H Yaghootkar

List of Publications by Year
in descending order

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90 papers	13,471 citations	47006 47 h-index	45317 90 g-index
119 all docs	119 docs citations	119 times ranked	25121 citing authors

#	Article	IF	Citations
1	Disease consequences of higher adiposity uncoupled from its adverse metabolic effects using Mendelian randomisation. ELife, 2022, 11, .	6.0	10
2	Estimating the Effect of Liver and Pancreas Volume and Fat Content on Risk of Diabetes: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 460-468.	8.6	27
3	Investigating Genetic Mutations in a Large Cohort of Iranian Patients with Congenital Hyperinsulinism. JCRPE Journal of Clinical Research in Pediatric Endocrinology, 2022, 14, 87-95.	0.9	5
4	A rare genetic variant in the manganese transporter SLC30A10 and elevated liver enzymes in the general population. Hepatology International, 2022, 16, 702-711.	4.2	4
5	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. Human Molecular Genetics, 2022, 31, 1762-1775.	2.9	2
6	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	3.7	77
7	Genetically defined favourable adiposity is not associated with a clinically meaningful difference in clinical course in people with type 2 diabetes but does associate with a favourable metabolic profile. Diabetic Medicine, 2021, 38, e14531.	2.3	1
8	Genetic Evidence for Different Adiposity Phenotypes and Their Opposing Influences on Ectopic Fat and Risk of Cardiometabolic Disease. Diabetes, 2021, 70, 1843-1856.	0.6	42
9	Higher adiposity and mental health: causal inference using Mendelian randomization. Human Molecular Genetics, 2021, 30, 2371-2382.	2.9	29
10	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	6.3	9
11	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
12	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
13	The MÄori and Pacific specific CREBRF variant and adult height. International Journal of Obesity, 2020, 44, 748-752.	3.4	15
14	Ethnic Differences in Body Fat Deposition and Liver Fat Content in Two UKâ€Based Cohorts. Obesity, 2020, 28, 2142-2152.	3.0	9
15	Using genetics to decipher the link between type 2 diabetes and cancer: shared aetiology or downstream consequence?. Diabetologia, 2020, 63, 1706-1717.	6.3	20
16	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
17	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. PLoS Computational Biology, 2020, 16, e1008044.	3.2	16
18	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	1.3	14

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19	Ethnic differences in adiposity and diabetes risk â€“ insights from genetic studies. Journal of Internal Medicine, 2020, 288, 271-283.	6.0	42
20	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. International Journal of Epidemiology, 2020, 49, 1270-1281.	1.9	20
21	Genome-wide and Mendelian randomisation studies of liver MRI yield insights into the pathogenesis of steatohepatitis. Journal of Hepatology, 2020, 73, 241-251.	3.7	83
22	A Mendelian Randomization Study Provides Evidence That Adiposity and Dyslipidemia Lead to Lower Urinary Albumin-to-Creatinine Ratio, a Marker of Microvascular Function. Diabetes, 2020, 69, 1072-1082.	0.6	10
23	Title is missing!. , 2020, 16, e1008044.		0
24	Title is missing!. , 2020, 16, e1008044.		0
25	Title is missing!. , 2020, 16, e1008044.		0
26	Title is missing!. , 2020, 16, e1008044.		0
27	Title is missing!. , 2020, 16, e1008044.		0
28	Title is missing!. , 2020, 16, e1008044.		0
29	A case of H syndrome with a novel mutation in SLC29A3. Meta Gene, 2019, 21, 100599.	0.6	1
30	Type 1 diabetes genetic risk score discriminates between monogenic and Type 1 diabetes in children diagnosed at the age of <5 years in the Iranian population. Diabetic Medicine, 2019, 36, 1694-1702.	2.3	13
31	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	12.8	417
32	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. Journal of Hepatology, 2019, 71, 594-602.	3.7	23
33	Wolcott-Rallison syndrome in Iran: a common cause of neonatal diabetes. Journal of Pediatric Endocrinology and Metabolism, 2019, 32, 607-613.	0.9	11
34	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
35	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
36	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	12.8	189

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37	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
38	Mosaic Turner syndrome shows reduced penetrance in an adult population study. Genetics in Medicine, 2019, 21, 877-886.	2.4	88
39	Using genetics to understand the causal influence of higher BMI on depression. International Journal of Epidemiology, 2019, 48, 834-848.	1.9	156
40	Response to Prakash et al.. Genetics in Medicine, 2019, 21, 1884-1885.	2.4	5
41	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
42	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. Diabetes, 2019, 68, 207-219.	0.6	72
43	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
44	Meta-analysis of genome-wide association studies for body fat distribution in 694Â649 individuals of European ancestry. Human Molecular Genetics, 2019, 28, 166-174.	2.9	752
45	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
46	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
47	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. Cell Reports, 2018, 23, 327-336.	6.4	76
48	DNA methylation and inflammation marker profiles associated with a history of depression. Human Molecular Genetics, 2018, 27, 2840-2850.	2.9	46
49	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
50	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40
51	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	7.9	63
52	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
53	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	1.9	159
54	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470

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55	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
56	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	21.4	452
57	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	2.5	49
58	Functional characterisation of ADIPOQ variants using individuals recruited by genotype. Molecular and Cellular Endocrinology, 2016, 428, 49-57.	3.2	12
59	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.6	122
60	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
61	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
62	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
63	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
64	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. BMJ, The, 2016, 352, i582.	6.0	247
65	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. Diabetologia, 2016, 59, 1214-1221.	6.3	65
66	Genetic evidence that lower circulating FSH levels lengthen menstrual cycle, increase age at menopause and impact female reproductive health. Human Reproduction, 2016, 31, 473-481.	0.9	51
67	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	2.9	10
68	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	3.5	308
69	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	3.1	113
70	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
71	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115
72	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. Diabetes, 2015, 64, 2676-2684.	0.6	114

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73	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at CCND2 Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. Diabetes, 2015, 64, 2279-2285.	0.6	24
74	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
75	Tumor Necrosis Factor-Alpha Polymorphism at Position -238 in Preeclampsia. Iranian Red Crescent Medical Journal, 2014, 16, e11195.	0.5	18
76	Genetic Evidence for a Normal-Weight â€œMetabolically Obeseâ€•Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. Diabetes, 2014, 63, 4369-4377.	0.6	185
77	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. Human Mutation, 2014, 35, 1524-1531.	2.5	45
78	Common Genetic Variants Highlight the Role of Insulin Resistance and Body Fat Distribution in Type 2 Diabetes, Independent of Obesity. Diabetes, 2014, 63, 4378-4387.	0.6	153
79	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
80	Recent progress in the use of genetics to understand links between type 2 diabetes and related metabolic traits. Genome Biology, 2013, 14, 203.	9.6	10
81	Parental diabetes and birthweight in 236 030 individuals in the UK Biobank Study. International Journal of Epidemiology, 2013, 42, 1714-1723.	1.9	65
82	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.6	116
83	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
84	Genetic origins of low birth weight. Current Opinion in Clinical Nutrition and Metabolic Care, 2012, 15, 258-264.	2.5	35
85	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
86	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
87	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	2.5	3
88	Allelic heterogeneity and more detailed analyses of known loci explain additional phenotypic variation and reveal complex patterns of association. Human Molecular Genetics, 2011, 20, 4082-4092.	2.9	61
89	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. Aging Cell, 2011, 10, 868-878.	6.7	230
90	Coding Variant In <i>LEP</i> Associated with Lower Leptin Concentrations Implicates Leptin in the Regulation of Early Adiposity. SSRN Electronic Journal, 0, , .	0.4	0