H Yaghootkar

List of Publications by Year in Descending Order

97 papers	8,314 citations	40 h-index	91 g-index
119 ext. papers	11,379 ext. citations	11.9 avg, IF	4.69 L-index

#	Paper	IF	Citations
97	A rare genetic variant in the manganese transporter SLC30A10 and elevated liver enzymes in the general population.. *Hepatology International*, **2022**, 1	8.8	0
96	Genetic Evidence for Different Adiposity Phenotypes and Their Opposing Influences on Ectopic Fat and Risk of Cardiometabolic Disease. *Diabetes*, **2021**, 70, 1843-1856	0.9	5
95	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. *Journal of Hepatology*, **2021**, 74, 20-30	13.4	24
94	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	3.5	0
93	Higher adiposity and mental health: causal inference using Mendelian randomization. *Human Molecular Genetics*, **2021**, 30, 2371-2382	5.6	4
92	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. *Diabetologia*, **2021**, 64, 2790-2802	10.3	0
91	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	36.3	60
90	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	7.9	6
89	Ethnic differences in adiposity and diabetes risk - insights from genetic studies. *Journal of Internal Medicine*, **2020**, 288, 271-283	10.8	15
88	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. *International Journal of Epidemiology*, **2020**, 49, 1270-1281	7.8	7
87	Genome-wide and Mendelian randomisation studies of liver MRI yield insights into the pathogenesis of steatohepatitis. *Journal of Hepatology*, **2020**, 73, 241-251	13.4	28
86	Ethnic Differences in Body Fat Deposition and Liver Fat Content in Two UK-Based Cohorts. *Obesity*, **2020**, 28, 2142-2152	8	1
85	Using genetics to decipher the link between type 2 diabetes and cancer: shared aetiology or downstream consequence?. *Diabetologia*, **2020**, 63, 1706-1717	10.3	7
84	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
83	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. *PLoS Computational Biology*, **2020**, 16, e1008044	5	5
82	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
81	The Māori and Pacific specific CREBRF variant and adult height. *International Journal of Obesity*, **2020**, 44, 748-752	5.5	10

80	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	9.9	7
79	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
78	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
77	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
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75	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
74	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
73	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. *Nature Communications*, **2019**, 10, 343	17.4	205
72	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. *Journal of Hepatology*, **2019**, 71, 594-602	13.4	10
71	Wolcott-Rallison syndrome in Iran: a common cause of neonatal diabetes. *Journal of Pediatric Endocrinology and Metabolism*, **2019**, 32, 607-613	1.6	6
70	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
69	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
68	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. *Nature Communications*, **2019**, 10, 1585	17.4	92
67	A case of H syndrome with a novel mutation in SLC29A3. *Meta Gene*, **2019**, 21, 100599	0.7	1
66	Type 1 diabetes genetic risk score discriminates between monogenic and Type 1 diabetes in children diagnosed at the age of . *Diabetic Medicine*, **2019**, 36, 1694-1702	3.5	8
65	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
64	Mosaic Turner syndrome shows reduced penetrance in an adult population study. *Genetics in Medicine*, **2019**, 21, 877-886	8.1	40
63	Using genetics to understand the causal influence of higher BMI on depression. *International Journal of Epidemiology*, **2019**, 48, 834-848	7.8	81

62	Response to Prakash et al. *Genetics in Medicine*, **2019**, 21, 1884-1885	8.1	4
61	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	36.3	259
60	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	0.9	46
59	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
58	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
57	Genome-wide association study of offspring birth weight in 86 577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. *Human Molecular Genetics*, **2018**, 27, 742-756	5.6	98
56	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
55	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	10.6	48
54	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
53	DNA methylation and inflammation marker profiles associated with a history of depression. *Human Molecular Genetics*, **2018**, 27, 2840-2850	5.6	23
52	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. *Molecular Psychiatry*, **2017**, 22, 192-201	15.1	31
51	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
50	Gene-obesogenic environment interactions in the UK Biobank study. *International Journal of Epidemiology*, **2017**, 46, 559-575	7.8	105
49	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
48	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
47	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
46	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. *PLoS ONE*, **2017**, 12, e0185083	3.7	28
45	Quantifying the extent to which index event biases influence large genetic association studies. *Human Molecular Genetics*, **2017**, 26, 1018-1030	5.6	30

44	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
43	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
42	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. *BMJ, The*, **2016**, 352, i582	5.9	153
41	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. *Diabetologia*, **2016**, 59, 1214-21	10.3	38
40	Genetic evidence that lower circulating FSH levels lengthen menstrual cycle, increase age at menopause and impact female reproductive health. *Human Reproduction*, **2016**, 31, 473-81	5.7	37
39	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
38	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. *PLoS Genetics*, **2016**, 12, e1006125	6	222
37	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. *Aging*, **2016**, 8, 547-60	5.6	84
36	Functional characterisation of ADIPOQ variants using individuals recruited by genotype. *Molecular and Cellular Endocrinology*, **2016**, 428, 49-57	4.4	9
35	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. *Diabetes*, **2016**, 65, 2448-60	0.9	86
34	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	32.4	266
33	Analysis with the exome array identifies multiple new independent variants in lipid loci. *Human Molecular Genetics*, **2016**, 25, 4094-4106	5.6	14
32	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81
31	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. *Diabetes*, **2015**, 64, 2676-84	0.9	83
30	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, 2279-85	0.9	20
29	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
28	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
27	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, 1524-31	4.7	37

26	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	0.9	127
25	Tumor necrosis factor-alpha polymorphism at position -238 in preeclampsia. *Iranian Red Crescent Medical Journal*, **2014**, 16, e11195	1.3	16
24	Genetic evidence for a normal-weight "metabolically obese" phenotype linking insulin resistance, hypertension, coronary artery disease, and type 2 diabetes. *Diabetes*, **2014**, 63, 4369-77	0.9	131
23	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
22	Recent progress in the use of genetics to understand links between type 2 diabetes and related metabolic traits. *Genome Biology*, **2013**, 14, 203	18.3	7
21	Parental diabetes and birthweight in 236 030 individuals in the UK biobank study. *International Journal of Epidemiology*, **2013**, 42, 1714-23	7.8	47
20	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. *Diabetes*, **2013**, 62, 3589-98	0.9	95
19	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
18	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
17	Genetic origins of low birth weight. *Current Opinion in Clinical Nutrition and Metabolic Care*, **2012**, 15, 258-64	3.8	28
16	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
15	Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. *PLoS ONE*, **2012**, 7, e31369	3.7	2
14	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. *Aging Cell*, **2011**, 10, 868-78	9.9	163
13	Allelic heterogeneity and more detailed analyses of known loci explain additional phenotypic variation and reveal complex patterns of association. *Human Molecular Genetics*, **2011**, 20, 4082-92	5.6	51
12	Higher maternal adiposity reduces offspring birth weight if associated with a metabolically favourable profile		1
11	HUMAN LONGEVITY IS INFLUENCED BY MANY GENETIC VARIANTS: EVIDENCE FROM 75,000 UK BIOBANK PARTICIPANTS		4
10	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
9	Mosaic Turner syndrome shows reduced phenotypic penetrance in an adult population study compared to clinically ascertained cases		5

List of Publications

8	rs641738C>T near MBOAT7 is positively associated with liver fat, ALT, and histological severity of NAFLD: a meta-analysis	3
7	Fetal alleles predisposing to metabolically favourable adiposity are associated with higher birth weight	1
6	A common allele in FGF21 associated with preference for sugar consumption lowers body fat in the lower body and increases blood pressure	2
5	Genetic studies of accelerometer-based sleep measures in 85,670 individuals yield new insights into human sleep behaviour	5
4	Genome-wide association analyses of chronotype in 697,828 individuals provides new insights into circadian rhythms in humans and links to disease	5
3	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry	1
2	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
1	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis	175