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	Association of birthweight and penetrance of diabetes in individuals with HNF4A-MODY: a cohort study. Diabetologia, 2022, 65, 246-249.	2.9	2
2	Systematic genetic testing for recessively inherited monogenic diabetes: a cross-sectional study in paediatric diabetes clinics. Diabetologia, 2022, 65, 336-342.	2.9	12
3	A Comparative Safety Analysis of Medicines Based on the UK Pharmacovigilance and General Practice Prescribing Data in England. In Vivo, 2022, 36, 780-800.	0.6	3
4	SavvyCNV: Genome-wide CNV calling from off-targetÂreads. PLoS Computational Biology, 2022, 18, e1009940.	1.5	18
5	PLIN1 Haploinsufficiency Causes a Favorable Metabolic Profile. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2318-e2323.	1.8	7
6	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
7	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 772-781.	4.3	25
8	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
9	Detection and characterization of male sex chromosome abnormalities in the UK Biobank study. Genetics in Medicine, 2022, 24, 1909-1919.	1.1	14
10	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
11	Sleep classification from wrist-worn accelerometer data using random forests. Scientific Reports, 2021, 11, 24.	1.6	51
12	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	5.8	136
13	Unreliability of genotyping arrays for detecting very rare variants in human genetic studies: Example from a recent study of MC4R. Cell, 2021, 184, 1651.	13.5	8
14	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
15	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
16	Using Mendelian Randomisation methods to understand whether diurnal preference is causally related to mental health. Molecular Psychiatry, 2021, 26, 6305-6316.	4.1	26
17	DR15-DQ6 remains dominantly protective against type 1 diabetes throughout the first five decades of life. Diabetologia, 2021, 64, 2258-2265.	2.9	8
18	Estimating disease prevalence in large datasets using genetic risk scores. Nature Communications, 2021, 12, 6441.	5.8	6

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19	Objective assessment of sleep regularity in 60 000 UK Biobank participants using an open-source package. Sleep, 2021, 44, .	0.6	13
20	Methods for quick, accurate and cost-effective determination of the type 1 diabetes genetic risk score (T1D-GRS). Clinical Chemistry and Laboratory Medicine, 2020, 58, e102-e104.	1.4	8
21	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
22	Assessment of MTNR1B Type 2 Diabetes Genetic Risk Modification by Shift Work and Morningness-Eveningness Preference in the UK Biobank. Diabetes, 2020, 69, 259-266.	0.3	11
23	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
24	A combined risk score enhances prediction of type 1 diabetes among susceptible children. Nature Medicine, 2020, 26, 1247-1255.	15.2	83
25	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
26	The clinical consequences of heterogeneity within and between different diabetes types. Diabetologia, 2020, 63, 2040-2048.	2.9	86
27	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
28	Large Copy-Number Variants in UK Biobank Caused by Clonal Hematopoiesis May Confound Penetrance Estimates. American Journal of Human Genetics, 2020, 107, 325-329.	2.6	6
29	Clinical Features and Genetic Risk of Demyelination Following Anti-TNF Treatment. Journal of Crohn's and Colitis, 2020, 14, 1653-1661.	0.6	9
30	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
31	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
32	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
33	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
34	A genome-wide association study implicates multiple mechanisms influencing raised urinary albuminâ€“creatinine ratio. Human Molecular Genetics, 2019, 28, 4197-4207.	1.4	16
35	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
36	0824 Using Mendelian Randomization To Understand How Chronotype Influences Breast Cancer Risk. Sleep, 2019, 42, A330-A331.	0.6	0

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37	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. Gut, 2019, 68, 854-865.	6.1	84
38	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	5.8	417
39	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
40	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
41	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
42	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
43	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
44	Chronotype Genetic Variant in PER2 is Associated with Intrinsic Circadian Period in Humans. Scientific Reports, 2019, 9, 5350.	1.6	24
45	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	5.8	189
46	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
47	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	9.4	250
48	P017â€...Differences in genetic risk for insomnia, hypersomnia and chronotype in bipolar disorder subtypes. , 2019, , .		0
49	OWE-16â€...Development and clinical validation of a genetic risk score for coeliac disease. , 2019, , .		0
50	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
51	Mosaic Turner syndrome shows reduced penetrance in an adult population study. Genetics in Medicine, 2019, 21, 877-886.	1.1	88
52	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
53	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
54	Using genetics to understand the causal influence of higher BMI on depression. International Journal of Epidemiology, 2019, 48, 834-848.	0.9	156

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55	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
56	Response to Prakash et al.. Genetics in Medicine, 2019, 21, 1884-1885.	1.1	5
57	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
58	The acute transcriptional response to resistance exercise: impact of age and contraction mode. Aging, 2019, 11, 2111-2126.	1.4	14
59	Refinement of the critical genomic region for hypoglycaemia in the Chromosome 9p deletion syndrome. Wellcome Open Research, 2019, 4, 149.	0.9	3
60	Refinement of the critical genomic region for congenital hyperinsulinismÂin the Chromosome 9p deletion syndrome. Wellcome Open Research, 2019, 4, 149.	0.9	5
61	Genetic risk scores in adult-onset type 1 diabetes â€“ Authors' reply. Lancet Diabetes and Endocrinology,the, 2018, 6, 169.	5.5	4
62	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
63	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
64	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
65	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
66	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
67	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
68	PLIN1 Haploinsufficiency Is Not Associated With Lipodystrophy. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3225-3230.	1.8	19
69	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
70	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
71	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
72	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.	1.4	1,541

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73	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
74	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	1.4	40
75	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	0.9	159
76	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
77	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
78	Heterozygous RFX6 protein truncating variants are associated with MODY with reduced penetrance. Nature Communications, 2017, 8, 888.	5.8	95
79	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
80	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
81	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
82	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. Clinical Epigenetics, 2017, 9, 47.	1.8	34
83	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	1.1	49
84	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
85	Events in Early Life are Associated with Female Reproductive Ageing: A UK Biobank Study. Scientific Reports, 2016, 6, 24710.	1.6	48
86	Pitfalls of haplotype phasing from amplicon-based long-read sequencing. Scientific Reports, 2016, 6, 21746.	1.6	62
87	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
88	From Association to Function: KCNJ11 and ABCC8. , 2016, , 363-377.		0
89	Type 1 Diabetes Genetic Risk Score: A Novel Tool to Discriminate Monogenic and Type 1 Diabetes. Diabetes, 2016, 65, 2094-2099.	0.3	146
90	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

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91	Length ofFMR1repeat alleles within the normal range does not substantially affect the risk of early menopause. Human Reproduction, 2016, 31, 2396-2403.	0.4	7
92	The Common p.R114W HNF4A Mutation Causes a Distinct Clinical Subtype of Monogenic Diabetes. Diabetes, 2016, 65, 3212-3217.	0.3	46
93	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
94	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. BMJ, The, 2016, 352, i582.	3.0	247
95	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
96	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
97	Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from advances in genomic technologies. Neuroscience Letters, 2016, 625, 47-55.	1.0	34
98	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
99	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
100	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	1.4	113
101	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	3.9	94
102	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
103	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
104	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
105	Using Genetic Variants to Assess the Relationship Between Circulating Lipids and Type 2 Diabetes. Diabetes, 2015, 64, 2676-2684.	0.3	114
106	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	9.4	120
107	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
108	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	1.4	8

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109	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
110	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
111	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
112	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. Nature Genetics, 2014, 46, 61-64.	9.4	255
113	HLA-DQA1â€“HLA-DRB1 variants confer susceptibility to pancreatitis induced by thiopurine immunosuppressants. Nature Genetics, 2014, 46, 1131-1134.	9.4	165
114	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
115	Another explanation for apparent epistasis. Nature, 2014, 514, E3-E5.	13.7	116
116	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
117	Genetic Variants Associated With Glycine Metabolism and Their Role in Insulin Sensitivity and Type 2 Diabetes. Diabetes, 2013, 62, 2141-2150.	0.3	70
118	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
119	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
120	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
121	Genome-Wide Association Studies of Human Growth Traits. Nestle Nutrition Institute Workshop Series, 2013, 71, 29-38.	1.5	0
122	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
123	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
124	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
125	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
126	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

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127	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
128	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
129	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
130	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
131	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
132	Adult height variants affect birth length and growth rate in children. Human Molecular Genetics, 2011, 20, 4069-4075.	1.4	47
133	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
134	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
135	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
136	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
137	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
138	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
139	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
140	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
141	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
142	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
143	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
144	Polygenic Risk Variants for Type 2 Diabetes Susceptibility Modify Age at Diagnosis in Monogenic HNF1A Diabetes. Diabetes, 2010, 59, 266-271.	0.3	37

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145	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
146	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
147	Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467.	0.3	93
148	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.3	109
149	Phosphodiesterase 8B Gene Polymorphism Is Associated with Subclinical Hypothyroidism in Pregnancy. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4608-4612.	1.8	30
150	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
151	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433.	0.3	135
152	Predicting human height by Victorian and genomic methods. European Journal of Human Genetics, 2009, 17, 1070-1075.	1.4	108
153	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
154	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. Nature Genetics, 2009, 41, 648-650.	9.4	266
155	A Genome-Wide Association Study Identifies Protein Quantitative Trait Loci (pQTLs). PLoS Genetics, 2008, 4, e1000072.	1.5	415
156	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
157	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
158	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
159	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
160	Reaching new heights: insights into the genetics of human stature. Trends in Genetics, 2008, 24, 595-603.	2.9	130
161	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
162	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

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163	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
164	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
165	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
166	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
167	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
168	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
169	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
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171	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	9.4	333
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