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List of Publications by Year
in descending order

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86	24,813	44444 50	58552 86
papers	citations	h-index	g-index

117	117	117	33356
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Epigenome-wide association study of incident type 2 diabetes: a meta-analysis of five prospective European cohorts. Diabetologia, 2022, 65, 763-776.	2.9	28
2	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1065-1077.	1.8	12
3	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	1.5	12
4	Detection and characterization of male sex chromosome abnormalities in the UK Biobank study. Genetics in Medicine, 2022, 24, 1909-1919.	1.1	14
5	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. Diabetes Care, 2021, 44, 98-106.	4.3	68
6	The potential shared role of inflammation in insulin resistance and schizophrenia: A bidirectional two-sample mendelian randomization study. PLoS Medicine, 2021, 18, e1003455.	3.9	37
7	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
8	Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. Nutrients, 2021, 13, 1868.	1.7	6
9	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.	1.8	2
10	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. Nature Communications, 2021, 12, 4178.	5.8	20
11	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	2.4	31
12	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
13	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.	2.1	14
14	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
15	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. Behavior Genetics, 2021, 51, 592-606.	1.4	13
16	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
17	MC3R links nutritional state to childhood growth and the timing of puberty. Nature, 2021, 599, 436-441.	13.7	59
18	Association of puberty timing with type 2 diabetes: A systematic review and meta-analysis. PLoS Medicine, 2020, 17, e1003017.	3.9	52

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19	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	1.8	40
20	Genetic basis of falling risk susceptibility in the UK Biobank Study. Communications Biology, 2020, 3, 543.	2.0	17
21	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: AÂmeta-analysis and Mendelian randomisation analysis. PLoS Medicine, 2020, 17, e1003394.	3.9	45
22	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. Nature Communications, 2020, 11, 1536.	5.8	36
23	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	15.2	384
24	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.	0.7	49
25	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.	4.1	44
26	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
27	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
28	Voice break in boysâ€"temporal relations with other pubertal milestones and likely causal effects of BMI. Human Reproduction, 2019, 34, 1514-1522.	0.4	31
29	Human Gain-of-Function MC4R Variants Show Signaling Bias and Protect against Obesity. Cell, 2019, 177, 597-607.e9.	13.5	192
30	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
31	Assessing the causal association of glycine with risk of cardio-metabolic diseases. Nature Communications, 2019, 10, 1060.	5.8	85
32	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
33	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.3	77
34	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
35	Genomeâ€"wide association study for risk taking propensity indicates shared pathways with body mass index. Communications Biology, 2018, 1, 36.	2.0	54
36	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341

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37	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.	3.8	152
38	Association of Genetically Enhanced Lipoprotein Lipaseâ€“Mediated Lipolysis and Low-Density Lipoprotein Cholesterolâ€“Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. JAMA Cardiology, 2018, 3, 957.	3.0	55
39	Elucidating the genetic architecture of reproductive ageing in the Japanese population. Nature Communications, 2018, 9, 1977.	5.8	44
40	Elucidating the genetic basis of social interaction and isolation. Nature Communications, 2018, 9, 2457.	5.8	156
41	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.	9.4	1,835
42	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
43	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. Nature Neuroscience, 2018, 21, 1161-1170.	7.1	436
44	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.	1.2	13
45	Associations between body mass index-related genetic variants and adult body composition: The Fenland cohort study. International Journal of Obesity, 2017, 41, 613-619.	1.6	14
46	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.	9.4	426
47	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	9.4	117
48	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.	1.2	170
49	Replication and characterization of CADM2 and MSRA genes on human behavior. Heliyon, 2017, 3, e00349.	1.4	80
50	Mediation and modification of genetic susceptibility to obesity by eating behaviors. American Journal of Clinical Nutrition, 2017, 106, 996-1004.	2.2	47
51	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
52	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	9.4	452
53	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
54	Identifying genetic variants that affect viability in large cohorts. PLoS Biology, 2017, 15, e2002458.	2.6	71

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55	Body shape and size in 6-year old children: assessment by three-dimensional photonic scanning. International Journal of Obesity, 2016, 40, 1012-1017.	1.6	8
56	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	9.4	158
57	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
58	Genome-wide association study identifies common and low-frequency variants at theAMHgene locus that strongly predict serum AMH levels in males. Human Molecular Genetics, 2016, 25, 382-388.	1.4	15
59	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
60	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
61	A Robust Example of Collider Bias in a Genetic Association Study. American Journal of Human Genetics, 2016, 98, 392-393.	2.6	95
62	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
63	Adiposity in Children Born Small for Gestational Age Is Associated With Î²-Cell Function, Genetic Variants for Insulin Resistance, and Response to Growth Hormone Treatment. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 131-142.	1.8	10
64	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. Nature Communications, 2015, 6, 8842.	5.8	100
65	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. PLoS Medicine, 2015, 12, e1001841.	3.9	153
66	Genetic Regulation of Puberty Timing in Humans. Neuroendocrinology, 2015, 102, 247-255.	1.2	43
67	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
68	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
69	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
70	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-E507.	1.8	10
71	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.	1.6	364
72	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045

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73	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	9.4	3,145
74	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
75	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
76	Season of birth is associated with birth weight, pubertal timing, adult body size and educational attainment: a UK Biobank study. Heliyon, 2015, 1, e00031.	1.4	44
77	Molecular insights into the aetiology of female reproductive ageing. Nature Reviews Endocrinology, 2015, 11, 725-734.	4.3	67
78	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
79	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
80	Quality control and conduct of genome-wide association meta-analyses. Nature Protocols, 2014, 9, 1192-1212.	5.5	398
81	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
82	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
83	Abstract 050: Meta-analysis of Genetic Associations in up to 339,224 Individuals Identify 66 New Loci for Bmi, Confirming a Neuronal Contribution to Body Weight Regulation and Implicating Several Novel Pathways. Circulation, 2013, 127, .	1.6	0
84	Developments in Obesity Genetics in the Era of Genome-Wide Association Studies. Journal of Nutrigenetics and Nutrigenomics, 2011, 4, 222-238.	1.8	134
85	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, 7559-7564.	3.3	84
86	Elucidating the genetic architecture underlying IGF1 levels and its impact on genomic instability and cancer risk. Wellcome Open Research, 0, 6, 20.	0.9	4