Timothy Frayling

List of Publications by Year
in descending order

170 papers	54,423 citations	6254 80 h-index	5255 165 g-index
199 all docs	199 docs citations	199 times ranked	50250 citing authors

#	Article	IF	Citations
1	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894.	12.6	3,884
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
4	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
5	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
8	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
9	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
10	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
11	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
12	Meta-analysis of genome-wide association studies for height and body mass index in â^¼700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	2.9	1,541
13	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. Nature Genetics, 2012, 44, 369-375.	21.4	1,338
14	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
15	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
16	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
17	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
18	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836

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19	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
20	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
21	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
22	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
23	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
24	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
25	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
26	Genomeâ€“wide association studies provide new insights into type 2 diabetes aetiology. Nature Reviews Genetics, 2007, 8, 657-662.	16.3	528
27	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
28	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	2.8	460
29	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
30	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
31	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
32	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	12.8	417
33	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
34	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
35	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	30.7	384
36	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383

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37	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
38	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. Nature Communications, 2019, 10, 1100.	12.8	369
39	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
40	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
41	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
42	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
43	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
44	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
45	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	3.5	308
46	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
47	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
48	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	21.4	250
49	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
50	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. BMJ, The, 2016, 352, i582.	6.0	247
51	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. Aging Cell, 2011, 10, 868-878.	6.7	230
52	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	21.4	227
53	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
54	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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55	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
56	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
57	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	12.0	177
58	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	2.9	176
59	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
60	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
61	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
62	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
63	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	1.9	159
64	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. American Journal of Human Genetics, 2019, 104, 275-286.	6.2	158
65	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
66	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
67	Using genetics to understand the causal influence of higher BMI on depression. International Journal of Epidemiology, 2019, 48, 834-848.	1.9	156
68	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
69	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	3.5	150
70	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002739.	8.4	144
71	A Putative Functional Polymorphism in the IGF-I Gene: Association Studies With Type 2 Diabetes, Adult Height, Glucose Tolerance, and Fetal Growth in U.K. Populations. Diabetes, 2002, 51, 2313-2316.	0.6	129
72	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

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73	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	21.4	120
74	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	12.8	117
75	Another explanation for apparent epistasis. Nature, 2014, 514, E3-E5.	27.8	116
76	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. Diabetes, 2015, 64, 2676-2684.	0.6	114
77	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	3.1	113
78	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
79	Phantasiaâ€"The psychological significance of lifelong visual imagery vividness extremes. Cortex, 2020, 130, 426-440.	2.4	106
80	Genetic predictors of participation in optional components of UK Biobank. Nature Communications, 2021, 12, 886.	12.8	106
81	New gene variants alter type 2 diabetes risk predominantly through reduced beta-cell function. Current Opinion in Clinical Nutrition and Metabolic Care, 2008, 11, 371-377.	2.5	102
82	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. Diabetes, 2017, 66, 2296-2309.	0.6	102
83	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
84	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
85	Mosaic Turner syndrome shows reduced penetrance in an adult population study. Genetics in Medicine, 2019, 21, 877-886.	2.4	88
86	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
87	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
88	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
89	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. BMJ: British Medical Journal, 2019, 365, l2327.	2.3	79
90	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

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91	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
92	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
93	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	12.8	68
94	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.6	67
95	Parental diabetes and birthweight in 236 030 individuals in the UK Biobank Study. International Journal of Epidemiology, 2013, 42, 1714-1723.	1.9	65
96	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
97	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
98	A Genome-Wide Scan in Families With Maturity-Onset Diabetes of the Young: Evidence for Further Genetic Heterogeneity. Diabetes, 2003, 52, 872-881.	0.6	62
99	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
100	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. Nature Communications, 2021, 12, 5647.	12.8	61
101	An Interleukin-18 Polymorphism Is Associated With Reduced Serum Concentrations and Better Physical Functioning in Older People. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2007, 62, 73-78.	3.6	55
102	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
103	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
104	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	2.5	49
105	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
106	Stratification by Smoking Status Reveals an Association of CHRNA5-A3-B4 Genotype with Body Mass Index in Never Smokers. PLoS Genetics, 2014, 10, e1004799.	3.5	45
107	Young-Onset Type 2 Diabetes Families Are the Major Contributors to Genetic Loci in the Diabetes UK Warren 2 Genome Scan and Identify Putative Novel Loci on Chromosomes 8q21, 21q22, and 22q11. Diabetes, 2003, 52, 1857-1863.	0.6	43
108	Effects of body mass index on relationship status, social contact and socio-economic position: Mendelian randomization and within-sibling study in UK Biobank. International Journal of Epidemiology, 2020, 49, 1173-1184.	1.9	42

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109	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
110	Effects of apolipoprotein B on lifespan and risks of major diseases including type 2 diabetes: a mendelian randomisation analysis using outcomes in first-degree relatives. The Lancet Healthy Longevity, 2021, 2, e317-e326.	4.6	41
111	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40
112	Associations Between Glycemic Traits and Colorectal Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2022, 114, 740-752.	6.3	35
113	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
114	Is disrupted sleep a risk factor for Alzheimerâ€™s disease? Evidence from a two-sample Mendelian randomization analysis. International Journal of Epidemiology, 2021, 50, 817-828.	1.9	31
115	Quantification of the overall contribution of gene-environment interaction for obesity-related traits. Nature Communications, 2020, 11, 1385.	12.8	31
116	Filaggrin gene mutations are associated with asthma and eczema in later life. Journal of Allergy and Clinical Immunology, 2008, 122, 834-836.	2.9	30
117	A rapid screening method for hepatocyte nuclear factor 1 alpha frameshift mutations; prevalence in maturity-onset diabetes of the young and late-onset non-insulin dependent diabetes. Human Genetics, 1997, 101, 351-354.	3.8	29
118	Higher adiposity and mental health: causal inference using Mendelian randomization. Human Molecular Genetics, 2021, 30, 2371-2382.	2.9	29
119	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.1	28
120	Influence of cell distribution and diabetes status on the association between mitochondrial <scp>DNA</scp> copy number and aging phenotypes in the In<scp>CHIANTI</scp> study. Aging Cell, 2018, 17, e12683.	6.7	26
121	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
122	Identifying molecular mediators of the relationship between body mass index and endometrial cancer risk: a Mendelian randomization analysis. BMC Medicine, 2022, 20, 125.	5.5	26
123	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 772-781.	8.6	25
124	Statins and type 2 diabetes: genetic studies on target. Lancet, The, 2015, 385, 310-312.	13.7	24
125	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
126	Chronotype Genetic Variant in PER2 is Associated with Intrinsic Circadian Period in Humans. Scientific Reports, 2019, 9, 5350.	3.3	24

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127	A genome-wide association study identifies 5 loci associated with frozen shoulder and implicates diabetes as a causal risk factor. PLoS Genetics, 2021, 17, e1009577.	3.5	23
128	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
129	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
130	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
131	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	2.8	18
132	Piecing together the FTO jigsaw. Genome Biology, 2011, 12, 104.	9.6	16
133	A genome-wide association study implicates multiple mechanisms influencing raised urinary albuminâ€“creatinine ratio. Human Molecular Genetics, 2019, 28, 4197-4207.	2.9	16
134	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
135	Mendelian Randomization Analyses Suggest Childhood Body Size Indirectly Influences End Points From Across the Cardiovascular Disease Spectrum Through Adult Body Size. Journal of the American Heart Association, 2021, 10, e021503.	3.7	16
136	Do sex hormones confound or mediate the effect of chronotype on breast and prostate cancer? A Mendelian randomization study. PLoS Genetics, 2022, 18, e1009887.	3.5	14
137	Are the causes of obesity primarily environmental? No. BMJ, The, 2012, 345, e5844-e5844.	6.0	13
138	An Ant Colony Optimization and Tabu List Approach to the Detection of Gene-Gene Interactions in Genome-Wide Association Studies [Research Frontier]. IEEE Computational Intelligence Magazine, 2015, 10, 54-65.	3.2	13
139	Mendelian randomisation in type 2 diabetes and coronary artery disease. Current Opinion in Genetics and Development, 2018, 50, 111-120.	3.3	13
140	Functional characterisation of ADIPOQ variants using individuals recruited by genotype. Molecular and Cellular Endocrinology, 2016, 428, 49-57.	3.2	12
141	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	2.9	10
142	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
143	Disease consequences of higher adiposity uncoupled from its adverse metabolic effects using Mendelian randomisation. ELife, 2022, 11, .	6.0	10
144	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	6.3	9

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145	Proposed mechanism for a novel insertion/deletion frameshift mutation (I414G415ATCG?CCA) in the hepatocyte nuclear factor 1 alpha (HNF-1?) gene which causes maturity-onset diabetes of the young (MODY). Human Mutation, 2000, 16, 273-273.	2.5	8
146	Commentary: Genetic association studies see light at the end of the tunnel. International Journal of Epidemiology, 2008, 37, 133-135.	1.9	8
147	Evaluation of Common Type 2 Diabetes Risk Variants in a South Asian Population of Sri Lankan Descent. PLoS ONE, 2014, 9, e98608.	2.5	8
148	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	2.9	8
149	Unreliability of genotyping arrays for detecting very rare variants in human genetic studies: Example from a recent study of MC4R. Cell, 2021, 184, 1651.	28.9	8
150	PLIN1 Haploinsufficiency Causes a Favorable Metabolic Profile. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2318-e2323.	3.6	7
151	Large Copy-Number Variants in UK Biobank Caused by Clonal Hematopoiesis May Confound Penetrance Estimates. American Journal of Human Genetics, 2020, 107, 325-329.	6.2	6
152	Physiology Helps GWAS Take a Step Closer to Mechanism. Diabetes, 2014, 63, 1836-1837.	0.6	5
153	Response to Prakash et al.. Genetics in Medicine, 2019, 21, 1884-1885.	2.4	5
154	Ant colony optimisation of decision tree and contingency table models for the discovery of geneâ€“gene interactions. IET Systems Biology, 2015, 9, 218-225.	1.5	4
155	Babies of South Asian and European Ancestry Show Similar Associations With Genetic Risk Score for Birth Weight Despite the Smaller Size of South Asian Newborns. Diabetes, 2022, 71, 821-836.	0.6	3
156	Simulated distributions from negative experiments highlight the importance of the body mass index distribution in explaining depressionâ€“body mass index genetic risk score interactions. International Journal of Epidemiology, 2022, 51, 1581-1592.	1.9	2
157	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. Human Molecular Genetics, 2022, 31, 1762-1775.	2.9	2
158	Commentary: A new dawn for genetic epidemiology?. International Journal of Epidemiology, 2009, 38, 975-977.	1.9	1
159	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.6	1
160	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
161	Recent Progress in the Identification of Genes Predisposing to the Metabolic Syndrome. , 2006, , 143-162.		0
162	The Hunt for Low-Frequency Alleles Predisposing to Type 2 Diabetes and Related Cardiovascular Risk Factors. Current Cardiovascular Risk Reports, 2015, 9, 1.	2.0	0

#	Article	IF	Citations
163	Authorsâ€™ reply to Toth. BMJ, The, 2016, 353, i1892.	6.0	0
164	Title is missing!. , 2020, 16, e1008044.		0
165	Title is missing!. , 2020, 16, e1008044.		0
166	Title is missing!. , 2020, 16, e1008044.		0
167	Title is missing!. , 2020, 16, e1008044.		0
168	Title is missing!. , 2020, 16, e1008044.		0
169	Title is missing!. , 2020, 16, e1008044.		0
170	130â€… Does visual imagery vividness have a genetic basis? A genome-wide associa- tion study of 1019 individuals. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A51.1-A51.	1.9	0