H Yaghootkar

List of Publications by Citations

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	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
96	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
95	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
94	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
93	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
92	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
91	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
90	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
89	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
88	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
87	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. *PLoS Genetics*, **2016**, 12, e1006125	6	222
86	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
85	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. *Nature Communications*, **2019**, 10, 343	17.4	205
84	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
83	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
82	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
81	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175

80	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. *Aging Cell*, **2011**, 10, 868-78	9.9	163
79	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. *BMJ, The*, **2016**, 352, i582	5.9	153
78	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
77	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
76	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
75	Gene-obesogenic environment interactions in the UK Biobank study. *International Journal of Epidemiology*, **2017**, 46, 559-575	7.8	105
74	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
73	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
72	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
71	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. *Nature Communications*, **2019**, 10, 1585	17.4	92
70	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
69	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. *Aging*, **2016**, 8, 547-60	5.6	84
68	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. *Diabetes*, **2015**, 64, 2676-84	0.9	83
67	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81
66	Using genetics to understand the causal influence of higher BMI on depression. *International Journal of Epidemiology*, **2019**, 48, 834-848	7.8	81
65	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
64	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
63	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

62	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
61	Parental diabetes and birthweight in 236 030 individuals in the UK biobank study. *International Journal of Epidemiology*, **2013**, 42, 1714-23	7.8	47
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	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
58	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
57	Mosaic Turner syndrome shows reduced penetrance in an adult population study. *Genetics in Medicine*, **2019**, 21, 877-886	8.1	40
56	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
55	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
54	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
53	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
52	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
51	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
50	Quantifying the extent to which index event biases influence large genetic association studies. *Human Molecular Genetics*, **2017**, 26, 1018-1030	5.6	30
49	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
48	Genetic origins of low birth weight. *Current Opinion in Clinical Nutrition and Metabolic Care*, **2012**, 15, 258-64	3.8	28
47	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. *PLoS ONE*, **2017**, 12, e0185083	3.7	28
46	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
45	DNA methylation and inflammation marker profiles associated with a history of depression. *Human Molecular Genetics*, **2018**, 27, 2840-2850	5.6	23

44	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
43	Tumor necrosis factor-alpha polymorphism at position -238 in preeclampsia. *Iranian Red Crescent Medical Journal*, **2014**, 16, e11195	1.3	16
42	Ethnic differences in adiposity and diabetes risk - insights from genetic studies. *Journal of Internal Medicine*, **2020**, 288, 271-283	10.8	15
41	Analysis with the exome array identifies multiple new independent variants in lipid loci. *Human Molecular Genetics*, **2016**, 25, 4094-4106	5.6	14
40	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
39	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
38	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
37	The Māori and Pacific specific CREBRF variant and adult height. *International Journal of Obesity*, **2020**, 44, 748-752	5.5	10
36	Functional characterisation of ADIPOQ variants using individuals recruited by genotype. *Molecular and Cellular Endocrinology*, **2016**, 428, 49-57	4.4	9
35	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
34	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
33	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
32	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
31	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
30	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	0.9	7
29	Wolcott-Rallison syndrome in Iran: a common cause of neonatal diabetes. *Journal of Pediatric Endocrinology and Metabolism*, **2019**, 32, 607-613	1.6	6
28	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
27	Mosaic Turner syndrome shows reduced phenotypic penetrance in an adult population study compared to clinically ascertained cases		5

26	Genetic studies of accelerometer-based sleep measures in 85,670 individuals yield new insights into human sleep behaviour		5
25	Genome-wide association analyses of chronotype in 697,828 individuals provides new insights into circadian rhythms in humans and links to disease		5
24	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
23	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
22	HUMAN LONGEVITY IS INFLUENCED BY MANY GENETIC VARIANTS: EVIDENCE FROM 75,000 UK BIOBANK PARTICIPANTS		4
21	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
20	Response to Prakash et al. *Genetics in Medicine*, **2019**, 21, 1884-1885	8.1	4
19	Higher adiposity and mental health: causal inference using Mendelian randomization. *Human Molecular Genetics*, **2021**, 30, 2371-2382	5.6	4
18	rs641738C>T near MBOAT7 is positively associated with liver fat, ALT, and histological severity of NAFLD: a meta-analysis		3
17	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
16	A common allele in FGF21 associated with preference for sugar consumption lowers body fat in the lower body and increases blood pressure		2
15	A case of H syndrome with a novel mutation in SLC29A3. *Meta Gene*, **2019**, 21, 100599	0.7	1
14	Higher maternal adiposity reduces offspring birth weight if associated with a metabolically favourable profile		1
13	Fetal alleles predisposing to metabolically favourable adiposity are associated with higher birth weight		1
12	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry		1
11	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
10	Ethnic Differences in Body Fat Deposition and Liver Fat Content in Two UK-Based Cohorts. *Obesity*, **2020**, 28, 2142-2152	8	1
9	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

List of Publications

8	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. *Diabetologia*, **2021**, 64, 2790-2802	10.3	0
7	A rare genetic variant in the manganese transporter SLC30A10 and elevated liver enzymes in the general population.. *Hepatology International*, **2022**, 1	8.8	0
6	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
5	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
4	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
3	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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