Michael N Weedon

List of Publications by Year
in descending order

195 papers	49,370 citations	4942 84 h-index	2940 189 g-index
229 all docs	229 docs citations	229 times ranked	47631 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.	6.0	3,884
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
4	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	6.0	2,040
5	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
6	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
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
8	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
9	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	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.	9.4	1,572
11	Meta-analysis of genome-wide association studies for height and body mass index in â^¼4700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	1.4	1,541
12	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. Nature Genetics, 2012, 44, 369-375.	9.4	1,338
13	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
14	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
15	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.	9.4	836
16	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
17	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
18	Large-Scale Association Studies of Variants in Genes Encoding the Pancreatic Â-Cell KATP Channel Subunits Kir6.2 (KCNJ11) and SUR1 (ABCC8) Confirm That the KCNJ11 E23K Variant Is Associated With Type 2 Diabetes. Diabetes, 2003, 52, 568-572.	0.3	688

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19	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
20	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
21	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
22	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
23	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
24	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	5.8	417
25	A Genome-Wide Association Study Identifies Protein Quantitative Trait Loci (pQTLs). PLoS Genetics, 2008, 4, e1000072.	1.5	415
26	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
27	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
28	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. Nature Communications, 2019, 10, 1100.	5.8	369
29	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.	0.3	335
30	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	9.4	333
31	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
32	Frequency and phenotype of type 1 diabetes in the first six decades of life: a cross-sectional, genetically stratified survival analysis from UK Biobank. Lancet Diabetes and Endocrinology,the, 2018, 6, 122-129.	5.5	291
33	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
34	Assessing the Combined Impact of 18 Common Genetic Variants of Modest Effect Sizes on Type 2 Diabetes Risk. Diabetes, 2008, 57, 3129-3135.	0.3	279
35	Common Variation in the FTO Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. Diabetes, 2008, 57, 1419-1426.	0.3	277
36	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. Nature Genetics, 2009, 41, 648-650.	9.4	266

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37	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. Nature Genetics, 2014, 46, 61-64.	9.4	255
38	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	9.4	250
39	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. BMJ, The, 2016, 352, i582.	3.0	247
40	Combining Information from Common Type 2 Diabetes Risk Polymorphisms Improves Disease Prediction. PLoS Medicine, 2006, 3, e374.	3.9	242
41	Association Analysis of 6,736 U.K. Subjects Provides Replication and ConfirmsTCF7L2as a Type 2 Diabetes Susceptibility Gene With a Substantial Effect on Individual Risk. Diabetes, 2006, 55, 2640-2644.	0.3	240
42	Exome Sequencing Identifies a DYNC1H1 Mutation in a Large Pedigree with Dominant Axonal Charcot-Marie-Tooth Disease. American Journal of Human Genetics, 2011, 89, 308-312.	2.6	233
43	A Type 1 Diabetes Genetic Risk Score Can Aid Discrimination Between Type 1 and Type 2 Diabetes in Young Adults. Diabetes Care, 2016, 39, 337-344.	4.3	231
44	Common Variants of the Novel Type 2 Diabetes GenesCDKAL1andHHEX/IDEAre Associated With Decreased Pancreatic Î²-Cell Function. Diabetes, 2007, 56, 3101-3104.	0.3	226
45	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
46	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190
47	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	5.8	189
48	Development and Standardization of an Improved Type 1 Diabetes Genetic Risk Score for Use in Newborn Screening and Incident Diagnosis. Diabetes Care, 2019, 42, 200-207.	4.3	187
49	Meta-Analysis and a Large Association Study Confirm a Role for Calpain-10 Variation in Type 2 Diabetes Susceptibility. American Journal of Human Genetics, 2003, 73, 1208-1212.	2.6	180
50	Evaluation of Common Variants in the Six Known Maturity-Onset Diabetes of the Young (MODY) Genes for Association With Type 2 Diabetes. Diabetes, 2007, 56, 685-693.	0.3	178
51	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	1.4	176
52	HLA-DQA1â€“HLA-DRB1 variants confer susceptibility to pancreatitis induced by thiopurine immunosuppressants. Nature Genetics, 2014, 46, 1131-1134.	9.4	165
53	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
54	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	0.9	159

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55	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. American Journal of Human Genetics, 2019, 104, 275-286.	2.6	158
56	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.	1.4	156
57	Using genetics to understand the causal influence of higher BMI on depression. International Journal of Epidemiology, 2019, 48, 834-848.	0.9	156
58	An in-frame deletion at the polymerase active site of POLD1 causes a multisystem disorder with lipodystrophy. Nature Genetics, 2013, 45, 947-950.	9.4	151
59	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
60	Type 1 Diabetes Genetic Risk Score: A Novel Tool to Discriminate Monogenic and Type 1 Diabetes. Diabetes, 2016, 65, 2094-2099.	0.3	146
61	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	5.8	136
62	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433.	0.3	135
63	A Common Variation in Deiodinase 1 Gene DIO1 Is Associated with the Relative Levels of Free Thyroxine and Triiodothyronine. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 3075-3081.	1.8	133
64	A common genetic variant in the 15q24 nicotinic acetylcholine receptor gene cluster (CHRNA5â€“CHRNA3â€“CHRNB4) is associated with a reduced ability of women to quit smoking in pregnancy. Human Molecular Genetics, 2009, 18, 2922-2927.	1.4	132
65	Reaching new heights: insights into the genetics of human stature. Trends in Genetics, 2008, 24, 595-603.	2.9	130
66	Association of Genetic Variants in NUDT15 With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease. JAMA - Journal of the American Medical Association, 2019, 321, 773.	3.8	129
67	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.3	122
68	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	9.4	120
69	A Common Haplotype of the Glucokinase Gene Alters Fasting Glucose and Birth Weight: Association in Six Studies and Population-Genetics Analyses. American Journal of Human Genetics, 2006, 79, 991-1001.	2.6	118
70	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
71	Another explanation for apparent epistasis. Nature, 2014, 514, E3-E5.	13.7	116
72	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. Diabetes, 2015, 64, 2676-2684.	0.3	114

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73	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	1.4	113
74	Type 2 Diabetes TCF7L2 Risk Genotypes Alter Birth Weight: A Study of 24,053 Individuals. American Journal of Human Genetics, 2007, 80, 1150-1161.	2.6	112
75	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.3	109
76	Predicting human height by Victorian and genomic methods. European Journal of Human Genetics, 2009, 17, 1070-1075.	1.4	108
77	A partially inactivating mutation in the sodium-dependent lysophosphatidylcholine transporter MFSD2A causes a non-lethal microcephaly syndrome. Nature Genetics, 2015, 47, 814-817.	9.4	108
78	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	1.4	104
79	A Type 1 Diabetes Genetic Risk Score Predicts Progression of Islet Autoimmunity and Development of Type 1 Diabetes in Individuals at Risk. Diabetes Care, 2018, 41, 1887-1894.	4.3	104
80	Genetic Regulation of Birth Weight and Fasting Glucose by a Common Polymorphism in the Islet Cell Promoter of the Glucokinase Gene. Diabetes, 2005, 54, 576-581.	0.3	103
81	Genetic scores to stratify risk of developing multiple islet autoantibodies and type 1 diabetes: A prospective study in children. PLoS Medicine, 2018, 15, e1002548.	3.9	101
82	Type 1 diabetes defined by severe insulin deficiency occurs after 30Âyears of age and is commonly treated as type 2 diabetes. Diabetologia, 2019, 62, 1167-1172.	2.9	100
83	Polycystic Kidney Disease with Hyperinsulinemic Hypoglycemia Caused by a Promoter Mutation in Phosphomannomutase 2. Journal of the American Society of Nephrology: JASN, 2017, 28, 2529-2539.	3.0	99
84	Heterozygous RFX6 protein truncating variants are associated with MODY with reduced penetrance. Nature Communications, 2017, 8, 888.	5.8	95
85	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	3.9	94
86	Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467.	0.3	93
87	Sex and BMI Alter the Benefits and Risks of Sulfonylureas and Thiazolidinediones in Type 2 Diabetes: A Framework for Evaluating Stratification Using Routine Clinical and Individual Trial Data. Diabetes Care, 2018, 41, 1844-1853.	4.3	91
88	Common Variants of the Hepatocyte Nuclear Factor-4Â P2 Promoter Are Associated With Type 2 Diabetes in the U.K. Population. Diabetes, 2004, 53, 3002-3006.	0.3	88
89	Mosaic Turner syndrome shows reduced penetrance in an adult population study. Genetics in Medicine, 2019, 21, 877-886.	1.1	88
90	Effects of the diabetes linked TCF7L2polymorphism in a representative older population. BMC Medicine, 2006, 4, 34.	2.3	87

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91	No Evidence of Association of ENPP1 Variants With Type 2 Diabetes or Obesity in a Study of 8,089 U.K. Caucasians. Diabetes, 2006, 55, 3175-3179.	0.3	86
92	The clinical consequences of heterogeneity within and between different diabetes types. Diabetologia, 2020, 63, 2040-2048.	2.9	86
93	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. Gut, 2019, 68, 854-865.	6.1	84
94	A combined risk score enhances prediction of type 1 diabetes among susceptible children. Nature Medicine, 2020, 26, 1247-1255.	15.2	83
95	TheHNF4AR76W mutation causes atypical dominant Fanconi syndrome in addition to a Î² cell phenotype. Journal of Medical Genetics, 2014, 51, 165-169.	1.5	82
96	Adherence to Oral Glucose-Lowering Therapies and Associations With 1-Year HbA1c: A Retrospective Cohort Analysis in a Large Primary Care Database. Diabetes Care, 2016, 39, 258-263.	4.3	79
97	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. BMJ: British Medical Journal, 2019, 365, l2327.	2.4	79
98	Mendelian Randomization Studies Do Not Support a Role for Raised Circulating Triglyceride Levels Influencing Type 2 Diabetes, Glucose Levels, or Insulin Resistance. Diabetes, 2011, 60, 1008-1018.	0.3	77
99	Association of the calpain-10 gene with type 2 diabetes in Europeans: Results of pooled and meta-analyses. Molecular Genetics and Metabolism, 2006, 89, 174-184.	0.5	76
100	Next-Generation Sequencing Reveals Deep Intronic Cryptic ABCC8 and HADH Splicing Founder Mutations Causing Hyperinsulinism by Pseudoexon Activation. American Journal of Human Genetics, 2013, 92, 131-136.	2.6	76
101	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.	2.9	76
102	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.	0.3	72
103	A meta-analysis of epigenome-wide association studies in Alzheimerâ€™s disease highlights novel differentially methylated loci across cortex. Nature Communications, 2021, 12, 3517.	5.8	72
104	Genetic Variants Associated With Glycine Metabolism and Their Role in Insulin Sensitivity and Type 2 Diabetes. Diabetes, 2013, 62, 2141-2150.	0.3	70
105	Absence of Islet Autoantibodies and Modestly Raised Glucose Values at Diabetes Diagnosis Should Lead to Testing for MODY: Lessons From a 5-Year Pediatric Swedish National Cohort Study. Diabetes Care, 2020, 43, 82-89.	4.3	68
106	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.	0.3	67
107	Precision Medicine in Type 2 Diabetes: Clinical Markers of Insulin Resistance Are Associated With Altered Short- and Long-term Glycemic Response to DPP-4 Inhibitor Therapy. Diabetes Care, 2018, 41, 705-712.	4.3	67
108	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. Diabetologia, 2016, 59, 1214-1221.	2.9	65

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109	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
110	Pitfalls of haplotype phasing from amplicon-based long-read sequencing. Scientific Reports, 2016, 6, 21746.	1.6	62
111	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.	1.4	61
112	Imputation of Variants from the 1000 Genomes Project Modestly Improves Known Associations and Can Identify Low-frequency Variant - Phenotype Associations Undetected by HapMap Based Imputation. PLoS ONE, 2013, 8, e64343.	1.1	61
113	Common genetic variants are significant risk factors for early menopause: results from the Breakthrough Generations Study. Human Molecular Genetics, 2011, 20, 186-192.	1.4	59
114	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.	1.7	55
115	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. American Journal of Human Genetics, 2019, 104, 157-163.	2.6	55
116	Genetic Variation in the Small Heterodimer Partner Gene and Young-Onset Type 2 Diabetes, Obesity, and Birth Weight in U.K. Subjects. Diabetes, 2003, 52, 1276-1279.	0.3	53
117	A Large-Scale Association Analysis of Common Variation of the HNF1Â Gene With Type 2 Diabetes in the U.K. Caucasian Population. Diabetes, 2005, 54, 2487-2491.	0.3	51
118	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.	0.4	51
119	Sleep classification from wrist-worn accelerometer data using random forests. Scientific Reports, 2021, 11, 24.	1.6	51
120	Common Variants Show Predicted Polygenic Effects on Height in the Tails of the Distribution, Except in Extremely Short Individuals. PLoS Genetics, 2011, 7, e1002439.	1.5	49
121	Development and validation of multivariable clinical diagnostic models to identify type 1 diabetes requiring rapid insulin therapy in adults aged 18â€“50 years. BMJ Open, 2019, 9, e031586.	0.8	49
122	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	1.1	49
123	Events in Early Life are Associated with Female Reproductive Ageing: A UK Biobank Study. Scientific Reports, 2016, 6, 24710.	1.6	48
124	Adult height variants affect birth length and growth rate in children. Human Molecular Genetics, 2011, 20, 4069-4075.	1.4	47
125	The Common p.R114W HNF4A Mutation Causes a Distinct Clinical Subtype of Monogenic Diabetes. Diabetes, 2016, 65, 3212-3217.	0.3	46
126	Next generation sequencing of chromosomal rearrangements in patients with split-hand/split-foot malformation provides evidence forDYNC1I1exonic enhancers ofDLX5/6expression in humans. Journal of Medical Genetics, 2014, 51, 264-267.	1.5	43

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127	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	1.4	40
128	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
129	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.3	37
130	Polygenic Risk Variants for Type 2 Diabetes Susceptibility Modify Age at Diagnosis in Monogenic HNF1A Diabetes. Diabetes, 2010, 59, 266-271.	0.3	37
131	Rare genetic variants in genes and loci linked to dominant monogenic developmental disorders cause milder related phenotypes in the general population. American Journal of Human Genetics, 2022, 109, 1308-1316.	2.6	35
132	Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from advances in genomic technologies. Neuroscience Letters, 2016, 625, 47-55.	1.0	34
133	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. Clinical Epigenetics, 2017, 9, 47.	1.8	34
134	Genome-Wide Association Study of Microscopic Colitis in the UK Biobank Confirms Immune-Related Pathogenesis. Journal of Crohn's and Colitis, 2019, 13, 1578-1582.	0.6	32
135	Comparison of Genetic Liability for Sleep Traits Among Individuals With Bipolar Disorder I or II and Control Participants. JAMA Psychiatry, 2020, 77, 303.	6.0	32
136	Targeted Allelic Expression Profiling in Human Islets Identifies cis-Regulatory Effects for Multiple Variants Identified by Type 2 Diabetes Genome-Wide Association Studies. Diabetes, 2015, 64, 1484-1491.	0.3	31
137	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.	0.9	31
138	Phosphodiesterase 8B Gene Polymorphism Is Associated with Subclinical Hypothyroidism in Pregnancy. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4608-4612.	1.8	30
139	Cohort profile for the MASTERMIND study: using the Clinical Practice Research Datalink (CPRD) to investigate stratification of response to treatment in patients with type 2 diabetes. BMJ Open, 2017, 7, e017989.	0.8	28
140	Meta-genome-wide association studies identify a locus on chromosome 1 and multiple variants in the MHC region for serum C-peptide in type 1 diabetes. Diabetologia, 2018, 61, 1098-1111.	2.9	26
141	Using Mendelian Randomisation methods to understand whether diurnal preference is causally related to mental health. Molecular Psychiatry, 2021, 26, 6305-6316.	4.1	26
142	Type 1 diabetes genetic risk score is discriminative of diabetes in non-Europeans: evidence from a study in India. Scientific Reports, 2020, 10, 9450.	1.6	25
143	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 772-781.	4.3	25
144	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.	0.3	24

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145	Chronotype Genetic Variant in PER2 is Associated with Intrinsic Circadian Period in Humans. Scientific Reports, 2019, 9, 5350.	1.6	24
146	Clinical and research uses of genetic risk scores in type 1 diabetes. Current Opinion in Genetics and Development, 2018, 50, 96-102.	1.5	23
147	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.	1.5	23
148	Utility of Diabetes Typeâ€“Specific Genetic Risk Scores for the Classification of Diabetes Type Among Multiethnic Youth. Diabetes Care, 2022, 45, 1124-1131.	4.3	22
149	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. International Journal of Epidemiology, 2020, 49, 1270-1281.	0.9	20
150	PLIN1 Haploinsufficiency Is Not Associated With Lipodystrophy. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3225-3230.	1.8	19
151	Zinc Transporter 8 Autoantibodies (ZnT8A) and a Type 1 Diabetes Genetic Risk Score Can Exclude Individuals With Type 1 Diabetes From Inappropriate Genetic Testing for Monogenic Diabetes. Diabetes Care, 2019, 42, e16-e17.	4.3	19
152	SavvyCNV: Genome-wide CNV calling from off-targetÂreads. PLoS Computational Biology, 2022, 18, e1009940.	1.5	18
153	The functional "KL-VS" variant of KLOTHO is not associated with type 2 diabetes in 5028 UK Caucasians. BMC Medical Genetics, 2006, 7, 51.	2.1	17
154	Relationship between E23K (an established type II diabetes-susceptibility variant within KCNJ11), polycystic ovary syndrome and androgen levels. European Journal of Human Genetics, 2007, 15, 679-684.	1.4	17
155	Analysis of large-scale sequencing cohorts does not support the role of variants inUCP2as a cause of hyperinsulinaemic hypoglycaemia. Human Mutation, 2017, 38, 1442-1444.	1.1	17
156	A single nucleotide polymorphism genetic risk score to aid diagnosis of coeliac disease: a pilot study in clinical care. Alimentary Pharmacology and Therapeutics, 2020, 52, 1165-1173.	1.9	17
157	A cautionary tale: the non-causal association between type 2 diabetes risk SNP, rs7756992, and levels of non-coding RNA, CDKAL1-v1. Diabetologia, 2015, 58, 745-748.	2.9	16
158	A genome-wide association study implicates multiple mechanisms influencing raised urinary albuminâ€“creatinine ratio. Human Molecular Genetics, 2019, 28, 4197-4207.	1.4	16
159	Novel homozygous missense mutation in GAN associated with Charcot-Marie-Tooth disease type 2 in a large consanguineous family from Israel. BMC Medical Genetics, 2016, 17, 82.	2.1	15
160	IgA Nephropathy Genetic Risk Score to Estimate the Prevalence of IgA Nephropathy in UK Biobank. Kidney International Reports, 2020, 5, 1643-1650.	0.4	15
161	Retrovirally Expressed Metal Response Element-Binding Transcription Factor-1 Normalizes Metallothionein-1 Gene Expression and Protects Cells against Zinc, but Not Cadmium, Toxicity. Toxicology and Applied Pharmacology, 2002, 178, 93-101.	1.3	14
162	The acute transcriptional response to resistance exercise: impact of age and contraction mode. Aging, 2019, 11, 2111-2126.	1.4	14

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163	Detection and characterization of male sex chromosome abnormalities in the UK Biobank study. Genetics in Medicine, 2022, 24, 1909-1919.	1.1	14
164	Assessment of the Role of Common Genetic Variation in the Transient Neonatal Diabetes Mellitus (TNDM) Region in Type 2 Diabetes: A Comparative Genomic and Tagging Single Nucleotide Polymorphism Approach. Diabetes, 2006, 55, 2272-2276.	0.3	13
165	Objective assessment of sleep regularity in 60 000 UK Biobank participants using an open-source package. Sleep, 2021, 44, .	0.6	13
166	The Common HNF1A Variant I27L Is a Modifier of Age at Diabetes Diagnosis in Individuals With HNF1A-MODY. Diabetes, 2018, 67, 1903-1907.	0.3	12
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