes Care*, **2021**, 44, 98-106	14.6	21
90	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. *Nature Human Behaviour*, **2021**,	12.8	5
89	Incident disease associations with mosaic chromosomal alterations on autosomes, X and Y chromosomes: insights from a phenome-wide association study in the UK Biobank. *Cell and Bioscience*, **2021**, 11, 143	9.8	1
88	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
87	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. *Behavior Genetics*, **2021**, 51, 592-606	3.2	2
86	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
85	Identification of rare loss of function genetic variation regulating body fat distribution. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	1
84	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. *Nature Communications*, **2020**, 11, 1536	17.4	12

83	Using human genetics to understand the disease impacts of testosterone in men and women. *Nature Medicine*, **2020**, 26, 252-258	50.5	121
82	Association of puberty timing with type 2 diabetes: A systematic review and meta-analysis. *PLoS Medicine*, **2020**, 17, e1003017	11.6	13
81	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	17
80	Genetic basis of falling risk susceptibility in the UK Biobank Study. *Communications Biology*, **2020**, 3, 543	6.7	3
79	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: A meta-analysis and Mendelian randomisation analysis. *PLoS Medicine*, **2020**, 17, e1003394	11.6	15
78	A genome-wide association study of polycystic ovary syndrome identified from electronic health records. *American Journal of Obstetrics and Gynecology*, **2020**, 223, 559.e1-559.e21	6.4	20
77	Voice break in boys-temporal relations with other pubertal milestones and likely causal effects of BMI. *Human Reproduction*, **2019**, 34, 1514-1522	5.7	14
76	Human Gain-of-Function MC4R Variants Show Signaling Bias and Protect against Obesity. *Cell*, **2019** , 177, 597-607.e9	56.2	113
75	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
74	Assessing the causal association of glycine with risk of cardio-metabolic diseases. *Nature Communications*, **2019**, 10, 1060	17.4	38
73	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. *Molecular Psychiatry*, **2019**, 24, 1920-1932	15.1	30
72	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
71	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. *Nature Communications*, **2019**, 10, 4857	17.4	34
70	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
69	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. *Diabetes*, **2019**, 68, 2315-2326	0.9	40
68	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. *Nature Communications*, **2018**, 9, 387	17.4	106
67	Genome-wide association study for risk taking propensity indicates shared pathways with body mass index. *Communications Biology*, **2018**, 1, 36	6.7	30
66	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

65	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
64	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal influence of schizophrenia. *Nature Neuroscience*, **2018**, 21, 1161-1170	25.5	270
63	Genetic risk score for adult body mass index associations with childhood and adolescent weight gain in an African population. *Genes and Nutrition*, **2018**, 13, 24	4.3	9
62	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genetics*, **2018**, 14, e1007813	6	166
61	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. *JAMA - Journal of the American Medical Association*, **2018**, 320, 2553-2563	27.4	78
60	Association of Genetically Enhanced Lipoprotein Lipase-Mediated Lipolysis and Low-Density Lipoprotein Cholesterol-Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. *JAMA Cardiology*, **2018**, 3, 957-966	16.2	30
59	Elucidating the genetic architecture of reproductive ageing in the Japanese population. *Nature Communications*, **2018**, 9, 1977	17.4	28
58	Elucidating the genetic basis of social interaction and isolation. *Nature Communications*, **2018**, 9, 2457	17.4	81
57	Associations between body mass index-related genetic variants and adult body composition: The Fenland cohort study. *International Journal of Obesity*, **2017**, 41, 613-619	5.5	9
56	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
55	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. *Nature Genetics*, **2017**, 49, 674-679	36.3	70
54	Identifying genetic variants that affect viability in large cohorts. *PLoS Biology*, **2017**, 15, e2002458	9.7	49
53	Dissecting Causal Pathways Using Mendelian Randomization with Summarized Genetic Data: Application to Age at Menarche and Risk of Breast Cancer. *Genetics*, **2017**, 207, 481-487	4	91
52	Replication and characterization of and genes on human behavior. *Heliyon*, **2017**, 3, e00349	3.6	61
51	Mediation and modification of genetic susceptibility to obesity by eating behaviors. *American Journal of Clinical Nutrition*, **2017**, 106, 996-1004	7	37
50	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
49	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. *Nature Genetics*, **2017**, 49, 17-26	36.3	312
48	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180

(2015-2016)

47	A Robust Example of Collider Bias in a Genetic Association Study. *American Journal of Human Genetics*, **2016**, 98, 392-3	11	60
46	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
45	Adiposity in Children Born Small for Gestational Age Is Associated With βCell Function, Genetic Variants for Insulin Resistance, and Response to Growth Hormone Treatment. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 131-42	5.6	8
44	Across-cohort QC analyses of GWAS summary statistics from complex traits. *European Journal of Human Genetics*, **2016**, 25, 137-146	5.3	13
43	Body shape and size in 6-year old children: assessment by three-dimensional photonic scanning. *International Journal of Obesity*, **2016**, 40, 1012-7	5.5	4
42	Physical and neurobehavioral determinants of reproductive onset and success. *Nature Genetics*, **2016**, 48, 617-623	36.3	118
41	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. *American Journal of Human Genetics*, **2016**, 98, 898-908	11	66
40	Genome-wide association study identifies common and low-frequency variants at the AMH gene locus that strongly predict serum AMH levels in males. *Human Molecular Genetics*, **2016**, 25, 382-8	5.6	12
39	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
38	Genetic markers of insulin sensitivity and insulin secretion are associated with spontaneous postnatal growth and response to growth hormone treatment in short SGA children: the North European SGA Study (NESGAS). *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E503-7	5.6	8
37	Puberty timing associated with diabetes, cardiovascular disease and also diverse health outcomes in men and women: the UK Biobank study. *Scientific Reports*, **2015**, 5, 11208	4.9	254
36	Partitioning heritability by functional annotation using genome-wide association summary statistics. *Nature Genetics*, **2015**, 47, 1228-35	36.3	1143
35	An atlas of genetic correlations across human diseases and traits. *Nature Genetics*, **2015**, 47, 1236-41	36.3	1841
34	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
33	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. *Nature Communications*, **2015**, 6, 8464	17.4	203
32	Season of birth is associated with birth weight, pubertal timing, adult body size and educational attainment: a UK Biobank study. *Heliyon*, **2015**, 1, e00031	3.6	31
31	Molecular insights into the aetiology of female reproductive ageing. *Nature Reviews Endocrinology*, **2015**, 11, 725-34	15.2	47
30	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. *Nature Communications*, **2015**, 6, 8842	17.4	75

29	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. *PLoS Medicine*, **2015**, 12, e1001841; discussion e1001841	11.6	115
28	Genetic Regulation of Puberty Timing in Humans. *Neuroendocrinology*, **2015**, 102, 247-255	5.6	30
27	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
26	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
25	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
24	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
23	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
22	Quality control and conduct of genome-wide association meta-analyses. *Nature Protocols*, **2014**, 9, 1192-1212	18.8	278
21	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
20	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
19	Developments in obesity genetics in the era of genome-wide association studies. *Journal of Nutrigenetics and Nutrigenomics*, **2011**, 4, 222-38		113
18	Statistical estimation of cell-cycle progression and lineage commitment in Plasmodium falciparum reveals a homogeneous pattern of transcription in ex vivo culture. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 7559-64	11.5	64
17	Genome-wide association analysis of lifetime cannabis use (N=184,765) identifies new risk loci, genetic overlap with mental health, and a causal influence of schizophrenia on cannabis use		1
16	Partitioning heritability by functional category using GWAS summary statistics		11
15	An Atlas of Genetic Correlations across Human Diseases and Traits		24
14	Identifying genetic variants that affect viability in large cohorts		3
13	Genetic analyses identify widespread sex-differential participation bias		15
12	Identification of 370 genetic loci for age at first sex and birth linked to externalising behaviour		3

LIST OF PUBLICATIONS

11	Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus		2
10	Development and validation of total and regional body composition prediction equations from anthropometry and single frequency segmental bioelectrical impedance with DEXA		1
9	Genome-wide scan and fine-mapping of rare nonsynonymous associations implicates intracellular lipolysis genes in fat distribution and cardio-metabolic risk		2
8	Expanded genomic analyses for male voice-breaking highlights a shared phenotypic and genetic basis between puberty timing and hair colour		1
7	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers		5
6	Using genetic variation to disentangle the complex relationship between food intake and health outcomes		6
5	Genetic Association Study of Childhood Aggression across raters, instruments and age		4
4	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
3	GWAS of epigenetic ageing rates in blood reveals a critical role forTERT		1
2	Dissecting causal pathways using Mendelian randomization with summarized genetic data: application to age at menarche and risk of breast cancer		2
1	Elucidating the genetic architecture underlying IGF1 levels and its impact on genomic instability and cancer risk. *Wellcome Open Research*,6, 20	4.8	1