Andrew Hattersley

List of Publications by Year
in descending order

708 papers	99,813 citations	256 142 h-index	336 286 g-index
748 all docs	748 docs citations	748 times ranked	63560 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	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	12.6	2,040
6	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
7	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
8	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
9	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
10	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.	21.4	1,683
11	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
12	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
13	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
14	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
15	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	21.4	1,298
16	Mutations in the hepatocyte nuclear factor-1Î± gene in maturity-onset diabetes of the young (MODY3). Nature, 1996, 384, 455-458.	27.8	1,240
17	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
18	Activating Mutations in the Gene Encoding the ATP-Sensitive Potassium-Channel Subunit Kir6.2 and Permanent Neonatal Diabetes. New England Journal of Medicine, 2004, 350, 1838-1849.	27.0	1,077

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19	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
20	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
21	Switching from Insulin to Oral Sulfonylureas in Patients with Diabetes Due to Kir6.2 Mutations. New England Journal of Medicine, 2006, 355, 467-477.	27.0	878
22	The fetal insulin hypothesis: an alternative explanation of the association of low bir thweight with diabetes and vascular disease. Lancet, The, 1999, 353, 1789-1792.	13.7	857
23	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
24	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
25	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	21.4	742
26	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
27	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.	0.6	688
28	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
29	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
30	Mutations in the glucokinase gene of the fetus result in reduced birth weight. Nature Genetics, 1998, 19, 268-270.	21.4	565
31	Maturity-onset diabetes of the young (MODY): how many cases are we missing?. Diabetologia, 2010, 53, 2504-2508.	6.3	560
32	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
33	Genetic cause of hyperglycaemia and response to treatment in diabetes. Lancet, The, 2003, 362, 1275-1281.	13.7	526
34	Insulin gene mutations as a cause of permanent neonatal diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15040-15044.	7.1	494
35	Excess mortality and cardiovascular disease in young adults with type 1 diabetes in relation to age at onset: a nationwide, register-based cohort study. Lancet, The, 2018, 392, 477-486.	13.7	492
36	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	21.4	469

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37	What makes a good genetic association study?. Lancet, The, 2005, 366, 1315-1323.	13.7	464
38	Hypomethylation of multiple imprinted loci in individuals with transient neonatal diabetes is associated with mutations in ZFP57. Nature Genetics, 2008, 40, 949-951.	21.4	460
39	The clinical utility of Câ€peptide measurement in the care of patients with diabetes. Diabetic Medicine, 2013, 30, 803-817.	2.3	455
40	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
41	Clinical implications of a molecular genetic classification of monogenic Î²-cell diabetes. Nature Clinical Practice Endocrinology and Metabolism, 2008, 4, 200-213.	2.8	439
42	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.	3.5	419
43	Activating germline mutations in STAT3 cause early-onset multi-organ autoimmune disease. Nature Genetics, 2014, 46, 812-814.	21.4	411
44	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
45	Mutations in PTF1A cause pancreatic and cerebellar agenesis. Nature Genetics, 2004, 36, 1301-1305.	21.4	405
46	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
47	Activating Mutations in Kir6.2 and Neonatal Diabetes. Diabetes, 2005, 54, 2503-2513.	0.6	399
48	Linkage of type 2 diabetes to the glucokinase gene. Lancet, The, 1992, 339, 1307-1310.	13.7	392
49	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. Nature Genetics, 2011, 43, 117-120.	21.4	390
50	Best practice guidelines for the molecular genetic diagnosis of maturity-onset diabetes of the young. Diabetologia, 2008, 51, 546-553.	6.3	376
51	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	21.4	373
52	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
53	Mutations in the human Delta homologue, DLL3, cause axial skeletal defects in spondylocostal dysostosis. Nature Genetics, 2000, 24, 438-441.	21.4	362
54	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

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55	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
56	Permanent Neonatal Diabetes due to Mutations in KCNJ11 Encoding Kir6.2. Diabetes, 2004, 53, 2713-2718.	0.6	350
57	Macrosomia and Hyperinsulinaemic Hypoglycaemia in Patients with Heterozygous Mutations in the HNF4A Gene. PLoS Medicine, 2007, 4, e118.	8.4	349
58	Insulin Mutation Screening in 1,044 Patients With Diabetes. Diabetes, 2008, 57, 1034-1042.	0.6	347
59	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
60	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	21.4	333
61	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
62	Mutations in ATP-Sensitive K+ Channel Genes Cause Transient Neonatal Diabetes and Permanent Diabetes in Childhood or Adulthood. Diabetes, 2007, 56, 1930-1937.	0.6	320
63	Prevalence, Characteristics and Clinical Diagnosis of Maturity Onset Diabetes of the Young Due to Mutations in HNF1A, HNF4A, and Glucokinase: Results From the SEARCH for Diabetes in Youth. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 4055-4062.	3.6	310
64	A Genomewide Scan for Loci Predisposing to Type 2 Diabetes in a U.K. Population (The Diabetes UK) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Locus on Chromosome 1q. American Journal of Human Genetics, 2001, 69, 553-569.	6.2	300
65	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. Lancet, The, 2005, 366, 1954-1959.	13.7	300
66	Rfx6 directs islet formation and insulin production in mice and humans. Nature, 2010, 463, 775-780.	27.8	300
67	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
68	Mutations in hepatocyte nuclear factor-1Â and their related phenotypes. Journal of Medical Genetics, 2005, 43, 84-90.	3.2	291
69	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.	11.4	291
70	Common Variation in the DIO2 Gene Predicts Baseline Psychological Well-Being and Response to Combination Thyroxine Plus Triiodothyronine Therapy in Hypothyroid Patients. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 1623-1629.	3.6	287
71	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
72	Variation in TCF7L2 Influences Therapeutic Response to Sulfonylureas. Diabetes, 2007, 56, 2178-2182.	0.6	284

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73	Disease progression and treatment response in data-driven subgroups of type 2 diabetes compared with models based on simple clinical features: an analysis using clinical trial data. Lancet Diabetes and Endocrinology,the, 2019, 7, 442-451.	11.4	280
74	Assessing the Combined Impact of 18 Common Genetic Variants of Modest Effect Sizes on Type 2 Diabetes Risk. Diabetes, 2008, 57, 3129-3135.	0.6	279
75	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.	0.6	277
76	Regulation ofFto/Ftmgene expression in mice and humans. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2008, 294, R1185-R1196.	1.8	270
77	Mutations in the Hepatocyte Nuclear Factor-1Î² Gene Are Associated with Familial Hypoplastic Glomerulocystic Kidney Disease. American Journal of Human Genetics, 2001, 68, 219-224.	6.2	263
78	Prevalence of Vascular Complications Among Patients With Glucokinase Mutations and Prolonged, Mild Hyperglycemia. JAMA - Journal of the American Medical Association, 2014, 311, 279.	7.4	257
79	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. Nature Genetics, 2014, 46, 61-64.	21.4	255
80	Definition, epidemiology and classification of diabetes in children and adolescents. Pediatric Diabetes, 2009, 10, 3-12.	2.9	252
81	The effect of early, comprehensive genomic testing on clinical care in neonatal diabetes: an international cohort study. Lancet, The, 2015, 386, 957-963.	13.7	250
82	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
83	GATA6 haploinsufficiency causes pancreatic agenesis in humans. Nature Genetics, 2012, 44, 20-22.	21.4	249
84	Improved genetic testing for monogenic diabetes using targeted next-generation sequencing. Diabetologia, 2013, 56, 1958-1963.	6.3	248
85	Altered Insulin Secretory Responses to Glucose in Diabetic and Nondiabetic Subjects With Mutations in the Diabetes Susceptibility Gene MODY3 on Chromosome 12. Diabetes, 1996, 45, 1503-1510.	0.6	245
86	Sensitivity to sulphonylureas in patients with hepatocyte nuclear factor-1alpha gene mutations: evidence for pharmacogenetics in diabetes. Diabetic Medicine, 2000, 17, 543-545.	2.3	244
87	The diagnosis and management of monogenic diabetes in children and adolescents. Pediatric Diabetes, 2009, 10, 33-42.	2.9	243
88	Combining Information from Common Type 2 Diabetes Risk Polymorphisms Improves Disease Prediction. PLoS Medicine, 2006, 3, e374.	8.4	242
89	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.	0.6	240
90	The majority of patients with long-duration type 1 diabetes are insulin microsecretors and have functioning beta cells. Diabetologia, 2014, 57, 187-191.	6.3	240

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91	Effective Treatment With Oral Sulfonylureas in Patients With Diabetes Due to Sulfonylurea Receptor 1 (SUR1) Mutations. Diabetes Care, 2008, 31, 204-209.	8.6	239
92	The fat massâ€“and obesity-associated locus and dietary intake in children. American Journal of Clinical Nutrition, 2008, 88, 971-978.	4.7	239
93	The development and validation of a clinical prediction model to determine the probability of MODY in patients with young-onset diabetes. Diabetologia, 2012, 55, 1265-1272.	6.3	238
94	Maturity-onset diabetes of the young: clinical heterogeneity explained by genetic heterogeneity. Diabetic Medicine, 1998, 15, 15-24.	2.3	237
95	HNF1B-associated renal and extra-renal diseaseâ€”an expanding clinical spectrum. Nature Reviews Nephrology, 2015, 11, 102-112.	9.6	237
96	Precision diabetes: learning from monogenic diabetes. Diabetologia, 2017, 60, 769-777.	6.3	237
97	Beta-cell genes and diabetes: molecular and clinical characterization of mutations in transcription factors. Diabetes, 2001, 50, S94-S100.	0.6	235
98	The genetic abnormality in the beta cell determines the response to an oral glucose load. Diabetologia, 2002, 45, 427-435.	6.3	235
99	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.	8.6	231
100	Clinical features, diagnosis and management of maternally inherited diabetes and deafness (MIDD) associated with the 3243A>G mitochondrial point mutation. Diabetic Medicine, 2008, 25, 383-399.	2.3	229
101	ISPAD Clinical Practice Consensus Guidelines 2018: The diagnosis and management of monogenic diabetes in children and adolescents. Pediatric Diabetes, 2018, 19, 47-63.	2.9	227
102	Common Variants of the Novel Type 2 Diabetes GenesCDKAL1andHHEX/IDEAre Associated With Decreased Pancreatic Î²-Cell Function. Diabetes, 2007, 56, 3101-3104.	0.6	226
103	Common variants in the TCF7L2 gene are strongly associated with type 2 diabetes mellitus in the Indian population. Diabetologia, 2006, 50, 63-67.	6.3	225
104	Molecular basis of Kir6.2 mutations associated with neonatal diabetes or neonatal diabetes plus neurological features. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17539-17544.	7.1	223
105	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	21.4	223
106	Mutations in KCNJ11, which encodes Kir6.2, are a common cause of diabetes diagnosed in the first 6Âmonths of life, with the phenotype determined by genotype. Diabetologia, 2006, 49, 1190-1197.	6.3	221
107	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
108	Recognition and Management of Individuals With Hyperglycemia Because of a Heterozygous Glucokinase Mutation. Diabetes Care, 2015, 38, 1383-1392.	8.6	217

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109	Missense mutations in the insulin promoter factor-1 gene predispose to type 2 diabetes. Journal of Clinical Investigation, 1999, 104, R33-R39.	8.2	216
110	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. PLoS ONE, 2010, 5, e14040.	2.5	215
111	A genetic diagnosis of HNF1A diabetes alters treatment and improves glycaemic control in the majority of insulinâ€treated patients. Diabetic Medicine, 2009, 26, 437-441.	2.3	205
112	Precision Medicine in Diabetes: A Consensus Report From the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). Diabetes Care, 2020, 43, 1617-1635.	8.6	204
113	Molecular genetics and phenotypic characteristics of MODY caused by hepatocyte nuclear factor 4Î± mutations in a large European collection. Diabetologia, 2005, 48, 878-885.	6.3	203
114	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
115	A heterozygous activating mutation in the sulphonylurea receptor SUR1 (ABCC8) causes neonatal diabetes. Human Molecular Genetics, 2006, 15, 1793-1800.	2.9	196
116	Permanent Neonatal Diabetes Caused by Dominant, Recessive, or Compound Heterozygous SUR1 Mutations with Opposite Functional Effects. American Journal of Human Genetics, 2007, 81, 375-382.	6.2	194
117	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	3.5	194
118	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.	3.5	190
119	A distant upstream promoter of the HNF-4alpha gene connects the transcription factors involved in maturity-onset diabetes of the young. Human Molecular Genetics, 2001, 10, 2089-2097.	2.9	186
120	Mutations in the Hepatocyte Nuclear Factorâ€“1Î± Gene Are a Common Cause of Maturity-Onset Diabetes of the Young in the U.K.. Diabetes, 1997, 46, 720-725.	0.6	185
121	Recessive mutations in the INS gene result in neonatal diabetes through reduced insulin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3105-3110.	7.1	185
122	Analysis of parent-offspring trios provides evidence for linkage and association between the insulin gene and type 2 diabetes mediated exclusively through paternally transmitted class III variable number tandem repeat alleles. Diabetes, 2000, 49, 126-130.	0.6	184
123	Relapsing diabetes can result from moderately activating mutations in KCNJ11. Human Molecular Genetics, 2005, 14, 925-934.	2.9	184
124	A high prevalence of glucokinase mutations in gestational diabetic subjects selected by clinical criteria. Diabetologia, 2000, 43, 250-253.	6.3	183
125	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.	6.2	180
126	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.	0.6	178

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127	Common Nonsynonymous Substitutions in SLCO1B1 Predispose to Statin Intolerance in Routinely Treated Individuals With Type 2 Diabetes: A Go-DARTS Study. Clinical Pharmacology and Therapeutics, 2011, 89, 210-216.	4.7	177
128	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
129	Islet autoantibodies can discriminate maturityâ€onset diabetes of the young (MODY) from Typeâ€ƒ1 diabetes. Diabetic Medicine, 2011, 28, 1028-1033.	2.3	173
130	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
131	First UK survey of paediatric type 2 diabetes and MODY. Archives of Disease in Childhood, 2004, 89, 526-529.	1.9	172
132	Systematic Population Screening, Using Biomarkers and Genetic Testing, Identifies 2.5% of the U.K. Pediatric Diabetes Population With Monogenic Diabetes. Diabetes Care, 2016, 39, 1879-1888.	8.6	172
133	Studies of Association between the Gene for Calpain-10 and Type 2 Diabetes Mellitus in the United Kingdom. American Journal of Human Genetics, 2001, 69, 544-552.	6.2	171
134	Kir6.2 Mutations Are a Common Cause of Permanent Neonatal Diabetes in a Large Cohort of French Patients. Diabetes, 2004, 53, 2719-2722.	0.6	171
135	The diagnosis and management of monogenic diabetes in children and adolescents. Pediatric Diabetes, 2014, 15, 47-64.	2.9	170
136	FTO gene variants are strongly associated with type 2 diabetes in South Asian Indians. Diabetologia, 2009, 52, 247-252.	6.3	168
137	Cross-sectional and longitudinal studies suggest pharmacological treatment used in patients with glucokinase mutations does not alter glycaemia. Diabetologia, 2014, 57, 54-56.	6.3	164
138	Renal cysts and diabetes syndrome resulting from mutations in hepatocyte nuclear factor-1Â. Nephrology Dialysis Transplantation, 2004, 19, 2703-2708.	0.7	163
139	Abnormal nephron development associated with a frameshift mutation in the transcription factor hepatocyte nuclear factor-1Î²1. Kidney International, 2000, 57, 898-907.	5.2	162
140	Exploring the Developmental Overnutrition Hypothesis Using Parentalâ€“Offspring Associations and FTO as an Instrumental Variable. PLoS Medicine, 2008, 5, e33.	8.4	162
141	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
142	Different genes, different diabetes: lessons from maturity-onset diabetes of the young. Annals of Medicine, 2002, 34, 207-216.	3.8	156
143	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
144	Reduced-Function SLC22A1 Polymorphisms Encoding Organic Cation Transporter 1 and Glycemic Response to Metformin: A GoDARTS Study. Diabetes, 2009, 58, 1434-1439.	0.6	153

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145	An in-frame deletion at the polymerase active site of POLD1 causes a multisystem disorder with lipodystrophy. Nature Genetics, 2013, 45, 947-950.	21.4	151
146	Insights Into the Biochemical and Genetic Basis of Glucokinase Activation From Naturally Occurring Hypoglycemia Mutations. Diabetes, 2003, 52, 2433-2440.	0.6	150
147	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	3.5	150
148	Type 1 Diabetes Genetic Risk Score: A Novel Tool to Discriminate Monogenic and Type 1 Diabetes. Diabetes, 2016, 65, 2094-2099.	0.6	146
149	Homozygous Mutations inNEUROD1Are Responsible for a Novel Syndrome of Permanent Neonatal Diabetes and Neurological Abnormalities. Diabetes, 2010, 59, 2326-2331.	0.6	143
150	Atypical familial juvenile hyperuricemic nephropathy associated with a hepatocyte nuclear factor-1Î² gene mutation. Kidney International, 2003, 63, 1645-1651.	5.2	142
151	Hepatocyte nuclear factorâ€1 beta mutations cause neonatal diabetes and intrauterine growth retardation: support for a critical role of HNFâ€1Î² in human pancreatic development. Diabetic Medicine, 2006, 23, 1301-1306.	2.3	142
152	Missense glucokinase mutation in maturityâ€“onset diabetes of the young and mutation screening in lateâ€“onset diabetes. Nature Genetics, 1992, 2, 153-156.	21.4	141
153	Loss-of-Function CYP2C9 Variants Improve Therapeutic Response to Sulfonylureas in Type 2 Diabetes: A Go-DARTS Study. Clinical Pharmacology and Therapeutics, 2010, 87, 52-56.	4.7	141
154	Heterozygous ABCC8 mutations are a cause of MODY. Diabetologia, 2012, 55, 123-127.	6.3	141
155	Type 2 Diabetes and COVID-19â€“Related Mortality in the Critical Care Setting: A National Cohort Study in England, Marchâ€“July 2020. Diabetes Care, 2021, 44, 50-57.	8.6	139
156	ISPAD Clinical Practice Consensus Guidelines 2006?2007 The diagnosis and management of monogenic diabetes in children. Pediatric Diabetes, 2006, 7, 352-360.	2.9	138
157	Permanent Neonatal Diabetes and Enteric Anendocrinosis Associated With Biallelic Mutations in NEUROG3. Diabetes, 2011, 60, 1349-1353.	0.6	138
158	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433.	0.6	135
159	KCNJ11 activating mutations are associated with developmental delay, epilepsy and neonatal diabetes syndrome and other neurological features. European Journal of Human Genetics, 2006, 14, 824-830.	2.8	134
160	Solitary functioning kidney and diverse genital tract malformations associated with hepatocyte nuclear factor-1Î² mutations. Kidney International, 2002, 61, 1243-1251.	5.2	133
161	Persistent Hyperinsulinemic Hypoglycemia and Maturity-Onset Diabetes of the Young Due to Heterozygous HNF4A Mutations. Diabetes, 2008, 57, 1659-1663.	0.6	133
162	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.	3.6	133

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163	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.	2.9	132
164	Markers of Î²-Cell Failure Predict Poor Glycemic Response to GLP-1 Receptor Agonist Therapy in Type 2 Diabetes. Diabetes Care, 2016, 39, 250-257.	8.6	132
165	KCNJ11activating mutations in Italian patients with permanent neonatal diabetes. Human Mutation, 2005, 25, 22-27.	2.5	131
166	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
167	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
168	Maturity-onset diabetes of the young: from clinical description to molecular genetic characterization. Best Practice and Research in Clinical Endocrinology and Metabolism, 2001, 15, 309-323.	4.7	128
169	GATA6 Mutations Cause a Broad Phenotypic Spectrum of Diabetes From Pancreatic Agenesis to Adult-Onset Diabetes Without Exocrine Insufficiency. Diabetes, 2013, 62, 993-997.	0.6	128
170	Wolcott-Rallison Syndrome Is the Most Common Genetic Cause of Permanent Neonatal Diabetes in Consanguineous Families. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4162-4170.	3.6	127
171	Urinary C-Peptide Creatinine Ratio Is a Practical Outpatient Tool for Identifying Hepatocyte Nuclear Factor 1-Î±/Hepatocyte Nuclear Factor 4-Î± Maturity-Onset Diabetes of the Young From Long-Duration Type 1 Diabetes. Diabetes Care, 2011, 34, 286-291.	8.6	123
172	Analysis of Transcription Factors Key for Mouse Pancreatic Development Establishes NKX2-2 and MNX1 Mutations as Causes of Neonatal Diabetes in Man. Cell Metabolism, 2014, 19, 146-154.	16.2	123
173	The 0.1% of the Population With Glucokinase Monogenic Diabetes Can Be Recognized by Clinical Characteristics in Pregnancy: The Atlantic Diabetes in Pregnancy Cohort. Diabetes Care, 2014, 37, 1230-1236.	8.6	122
174	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
175	Regulation of Apolipoprotein M Gene Expression by MODY3 Gene Hepatocyte Nuclear Factor-1Â: Haploinsufficiency Is Associated With Reduced Serum Apolipoprotein M Levels. Diabetes, 2003, 52, 2989-2995.	0.6	121
176	Improved motor development and good long-term glycaemic control with sulfonylurea treatment in a patient with the syndrome of intermediate developmental delay, early-onset generalised epilepsy and neonatal diabetes associated with the V59M mutation in the KCNJ11 gene. Diabetologia, 2006, 49, 2559-2563.	6.3	121
177	Referral rates for diagnostic testing support an incidence of permanent neonatal diabetes in three European countries of at least 1 in 260,000 live births. Diabetologia, 2009, 52, 1683-1685.	6.3	120
178	Effectiveness and safety of long-term treatment with sulfonylureas in patients with neonatal diabetes due to KCNJ11 mutations: an international cohort study. Lancet Diabetes and Endocrinology,the, 2018, 6, 637-646.	11.4	120
179	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	6.3	119
180	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.	6.2	118

#	Article	IF	Citations
181	Hypoglycaemic counter-regulation at normal blood glucose concentrations in patients with well controlled type-2 diabetes. Lancet, The, 2000, 356, 1970-1974.	13.7	117
182	Beta-cell genes and diabetes: quantitative and qualitative differences in the pathophysiology of hepatic nuclear factor-1alpha and glucokinase mutations. Diabetes, 2001, 50, S101-S107.	0.6	117
183	Minireview: Pharmacogenetics and Beyond: The Interaction of Therapeutic Response, Î²-Cell Physiology, and Genetics in Diabetes. Endocrinology, 2006, 147, 2657-2663.	2.8	116
184	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.6	116
185	No Deterioration in Glycemic Control in HNF-1Â Maturity-Onset Diabetes of the Young Following Transfer From Long-Term Insulin to Sulphonylureas. Diabetes Care, 2003, 26, 3191-3192.	8.6	115
186	Isomers of the TCF1 gene encoding hepatocyte nuclear factor-1 alpha show differential expression in the pancreas and define the relationship between mutation position and clinical phenotype in monogenic diabetes. Human Molecular Genetics, 2006, 15, 2216-2224.	2.9	115
187	Contrasting Diabetes Phenotypes Associated With Hepatocyte Nuclear Factor-1Â and -1Â Mutations. Diabetes Care, 2004, 27, 1102-1107.	8.6	114
188	SLC2A2 mutations can cause neonatal diabetes, suggesting GLUT2 may have a role in human insulin secretion. Diabetologia, 2012, 55, 2381-2385.	6.3	113
189	Clinical presentation of 6q24 transient neonatal diabetes mellitus (6q24 TNDM) and genotypeâ€“phenotype correlation in an international cohort of patients. Diabetologia, 2013, 56, 758-762.	6.3	113
190	Type 2 Diabetes TCF7L2 Risk Genotypes Alter Birth Weight: A Study of 24,053 Individuals. American Journal of Human Genetics, 2007, 80, 1150-1161.	6.2	112
191	Influence of maternal and fetal glucokinase mutations in gestational diabetes. American Journal of Obstetrics and Gynecology, 2001, 185, 240-241.	1.3	111
192	Population-Based Assessment of a Biomarker-Based Screening Pathway to Aid Diagnosis of Monogenic Diabetes in Young-Onset Patients. Diabetes Care, 2017, 40, 1017-1025.	8.6	111
193	Heritability estimates for beta cell function and features of the insulin resistance syndrome in UK families with an increased susceptibility to Type 2 diabetes. Diabetologia, 2004, 47, 732-738.	6.3	110
194	Learning From Molecular Genetics. Diabetes, 2008, 57, 2889-2898.	0.6	110
195	Hepatocyte Nuclear Factor-1Î². Journal of the American Society of Nephrology: JASN, 2001, 12, 2175-2180.	6.1	110
196	HLA Genotyping Supports a Nonautoimmune Etiology in Patients Diagnosed With Diabetes Under the Age of 6 Months. Diabetes, 2006, 55, 1895-1898.	0.6	109
197	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.6	109
198	Clinical improvement in cystic fibrosis with early insulin treatment. Archives of Disease in Childhood, 2002, 87, 430-431.	1.9	108

#	Article	IF	Citations
199	Â-Cell Dysfunction, Insulin Sensitivity, and Glycosuria Precede Diabetes in Hepatocyte Nuclear Factor-1Â Mutation Carriers. Diabetes Care, 2005, 28, 1751-1756.	8.6	108
200	Pregnancy outcome in patients with raised blood glucose due to a heterozygous glucokinase gene mutation. Diabetic Medicine, 2009, 26, 14-18.	2.3	108
201	GATA4 Mutations Are a Cause of Neonatal and Childhood-Onset Diabetes. Diabetes, 2014, 63, 2888-2894.	0.6	108
202	Sulphonylurea therapy improves cognition in a patient with the V59M KCNJ11 mutation. Diabetic Medicine, 2008, 25, 277-281.	2.3	106
203	Phantasiaâ€"The psychological significance of lifelong visual imagery vividness extremes. Cortex, 2020, 130, 426-440.	2.4	106
204	Clinical Heterogeneity in Patients With FOXP3 Mutations Presenting With Permanent Neonatal Diabetes. Diabetes Care, 2009, 32, 111-116.	8.6	104
205	Most People With Long-Duration Type 1 Diabetes in a Large Population-Based Study Are Insulin Microsecretors. Diabetes Care, 2015, 38, 323-328.	8.6	104
206	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.	0.6	103
207	tRNA Methyltransferase Homolog Gene TRMT10A Mutation in Young Onset Diabetes and Primary Microcephaly in Humans. PLoS Genetics, 2013, 9, e1003888.	3.5	103
208	Intrauterine Hyperglycemia Is Associated With an Earlier Diagnosis of Diabetes in HNF-1Â Gene Mutation Carriers. Diabetes Care, 2002, 25, 2287-2291.	8.6	102
209	Conventional measures underestimate glycaemia in cystic fibrosis patients. Diabetic Medicine, 2004, 21, 691-696.	2.3	102
210	Precision medicine in diabetes: a Consensus Report from the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). Diabetologia, 2020, 63, 1671-1693.	6.3	102
211	An evaluation of HapMap sample size and tagging SNP performance in large-scale empirical and simulated data sets. Nature Genetics, 2005, 37, 1320-1322.	21.4	101
212	A novel mutation causing DEND syndrome. Neurology, 2007, 69, 1342-1349.	1.1	101
213	Genetic scores to stratify risk of developing multiple islet autoantibodies and type 1 diabetes: A prospective study in children. PLoS Medicine, 2018, 15, e1002548.	8.4	101
214	Use of HbA1c in the Identification of Patients with Hyperglycaemia Caused by a Glucokinase Mutation: Observational Case Control Studies. PLoS ONE, 2013, 8, e65326.	2.5	101
215	Prevalence of Permanent Neonatal Diabetes in Slovakia and Successful Replacement of Insulin with Sulfonylurea Therapy in KCNJ11 and ABCC8 Mutation Carriers. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 1276-1282.	3.6	100
216	Genetic variation at CHRNA5-CHRNA3-CHRNB4 interacts with smoking status to influence body mass index. International Journal of Epidemiology, 2011, 40, 1617-1628.	1.9	100

#	Article	IF	Citations
217	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.	6.3	100
218	A gating mutation at the internal mouth of the Kir6.2 pore is associated with DEND syndrome. EMBO Reports, 2005, 6, 470-475.	4.5	99
219	Studies of insulin and proinsulin in pancreas and serum support the existence of aetiopathological endotypes of type 1 diabetes associated with age at diagnosis. Diabetologia, 2020, 63, 1258-1267.	6.3	98
220	Fetal Thyroid Hormone Level at Birth Is Associated with Fetal Growth. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E934-E938.	3.6	97
221	Increased allâ€cause and cardiovascular mortality in monogenic diabetes as a result of mutations in the HNF1A gene. Diabetic Medicine, 2010, 27, 157-161.	2.3	96
222	Hepatocyte nuclear factor-1Â gene deletions--a common cause of renal disease. Nephrology Dialysis Transplantation, 2007, 23, 627-635.	0.7	95
223	Hyperglycemia and Adverse Pregnancy Outcome (HAPO) Study: Common Genetic Variants in GCK and TCF7L2 Are Associated With Fasting and Postchallenge Glucose Levels in Pregnancy and With the New Consensus Definition of Gestational Diabetes Mellitus From the International Association of Diabetes and Pregnancy Study Groups. Diabetes, 2010, 59, 2682-2689.	0.6	95
224	Heterozygous RFX6 protein truncating variants are associated with MODY with reduced penetrance. Nature Communications, 2017, 8, 888.	12.8	95
225	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	3.5	95
226	Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467.	0.6	93
227	Detection of an MEN1 gene mutation depends on clinical features and supports current referral criteria for diagnostic molecular genetic testing. Clinical Endocrinology, 2005, 62, 169-175.	2.4	91
228	FTOgene variation and measures of body mass in an African population. BMC Medical Genetics, 2009, 10, 21.	2.1	91
229	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.	8.6	91
230	High-Sensitivity CRP Discriminates HNF1A-MODY From Other Subtypes of Diabetes. Diabetes Care, 2011, 34, 1860-1862.	8.6	90
231	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
232	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.	0.6	88
233	Permanent Neonatal Diabetes due to Paternal Germline Mosaicism for an Activating Mutation of the KCNJ11 Gene Encoding the Kir6.2 Subunit of the Î²-Cell Potassium Adenosine Triphosphate Channel. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 3932-3935.	3.6	87
234	Insights into the Structure and Regulation of Glucokinase from a Novel Mutation (V62M), Which Causes Maturity-onset Diabetes of the Young. Journal of Biological Chemistry, 2005, 280, 14105-14113.	3.4	87

#	Article	IF	Citations
235	Mutations in the Kir6.2 subunit of the KATPchannel and permanent neonatal diabetes: New insights and new treatment. Annals of Medicine, 2005, 37, 186-195.	3.8	87
236	Association Studies of Genetic Variation in the WFS1 Gene and Type 2 Diabetes in U.K. Populations. Diabetes, 2002, 51, 1287-1290.	0.6	86
237	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.	0.6	86
238	Novel GLIS3 mutations demonstrate an extended multisystem phenotype. European Journal of Endocrinology, 2011, 164, 437-443.	3.7	86
239	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
240	Identifying Hepatic Nuclear Factor 1Â Mutations in Children and Young Adults With a Clinical Diagnosis of Type 1 Diabetes. Diabetes Care, 2003, 26, 333-337.	8.6	84
241	Entities and frequency of neonatal diabetes: data from the diabetes documentation and quality management system (DPV). Diabetic Medicine, 2010, 27, 709-712.	2.3	84
242	Incidence, genetics, and clinical phenotype of permanent neonatal diabetes mellitus in northwest Saudi Arabia. Pediatric Diabetes, 2012, 13, 499-505.	2.9	84
243	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
244	TheHNF4AR76W mutation causes atypical dominant Fanconi syndrome in addition to a Î² cell phenotype. Journal of Medical Genetics, 2014, 51, 165-169.	3.2	82
245	A Gene for Autosomal Recessive Spondylocostal Dysostosis Maps to 19q13.1-q13.3. American Journal of Human Genetics, 1999, 65, 175-182.	6.2	81
246	Pigmentary retinal dystrophy and the syndrome of maternally inherited diabetes and deafness caused by the mitochondrial DNA 3243 tRNALeu A to G mutation11The authors have no proprietary interest in the development or marketing of any device or medications mentioned in the article or any competing device.. Ophthalmology, 1999, 106, 1101-1108.	5.2	81
247	Evidence that single nucleotide polymorphism in the uncoupling protein 3 (UCP3) gene influences fat distribution in women of European and Asian origin. Diabetologia, 2000, 43, 1558-1564.	6.3	81
248	Mutations in the ABCC8 gene encoding the SUR1 subunit of the K_{ATP} channel cause transient neonatal diabetes, permanent neonatal diabetes or permanent diabetes diagnosed outside the neonatal period. Diabetes, Obesity and Metabolism, 2007, 9, 28-39.	4.4	81
249	Can clinical features be used to differentiate type 1 from type 2 diabetes? A systematic review of the literature. BMJ Open, 2015, 5, e009088.	1.9	81
250	C-Peptide Decline in Type 1 Diabetes Has Two Phases: An Initial Exponential Fall and a Subsequent Stable Phase. Diabetes Care, 2018, 41, 1486-1492.	8.6	81
251	A common variant of the p16INK4a genetic region is associated with physical function in older people. Mechanisms of Ageing and Development, 2007, 128, 370-377.	4.6	80
252	Variation in the Calpain-10 Gene Affects Blood Glucose Levels in the British Population. Diabetes, 2002, 51, 247-250.	0.6	79

#	Article	IF	Citations
253	Role of the mitochondrial DNA 16184â€“16193 poly-C tract in type 2 diabetes. Lancet, The, 2005, 366, 1650-1651.	13.7	79
254	The effect of obesity on glycaemic response to metformin or sulphonylureas in Type 2 diabetes. Diabetic Medicine, 2006, 23, 128-133.	2.3	79
255	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.	8.6	79
256	Distinct Molecular and Morphogenetic Properties of Mutations in the Human HNF1Î² Gene That Lead to Defective Kidney Development. Journal of the American Society of Nephrology: JASN, 2003, 14, 2033-2041.	6.1	78
257	Paradoxical Lower Serum Triglyceride Levels and Higher Type 2 Diabetes Mellitus Susceptibility in Obese Individuals with the PNPLA3 148M Variant. PLoS ONE, 2012, 7, e39362.	2.5	78
258	High-Dose Glibenclamide Can Replace Insulin Therapy Despite Transitory Diarrhea in Early-Onset Diabetes Caused by a Novel R201L Kir6.2 Mutation. Diabetes Care, 2005, 28, 758-759.	8.6	77
259	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.	0.6	77
260	Dominant ER Stressâ€“Inducing WFS1 Mutations Underlie a Genetic Syndrome of Neonatal/Infancy-Onset Diabetes, Congenital Sensorineural Deafness, and Congenital Cataracts. Diabetes, 2017, 66, 2044-2053.	0.6	77
261	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.	1.1	76
262	Association of low birth weight with beta cell function in the adult first degree relatives of non-insulin dependent diabetic subjects.. BMJ: British Medical Journal, 1993, 306, 302-306.	2.3	75
263	Type II Diabetes: Clinical Aspects of Molecular Biological Studies. Diabetes, 1995, 44, 1-10.	0.6	75
264	Evidence of genetic regulation of fetal longitudinal growth. Early Human Development, 2005, 81, 823-831.	1.8	75
265	The identification of a R201H mutation in KCNJ11, which encodes Kir6.2, and successful transfer to sustained-release sulphonylurea therapy in a subject with neonatal diabetes: evidence for heterogeneity of beta cell function among carriers of the R201H mutation. Diabetologia, 2005, 48, 1029-1031.	6.3	75
266	TCF7L2 in the Go-DARTS study: evidence for a gene dose effect on both diabetes susceptibility and control of glucose levels. Diabetologia, 2007, 50, 1186-1191.	6.3	74
267	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
268	Lower Circulating B12 Is Associated with Higher Obesity and Insulin Resistance during Pregnancy in a Non-Diabetic White British Population. PLoS ONE, 2015, 10, e0135268.	2.5	74
269	Identification of 21 novel glucokinase (GCK) mutations in UK and European Caucasians with maturity-onset diabetes of the young (MODY). Human Mutation, 2003, 22, 417-417.	2.5	73
270	The mutated human gene encoding hepatocyte nuclear factor 1beta inhibits kidney formation in developing Xenopus embryos. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 4695-4700.	7.1	72

#	Article	IF	Citations
271	An association analysis of the HLA gene region in latent autoimmune diabetes in adults. Diabetologia, 2006, 50, 68-73.	6.3	72
272	Association between the T-381C polymorphism of the brain natriuretic peptide gene and risk of type 2 diabetes in human populations. Human Molecular Genetics, 2007, 16, 1343-1350.	2.9	72
273	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
274	A Missense Mutation in PPP1R15B Causes a Syndrome Including Diabetes, Short Stature, and Microcephaly. Diabetes, 2015, 64, 3951-3962.	0.6	71
275	Maternal diabetes alters birth weight in glucokinase-deficient (MODY2) kindred but has no influence on adult weight, height, insulin secretion or insulin sensitivity. Diabetologia, 2000, 43, 1060-1063.	6.3	70
276	ISPAD Clinical Practice Consensus Guidelines 2006?2007 Definition, epidemiology and classification. Pediatric Diabetes, 2006, 7, 343-351.	2.9	69
277	A meta-analysis of four European genome screens (GIFT Consortium) shows evidence for a novel region on chromosome 17p11.2-q22 linked to type 2 diabetes. Human Molecular Genetics, 2003, 12, 1865-1873.	2.9	68
278	Genetic variations in the gene encoding TFAP2B are associated with type 2 diabetes mellitus. Journal of Human Genetics, 2005, 50, 283-292.	2.3	68
279	Measurement of Cord Insulin and Insulin-Related Peptides Suggests That Girls Are More Insulin Resistant Than Boys at Birth. Diabetes Care, 2007, 30, 2661-2666.	8.6	68
280	Successful transfer to sulfonylureas in KCNJ11 neonatal diabetes is determined by the mutation and duration of diabetes. Diabetologia, 2016, 59, 1162-1166.	6.3	68
281	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.	8.6	68
282	Altered insulin secretory responses to glucose in diabetic and nondiabetic subjects with mutations in the diabetes susceptibility gene MODY3 on chromosome 12. Diabetes, 1996, 45, 1503-1510.	0.6	68
283	Clinical Characteristics of Subjects with a Missense Mutation in Glucokinase. Diabetic Medicine, 1995, 12, 209-217.	2.3	67
284	Naturally occurring mutations in the human HNF4alpha gene impair the function of the transcription factor to a varying degree. Nucleic Acids Research, 2000, 28, 430-437.	14.5	67
285	Variation within the Type 2 Diabetes Susceptibility Gene Calpain-10 and Polycystic Ovary Syndrome. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 2606-2610.	3.6	67
286	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.	8.6	67
287	Expanding the Clinical Spectrum Associated With GLIS3 Mutations. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E1362-E1369.	3.6	66
288	The Exeter Family Study of Childhood Health (EFSOCH): study protocol and methodology. Paediatric and Perinatal Epidemiology, 2006, 20, 172-179.	1.7	65

#	Article	IF	Citations
289	Incorrect and incomplete coding and classification of diabetes: a systematic review. Diabetic Medicine, 2010, 27, 491-497.	2.3	65
290	Parental diabetes and birthweight in 236 030 individuals in the UK Biobank Study. International Journal of Epidemiology, 2013, 42, 1714-1723.	1.9	65
291	A UK nationwide prospective study of treatment change in MODY: genetic subtype and clinical characteristics predict optimal glycaemic control after discontinuing insulin and metformin. Diabetologia, 2018, 61, 2520-2527.	6.3	65
292	Monogenic Diabetes: From Genetic Insights to Population-Based Precision in Care. Reflections From a Diabetes Care Editorsâ€™ Expert Forum. Diabetes Care, 2020, 43, 3117-3128.	8.6	65
293	Mutations at the Same Residue (R50) of Kir6.2 (KCNJ11) That Cause Neonatal Diabetes Produce Different Functional Effects. Diabetes, 2006, 55, 1705-1712.	0.6	64
294	The Diabetic Phenotype in HNF4A Mutation Carriers Is Moderated By the Expression of HNF4A Isoforms From the P1 Promoter During Fetal Development. Diabetes, 2008, 57, 1745-1752.	0.6	64
295	Cigarette Smoking during Pregnancy Is Associated with Alterations in Maternal and Fetal Thyroid Function. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 570-574.	3.6	64
296	Chromosome 17q12 microdeletions but not intragenic HNF1B mutations link developmental kidney disease and psychiatric disorder. Kidney International, 2016, 90, 203-211.	5.2	64
297	Time trends in prescribing of type 2 diabetes drugs, glycaemic response and risk factors: A retrospective analysis of primary care data, 2010â€“2017. Diabetes, Obesity and Metabolism, 2019, 21, 1576-1584.	4.4	64
298	Underlying Genetic Models of Inheritance in Established Type 2 Diabetes Associations. American Journal of Epidemiology, 2009, 170, 537-545.	3.4	63
299	Time trends and geographical variation in prescribing of drugs for diabetes in England from 1998 to 2017. Diabetes, Obesity and Metabolism, 2018, 20, 2159-2168.	4.4	63
300	Response to treatment with rosiglitazone in familial partial lipodystrophy due to a mutation in the LMNA gene. Diabetic Medicine, 2003, 20, 823-827.	2.3	62
301	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
302	The Impact of Maternal Glycemia and Obesity on Early Postnatal Growth in a Nondiabetic Caucasian Population. Diabetes Care, 2007, 30, 777-783.	8.6	62
303	Urine C-Peptide Creatinine Ratio Is a Noninvasive Alternative to the Mixed-Meal Tolerance Test in Children and Adults With Type 1 Diabetes. Diabetes Care, 2011, 34, 607-609.	8.6	62
304	Genetic variation in the 15q25 nicotinic acetylcholine receptor gene cluster (CHRNA5â€“CHRNA3â€“CHRNB4) interacts with maternal self-reported smoking status during pregnancy to influence birth weight. Human Molecular Genetics, 2012, 21, 5344-5358.	2.9	62
305	High prevalence of a missense mutation of the glucokinase gene in gestational diabetic patients due to a founder-effect in a local population. Diabetologia, 1996, 39, 1325-1328.	6.3	61
306	â€˜I don't feel like a diabetic any moreâ€™: the impact of stopping insulin in patients with maturity onset diabetes of the young following genetic testing. Clinical Medicine, 2004, 4, 144-147.	1.9	61

#	Article	IF	Citations
307	Mutations in the VNTR of the carboxyl-ester lipase gene (CEL) are a rare cause of monogenic diabetes. Human Genetics, 2010, 127, 55-64.	3.8	61
308	Lessons From the Mixed-Meal Tolerance Test. Diabetes Care, 2013, 36, 195-201.	8.6	61
309	Predictive genetic testing in maturity-onset diabetes of the young (MODY). Diabetic Medicine, 2001, 18, 417-421.	2.3	60
310	Stability and Reproducibility of a Single-Sample Urinary C-Peptide/Creatinine Ratio and Its Correlation with 24-h Urinary C-Peptide. Clinical Chemistry, 2009, 55, 2035-2039.	3.2	60
311	Practical Classification Guidelines for Diabetes in patients treated with insulin: a cross-sectional study of the accuracy of diabetes diagnosis. British Journal of General Practice, 2016, 66, e315-e322.	1.4	60
312	The role of genetic susceptibility in the association of low birth weight with type 2 diabetes. British Medical Bulletin, 2001, 60, 89-101.	6.9	59
313	Partial and whole gene deletion mutations of the GCK and HNF1A genes in maturity-onset diabetes of the young. Diabetologia, 2007, 50, 2313-2317.	6.3	59
314	Recessively InheritedLRBAMutations Cause Autoimmunity Presenting as Neonatal Diabetes. Diabetes, 2017, 66, 2316-2322.	0.6	59
315	Dietary Energy Density Affects Fat Mass in Early Adolescence and Is Not Modified by FTO Variants. PLoS ONE, 2009, 4, e4594.	2.5	58
316	Maternal hypothyroxinaemia in pregnancy is associated with obesity and adverse maternal metabolic parameters. European Journal of Endocrinology, 2016, 174, 51-57.	3.7	58
317	YIPF5 mutations cause neonatal diabetes and microcephaly through endoplasmic reticulum stress. Journal of Clinical Investigation, 2020, 130, 6338-6353.	8.2	58
318	A missense mutation in the hepatocyte nuclear factor 4 alpha gene in a UK pedigree with maturity-onset diabetes of the young. Diabetologia, 1997, 40, 859-862.	6.3	57
319	KATP channel mutations in infants with permanent diabetes diagnosed after 6 months of life. Pediatric Diabetes, 2012, 13, 322-325.	2.9	57
320	Recessive SLC19A2 mutations are a cause ofÂneonatal diabetes mellitus inÂthiamine-responsive megaloblastic anaemia. Pediatric Diabetes, 2012, 13, 314-321.	2.9	57
321	The Generalized Aminoaciduria Seen in Patients With Hepatocyte Nuclear Factor-1Â Mutations Is a Feature of All Patients With Diabetes and Is Associated With Glucosuria. Diabetes, 2001, 50, 2047-2052.	0.6	56
322	Etiological Investigation of Diabetes in Young Adults Presenting With Apparent Type 2 Diabetes. Diabetes Care, 2003, 26, 2088-2093.	8.6	56
323	Type 2 diabetes in grandparents and birth weight in offspring and grandchildren in the ALSPAC study. Journal of Epidemiology and Community Health, 2004, 58, 517-522.	3.7	54
324	Permanent neonatal diabetes mellitus: prevalence and genetic diagnosis in the SEARCH for Diabetes in Youth Study. Pediatric Diabetes, 2012, 14, n/a-n/a.	2.9	54

#	Article	IF	Citations
325	Understanding the manifestation of diabetes in sub Saharan Africa to inform therapeutic approaches and preventive strategies: a narrative review. Clinical Diabetes and Endocrinology, 2019, 5, 2.	2.7	54
326	Mutations in the hepatocyte nuclear factor-1alpha gene are a common cause of maturity-onset diabetes of the young in the U.K. Diabetes, 1997, 46, 720-725.	0.6	54
327	Evidence for Linkage of Stature to Chromosome 3p26 in a Large U.K. Family Data Set Ascertained for Type 2 Diabetes. American Journal of Human Genetics, 2002, 70, 543-546.	6.2	53
328	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.	0.6	53
329	Association and Haplotype Analysis of the Insulin-Degrading Enzyme (IDE) Gene, a Strong Positional and Biological Candidate for Type 2 Diabetes Susceptibility. Diabetes, 2003, 52, 1300-1305.	0.6	52
330	Origin of de Novo KCNJ11 Mutations and Risk of Neonatal Diabetes for Subsequent Siblings. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 1773-1777.	3.6	52
331	Mitochondrial DNA haplogroups and type 2 diabetes: a study of 897 cases and 1010 controls. Journal of Medical Genetics, 2007, 44, e80-e80.	3.2	52
332	A powerful approach to subâ€phenotype analysis in populationâ€based genetic association studies. Genetic Epidemiology, 2010, 34, 335-343.	1.3	52
333	Incidence of neonatal diabetes in Austria-calculation based on the Austrian Diabetes Register. Pediatric Diabetes, 2010, 11, 18-23.	2.9	52
334	Clinical characteristics and molecular genetic analysis of 22 patients with neonatal diabetes from the South-Eastern region of Turkey: predominance of non-KATP channel mutations. European Journal of Endocrinology, 2015, 172, 697-705.	3.7	52
335	Latent Autoimmune Diabetes of Adults (LADA) Is Likely to Represent a Mixed Population of Autoimmune (Type 1) and Nonautoimmune (Type 2) Diabetes. Diabetes Care, 2021, 44, 1243-1251.	8.6	52
336	The effect of long-and short-term corticosteroids on plasma calcitonin and parathyroid hormone levels. Calcified Tissue International, 1994, 54, 198-202.	3.1	51
337	Frequent Occurrence of an Intron 4 Mutation in Multiple Endocrine Neoplasia Type 1. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 2688-2693.	3.6	51
338	Activating Mutations in the KCNJ11 Gene Encoding the ATP-Sensitive K+ Channel Subunit Kir6.2 Are Rare in Clinically Defined Type 1 Diabetes Diagnosed Before 2 Years. Diabetes, 2004, 53, 2998-3001.	0.6	51
339	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.	0.6	51
340	Permanent neonatal diabetes in an Asian infant. Journal of Pediatrics, 2005, 146, 131-133.	1.8	51
341	Increased ATPase activity produced by mutations at arginine-1380 in nucleotide-binding domain 2 of ABCC8 causes neonatal diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18988-18992.	7.1	51
342	Persistently autoantibody negative (PAN) type 1 diabetes mellitus in children. Pediatric Diabetes, 2011, 12, 142-149.	2.9	51

#	Article	IF	Citations
343	Mutations in hepatocyte nuclear factor 1beta are not a common cause of maturity-onset diabetes of the young in the U.K. Diabetes, 1998, 47, 1152-1154.	0.6	50
344	Messenger RNA Transcripts of the Hepatocyte Nuclear Factor-1Â Gene Containing Premature Termination Codons Are Subject to Nonsense-Mediated Decay. Diabetes, 2004, 53, 500-504.	0.6	50
345	Antenatal Diagnosis of Fetal Genotype Determines if Maternal Hyperglycemia Due to a Glucokinase Mutation Requires Treatment. Diabetes Care, 2012, 35, 1832-1834.	8.6	50
346	Random nonâ€fasting Câ€“peptide: bringing robust assessment of endogenous insulin secretion to the clinic. Diabetic Medicine, 2016, 33, 1554-1558.	2.3	50
347	Prime suspect: the TCF7L2 gene and type 2 diabetes risk. Journal of Clinical Investigation, 2007, 117, 2077-2079.	8.2	50
348	Testing for monogenic diabetes among children and adolescents with antibodyâ€negative clinically defined Type 1 diabetes. Diabetic Medicine, 2009, 26, 1070-1074.	2.3	49
349	Mutations in the hepatocyte nuclear factor-1Î² (HNF1B) gene are common with combined uterine and renal malformations but are not found with isolated uterine malformations. American Journal of Obstetrics and Gynecology, 2010, 203, 364.e1-364.e5.	1.3	49
350	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.	1.9	49
351	Molecular genetics goes to the diabetes clinic. Clinical Medicine, 2005, 5, 476-481.	1.9	48
352	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: rationale and design of the epidemiological studies within the IMI DIRECT Consortium. Diabetologia, 2014, 57, 1132-1142.	6.3	48
353	Heterogeneity in phenotype, disease progression and drug response in type 2 diabetes. Nature Medicine, 2022, 28, 982-988.	30.7	48
354	Premature birth and low birth weight associated with nonautoimmune hyperthyroidism due to an activating thyrotropin receptor gene mutation. Clinical Endocrinology, 2004, 60, 711-718.	2.4	47
355	Optimisation of an Advanced Oxidation Protein Products Assay: Its Application to Studies of Oxidative Stress in Diabetes Mellitus. Oxidative Medicine and Cellular Longevity, 2015, 2015, 1-10.	4.0	47
356	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
357	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. PLoS Medicine, 2020, 17, e1003149.	8.4	47
358	Validation of Interstitial Fluid Continuous Glucose Monitoring in Cystic Fibrosis. Diabetes Care, 2003, 26, 1940-1941.	8.6	46
359	Lack of Support for a Role of the Insulin Gene Variable Number of Tandem Repeats Minisatellite (INS-VNTR) Locus in Fetal Growth or Type 2 Diabetes-Related Intermediate Traits in United Kingdom Populations. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 310-317.	3.6	46
360	Biallelic PDX1 (insulin promoter factorÂ1) mutations causing neonatal diabetes without exocrine pancreatic insufficiency. Diabetic Medicine, 2013, 30, e197-200.	2.3	46

#	Article	IF	Citations
361	The Common p.R114W HNF4A Mutation Causes a Distinct Clinical Subtype of Monogenic Diabetes. Diabetes, 2016, 65, 3212-3217.	0.6	46
362	Prevalence of diabetes in Australia: insights from the Fremantle Diabetes Study Phase II. Internal Medicine Journal, 2018, 48, 803-809.	0.8	46
363	Parent-offspring trios: a resource to facilitate the identification of type 2 diabetes genes. Diabetes, 1999, 48, 2475-2479.	0.6	45
364	Heterogeneity in young adult onset diabetes: aetiology alters clinical characteristics. Diabetic Medicine, 2002, 19, 758-761.	2.3	45
365	Large-scale studies of the association between variation at the TNF/LTA locus and susceptibility to type 2 diabetes. Diabetologia, 2005, 48, 2013-2017.	6.3	45
366	The position of premature termination codons in the hepatocyte nuclear factor â^'1 beta gene determines susceptibility to nonsense-mediated decay. Human Genetics, 2005, 118, 214-224.	3.8	45
367	Contrasting Insulin Sensitivity of Endogenous Glucose Production Rate in Subjects With Hepatocyte Nuclear Factor-1Â and -1Â Mutations. Diabetes, 2006, 55, 405-411.	0.6	45
368	Different genes, different diabetes: lessons from maturity-onset diabetes of the young. Annals of Medicine, 2002, 34, 207-216.	3.8	45
369	Different genes, different diabetes: lessons from maturity-onset diabetes of the young. Annals of Medicine, 2002, 34, 207-16.	3.8	45
370	Characteristics of maturity onset diabetes of the young in a large diabetes center. Pediatric Diabetes, 2016, 17, 360-367.	2.9	44
371	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
372	The Variable Number of Tandem Repeats Upstream of the Insulin Gene Is a Susceptibility Locus for Latent Autoimmune Diabetes in Adults. Diabetes, 2006, 55, 1890-1894.	0.6	43
373	A Kir6.2 Mutation Causing Neonatal Diabetes Impairs Electrical Activity and Insulin Secretion From INS-1 Â-Cells. Diabetes, 2006, 55, 3075-3082.	0.6	43
374	A Specific CNOT1 Mutation Results in a Novel Syndrome of Pancreatic Agenesis and Holoprosencephaly through Impaired Pancreatic and Neurological Development. American Journal of Human Genetics, 2019, 104, 985-989.	6.2	43
375	Risk factors for genital infections in people initiating SGLT2 inhibitors and their impact on discontinuation. BMJ Open Diabetes Research and Care, 2020, 8, e001238.	2.8	43
376	Five-Year Follow-Up for Women With Subclinical Hypothyroidism in Pregnancy. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1941-E1945.	3.6	42
377	UKPDS 21: Low Prevalence of the Mitochondrial Transfer RNA gene (tRNALeu(UUR)) Mutation at Position 3243bp in UK Caucasian Type 2 Diabetic Patients. , 1997, 14, 42-45.		41
378	Evidence From a Large U.K. Family Collection That Genes Influencing Age of Onset of Type 2 Diabetes Map to Chromosome 12p and to the MODY3/NIDDM2 Locus on 12q24. Diabetes, 2004, 53, 855-860.	0.6	41

#	Article	IF	Citations
379	Association Studies of Insulin Receptor Substrate 1 Gene (IRS1) Variants in Type 2 Diabetes Samples Enriched for Family History and Early Age of Onset. Diabetes, 2004, 53, 3319-3322.	0.6	41
380	Gene variants influencing measures of inflammation or predisposing to autoimmune and inflammatory diseases are not associated with the risk of type 2 diabetes. Diabetologia, 2008, 51, 2205-2213.	6.3	41
381	Phenotypic severity of homozygous GCK mutations causing neonatal or childhood-onset diabetes is primarily mediated through effects on protein stability. Human Molecular Genetics, 2014, 23, 6432-6440.	2.9	41
382	Type II diabetes: clinical aspects of molecular biological studies. Diabetes, 1995, 44, 1-10.	0.6	41
383	Searching for Type 2 Diabetes Genes in the Post-genome Era. Trends in Endocrinology and Metabolism, 2000, 11, 383-393.	7.1	40
384	ACE Gene Polymorphism as a Prognostic Indicator in Patients With Type 2 Diabetes and Established Renal Disease. Diabetes Care, 2001, 24, 2115-2120.	8.6	40
385	Activating Mutations in the Gene Encoding Kir6.2 Alter Fetal and Postnatal Growth and Also Cause Neonatal Diabetes. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 2782-2788.	3.6	40
386	A mutation (R826W) in nucleotideâ€binding domain 1 of ABCC8 reduces ATPase activity and causes transient neonatal diabetes. EMBO Reports, 2008, 9, 648-654.	4.5	40
387	Permanent neonatal diabetes: different aetiology in Arabs compared to Europeans. Archives of Disease in Childhood, 2012, 97, 721-723.	1.9	40
388	Molecular diagnostics in monogenic and multifactorial forms of Type 2 diabetes. Expert Review of Molecular Diagnostics, 2001, 1, 403-412.	3.1	39
389	Tooth Discoloration in Patients With Neonatal Diabetes After Transfer Onto Glibenclamide: A previously unreported side effect. Diabetes Care, 2009, 32, 1428-1430.	8.6	39
390	Lipoprotein composition in HNF1A-MODY: Differentiating between HNF1A-MODY and Type 2 diabetes. Clinica Chimica Acta, 2012, 413, 927-932.	1.1	39
391	EDTA Improves Stability of Whole Blood C-Peptide and Insulin to Over 24 Hours at Room Temperature. PLoS ONE, 2012, 7, e42084.	2.5	39
392	Association of maternal circulating 25(OH)D and calcium with birth weight: A mendelian randomisation analysis. PLoS Medicine, 2019, 16, e1002828.	8.4	39
393	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. Cell Reports Medicine, 2022, 3, 100477.	6.5	39
394	Linkage Analysis of Glucokinase Gene With NIDDM in Caucasian Pedigrees. Diabetes, 1992, 41, 1496-1500.	0.6	38
395	Fetal Genotype and Maternal Glucose Have Independent and Additive Effects on Birth Weight. Diabetes, 2018, 67, 1024-1029.	0.6	38
396	Abnormal splicing of hepatocyte nuclear factor-1 beta in the renal cysts and diabetes syndrome. Diabetologia, 2004, 47, 937-942.	6.3	37

#	Article	IF	Citations
397	Variation Within the Gene Encoding the Upstream Stimulatory Factor 1 Does Not Influence Susceptibility to Type 2 Diabetes in Samples From Populations With Replicated Evidence of Linkage to Chromosome 1q. Diabetes, 2006, 55, 2541-2548.	0.6	37
398	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.6	37
399	Glucokinase, the pancreatic glucose sensor, is not the gut glucose sensor. Diabetologia, 2009, 52, 154-159.	6.3	37
400	Polygenic Risk Variants for Type 2 Diabetes Susceptibility Modify Age at Diagnosis in Monogenic HNF1A Diabetes. Diabetes, 2010, 59, 266-271.	0.6	37
401	Beta cell function and ongoing autoimmunity in long-standing, childhood onset type 1 diabetes. Diabetologia, 2016, 59, 2722-2726.	6.3	37
402	Molecular reductions in glucokinase activity increase counter-regulatory responses to hypoglycemia in mice and humans with diabetes. Molecular Metabolism, 2018, 17, 17-27.	6.5	37
403	Loss of MANF Causes Childhood-Onset Syndromic Diabetes Due to Increased Endoplasmic Reticulum Stress. Diabetes, 2021, 70, 1006-1018.	0.6	37
404	Adjacent mutations in the gating loop of Kir6.2 produce neonatal diabetes and hyperinsulinism. EMBO Molecular Medicine, 2009, 1, 166-177.	6.9	36
405	A meta-analysis of the associations between common variation in the PDE8B gene and thyroid hormone parameters, including assessment of longitudinal stability of associations over time and effect of thyroid hormone replacement. European Journal of Endocrinology, 2011, 164, 773-780.	3.7	36
406	Maternal and fetal genetic contribution to gestational weight gain. International Journal of Obesity, 2018, 42, 775-784.	3.4	36
407	A survey of cytomegalovirus (CMV) DNA in primary sclerosing cholangitis (PSC) liver tissues using a sensitive polymerase chain reaction (PCR) based assay. Journal of Hepatology, 1992, 15, 396-399.	3.7	35
408	The long-term impact on offspring of exposure to hyperglycaemia in utero due to maternal glucokinase gene mutations. Diabetologia, 2007, 50, 620-624.	6.3	35
409	Mutations in the ABCC8 (SUR1 subunit of the K_{ATP} channel) gene are associated with a variable clinical phenotype. Clinical Endocrinology, 2009, 71, 358-362.	2.4	35
410	Type 2 Diabetes, SGLT2 Inhibitors, and Glucose Secretion. New England Journal of Medicine, 2015, 373, 974-976.	27.0	35
411	A Type 1 Diabetes Genetic Risk Score Can Identify Patients With GAD65 Autoantibodyâ€“Positive Type 2 Diabetes Who Rapidly Progress to Insulin Therapy. Diabetes Care, 2019, 42, 208-214.	8.6	35
412	Syndromic Monogenic Diabetes Genes Should Be Tested in Patients With a Clinical Suspicion of Maturity-Onset Diabetes of the Young. Diabetes, 2022, 71, 530-537.	0.6	35
413	Complete glucokinase deficiency is not a common cause of permanent neonatal diabetes. Diabetologia, 2002, 45, 290-290.	6.3	34
414	Common Variation in the LMNA Gene (Encoding Lamin A/C) and Type 2 Diabetes: Association Analyses in 9,518 Subjects. Diabetes, 2007, 56, 879-883.	0.6	34

#	Article	IF	Citations
415	Detailed Investigation of the Role of Common and Low-Frequency WFS1 Variants in Type 2 Diabetes Risk. Diabetes, 2010, 59, 741-746.	0.6	34
416	Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. Annals of Human Genetics, 2011, 75, 10-19.	0.8	34
417	HNF1B deletions in patients with youngâ€onset diabetes but no known renal disease. Diabetic Medicine, 2013, 30, 114-117.	2.3	34
418	Biallelic RFX6 mutations can cause childhood as well as neonatal onset diabetes mellitus. European Journal of Human Genetics, 2015, 23, 1744-1748.	2.8	34
419	Neonatal diabetes in Ukraine: incidence, genetics, clinical phenotype and treatment. Journal of Pediatric Endocrinology and Metabolism, 2015, 28, 1279-86.	0.9	34
420	Associations Between Systolic Interarm Differences in Blood Pressure and Cardiovascular Disease Outcomes and Mortality. Hypertension, 2021, 77, 650-661.	2.7	34
421	Non-linkage of the glucagon-like peptide 1 receptor gene with maturity onset diabetes of the young. Diabetologia, 1994, 37, 721-724.	6.3	33
422	A type 1 diabetes genetic risk score can discriminate monogenic autoimmunity with diabetes from early-onset clustering of polygenic autoimmunity with diabetes. Diabetologia, 2018, 61, 862-869.	6.3	33
423	GATA6 Cooperates with EOMES/SMAD2/3 to Deploy the Gene Regulatory Network Governing Human Definitive Endoderm and Pancreas Formation. Stem Cell Reports, 2019, 12, 57-70.	4.8	33
424	Prevalence of diabetes mellitus and impaired glucose tolerance in parents of women with gestational diabetes. Diabetologia, 1995, 38, 693-698.	6.3	32
425	Allelic drop-out in exon 2 of the hepatocyte nuclear factor-1alpha gene hinders the identification of mutations in three families with maturity-onset diabetes of the young. Diabetes, 1999, 48, 921-923.	0.6	32
426	Urine Câ€peptide creatinine ratio is an alternative to stimulated serum Câ€peptide measurement in lateâ€onset, insulinâ€treated diabetes. Diabetic Medicine, 2011, 28, 1034-1038.	2.3	32
427	Persistent Câ€peptide is associated with reduced hypoglycaemia but not HbA_{1c} in adults with longstanding Type 1 diabetes: evidence for lack of intensive treatment in UK clinical practice?. Diabetic Medicine, 2019, 36, 1092-1099.	2.3	32
428	Noninvasive Fetal Genotyping by Droplet Digital PCR to Identify Maternally Inherited Monogenic Diabetes Variants. Clinical Chemistry, 2020, 66, 958-965.	3.2	32
429	Segregation analysis of NIDDM in Caucasian families. Diabetologia, 1994, 37, 1231-1240.	6.3	31
430	Severe Intrauterine Growth Retardation and Atypical Diabetes Associated with a Translocation Breakpoint Disrupting Regulation of the Insulin-Like Growth Factor 2 Gene. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 4373-4380.	3.6	31
431	Monogenic autoimmune diseases of the endocrine system. Lancet Diabetes and Endocrinology,the, 2016, 4, 862-872.	11.4	31
432	Management of sulfonylureaâ€treated monogenic diabetes in pregnancy: implications of placental glibenclamide transfer. Diabetic Medicine, 2017, 34, 1332-1339.	2.3	31

#	Article	IF	Citations
433	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
434	Distribution of Type II Diabetes in Nuclear Families. Diabetes, 1993, 42, 106-112.	0.6	30
435	Predictive Genetic Testing in Diabetes: A Case Study of Multiple Perspectives. Qualitative Health Research, 2000, 10, 242-259.	2.1	30
436	Glucokinase mutations in a phenotypically selected multiethnic group of women with a history of gestational diabetes. Diabetic Medicine, 2001, 18, 683-684.	2.3	30
437	Reduced beta cell function in offspring of mothers with young-onset type 2 diabetes. Diabetologia, 2006, 49, 1876-1880.	6.3	30
438	Mutations in the Glucokinase Gene of the Fetus Result in Reduced Placental Weight. Diabetes Care, 2008, 31, 753-757.	8.6	30
439	Linkage Disequilibrium Mapping of the Replicated Type 2 Diabetes Linkage Signal on Chromosome 1q. Diabetes, 2009, 58, 1704-1709.	0.6	30
440	Phosphodiesterase 8B Gene Polymorphism Is Associated with Subclinical Hypothyroidism in Pregnancy. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4608-4612.	3.6	30
441	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
442	A simple pragmatic system for detecting new cases of type 2 diabetes and impaired fasting glycaemia in primary care. Family Practice, 2004, 21, 57-62.	1.9	29
443	Familial factors in diabetic nephropathy: an offspring study. Diabetic Medicine, 2006, 23, 331-334.	2.3	29
444	Sulfonylurea Treatment in Young Children With Neonatal Diabetes: Dealing with hyperglycemia, hypoglycemia, and sick days. Diabetes Care, 2007, 30, e28-e29.	8.6	29
445	A Kir6.2 mutation causing severe functional effects in vitro produces neonatal diabetes without the expected neurological complications. Diabetologia, 2008, 51, 802-810.	6.3	29
446	A role for coding functional variants in HNF4A in type 2 diabetes susceptibility. Diabetologia, 2011, 54, 111-119.	6.3	29
447	Home urine C-peptide creatinine ratio testing can identify type 2 and MODY in pediatric diabetes. Pediatric Diabetes, 2012, 14, n/a-n/a.	2.9	29
448	Validation of a singleâ€sample urinary Câ€peptide creatinine ratio as a reproducible alternative to serum Câ€peptide in patients with Type 2 diabetes. Diabetic Medicine, 2012, 29, 90-93.	2.3	29
449	De Novo Mutations in EIF2B1 Affecting eIF2 Signaling Cause Neonatal/Early-Onset Diabetes and Transient Hepatic Dysfunction. Diabetes, 2020, 69, 477-483.	0.6	29
450	Risk of Anemia With Metformin Use in Type 2 Diabetes: A MASTERMIND Study. Diabetes Care, 2020, 43, 2493-2499.	8.6	29

#	Article	IF	Citations
451	Increased prevalence of proteinuria in diabetic sibs of proteinuric type 2 diabetic subjects. American Journal of Kidney Diseases, 2000, 35, 708-712.	1.9	28
452	Evidence for Haploinsufficiency of the Human HNF1Î± Gene Revealed by Functional Characterization of MODY3-Associated Mutations. Biological Chemistry, 2002, 383, 1691-700.	2.5	28
453	Rapid and Sensitive Real-Time Polymerase Chain Reaction Method for Detection and Quantification of 3243A>G Mitochondrial Point Mutation. Journal of Molecular Diagnostics, 2006, 8, 225-230.	2.8	28
454	South Asian individuals with diabetes who are referred for MODY testing in the UK have a lower mutation pick-up rate than white European people. Diabetologia, 2016, 59, 2262-2265.	6.3	28
455	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.	1.9	28
456	The role of genetic susceptibility in diabetic nephropathy: evidence from family studies. Nephrology Dialysis Transplantation, 2002, 17, 1543-1546.	0.7	27
457	Maturity-Onset Diabetes of the Young Caused by a Balanced Translocation Where the 20q12 Break Point Results in Disruption Upstream of the Coding Region of Hepatocyte Nuclear Factor-4Â (HNF4A) Gene. Diabetes, 2002, 51, 2329-2333.	0.6	27
458	Analysis of the contribution to type 2 diabetes susceptibility of sequence variation in the gene encoding stearoyl-CoA desaturase, a key regulator of lipid and carbohydrate metabolism. Diabetologia, 2004, 47, 2168-2175.	6.3	27
459	The association of common genetic variants in the APOA5, LPL and GCK genes with longitudinal changes in metabolic and cardiovascular traits. Diabetologia, 2009, 52, 106-114.	6.3	27
460	Neurogenin 3 is important but not essential for pancreatic islet development in humans. Diabetologia, 2014, 57, 2421-2424.	6.3	27
461	Prematurity and Genetic Testing for Neonatal Diabetes. Pediatrics, 2016, 138, .	2.1	27
462	Analysis of cellâ€free fetal <scp>DNA</scp> for nonâ€invasive prenatal diagnosis in a family with neonatal diabetes. Diabetic Medicine, 2017, 34, 582-585.	2.3	27
463	Prediction algorithms: pitfalls in interpreting genetic variants of autosomal dominant monogenic diabetes. Journal of Clinical Investigation, 2019, 130, 14-16.	8.2	27
464	Evaluation of Evidence for Pathogenicity Demonstrates That BLK, KLF11, and PAX4 Should Not Be Included in Diagnostic Testing for MODY. Diabetes, 2022, 71, 1128-1136.	0.6	27
465	Genetic testing for glucokinase mutations in clinically selected patients with MODY: a worthwhile investment. Swiss Medical Weekly, 2005, 135, 352-6.	1.6	27
466	Association of the calpain-10 gene with microvascular function. Diabetologia, 2002, 45, 899-904.	6.3	26
467	Diabetes Susceptibility in the Canadian Oji-Cree Population Is Moderated by Abnormal mRNA Processing of HNF1A G319S Transcripts. Diabetes, 2008, 57, 1978-1982.	0.6	26
468	Pharmacogenomics in diabetes: outcomes of thiamine therapy in TRMA syndrome. Diabetologia, 2018, 61, 1027-1036.	6.3	26

#	Article	IF	Citations
469	Cognitive, Neurological, and Behavioral Features in Adults With KCNJ11 Neonatal Diabetes. Diabetes Care, 2019, 42, 215-224.	8.6	26
470	Should Studies of Diabetes Treatment Stratification Correct for Baseline HbA1c?. PLoS ONE, 2016, 11, e0152428.	2.5	26
471	Mutations of the Same Conserved Glutamate Residue in NBD2 of the Sulfonylurea Receptor 1 Subunit of the KATP Channel Can Result in Either Hyperinsulinism or Neonatal Diabetes. Diabetes, 2011, 60, 1813-1822.	0.6	25
472	Neonatal diabetes caused by a homozygous KCNJ11 mutation demonstrates that tiny changes in ATP sensitivity markedly affect diabetes risk. Diabetologia, 2016, 59, 1430-1436.	6.3	25
473	Psychiatric morbidity in children with <scp>KCNJ</scp>11 neonatal diabetes. Diabetic Medicine, 2016, 33, 1387-1391.	2.3	25
474	Significant Linkage of BMI to Chromosome 10p in the U.K. Population and Evaluation of GAD2 as a Positional Candidate. Diabetes, 2006, 55, 1884-1889.	0.6	24
475	IGF2/H19 hypomethylation in a patient with very low birthweight, preocious pubarche and insulin resistance. BMC Medical Genetics, 2012, 13, 42.	2.1	24
476	Hypoglycaemia following diabetes remission in patients with 6q24 methylation defects: expanding the clinical phenotype. Diabetologia, 2013, 56, 218-221.	6.3	24
477	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
478	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
479	Defining drug response for stratified medicine. Drug Discovery Today, 2017, 22, 173-179.	6.4	24
480	Are we missing hypoglycaemia? Elderly patients with insulin-treated diabetes present to primary care frequently with non-specific symptoms associated with hypoglycaemia. Primary Care Diabetes, 2018, 12, 139-146.	1.8	24
481	Type 1 diabetes can present before the age of 6Âmonths and is characterised by autoimmunity and rapid loss of beta cells. Diabetologia, 2020, 63, 2605-2615.	6.3	24
482	Long-term Follow-up of Glycemic and Neurological Outcomes in an International Series of Patients With Sulfonylurea-Treated ABCC8 Permanent Neonatal Diabetes. Diabetes Care, 2021, 44, 35-42.	8.6	24
483	Development of a bloodspot assay for insulin. Clinica Chimica Acta, 2001, 310, 141-150.	1.1	23
484	Severe hyperglycemia after renal transplantation in a pediatric patient with a mutation of the Hepatocyte Nuclear Factor-1Î² gene. American Journal of Kidney Diseases, 2002, 40, 1325-1330.	1.9	23
485	Abnormal splicing of hepatocyte nuclear factor 1 alpha in maturity-onset diabetes of the young. Diabetologia, 2002, 45, 1463-1467.	6.3	23
486	Apolipoprotein-E Influences Aspects of Intellectual Ability in Type 1 Diabetes. Diabetes, 2003, 52, 145-148.	0.6	23

#	Article	IF	Citations
487	Examining the relationships between the Pro12Ala variant in PPARG and Type 2 diabetes-related traits in UK samples. Diabetic Medicine, 2005, 22, 1696-1700.	2.3	23
488	Common variations in the ALMS1 gene do not contribute to susceptibility to type 2 diabetes in a large white UK population. Diabetologia, 2006, 49, 1209-1213.	6.3	23
489	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. Journal of Hepatology, 2019, 71, 594-602.	3.7	23
490	Microalbuminuria as a screening tool in cystic fibrosis-related diabetes. Pediatric Pulmonology, 2005, 39, 103-107.	2.0	22
491	Asian MODY: are we missing an important diagnosis?. Diabetic Medicine, 2006, 23, 1257-1260.	2.3	22
492	Genetics and type 2 diabetes in youth. Pediatric Diabetes, 2007, 8, 42-47.	2.9	22
493	Circulating Î²-carotene levels and type 2 diabetesâ€"cause or effect?. Diabetologia, 2009, 52, 2117-2121.	6.3	22
494	Isolated Pancreatic Aplasia Due to a Hypomorphic PTF1A Mutation. Diabetes, 2016, 65, 2810-2815.	0.6	22
495	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. Diabetologia, 2019, 62, 1601-1615.	6.3	22
496	Trisomy 21 Is a Cause of Permanent Neonatal Diabetes That Is Autoimmune but Not HLA Associated. Diabetes, 2019, 68, 1528-1535.	0.6	22
497	Homozygosity mapping provides supporting evidence of pathogenicity in recessive Mendelian disease. Genetics in Medicine, 2019, 21, 982-986.	2.4	22
498	Two decades since the fetal insulin hypothesis: what have we learned from genetics?. Diabetologia, 2021, 64, 717-726.	6.3	22
499	Availability of Type II Diabetic Families for Detection of Diabetes Susceptibility Genes. Diabetes, 1993, 42, 1536-1543.	0.6	21
500	Mesangiocapillary Glomerulonephritis Type 2 Associated with Familial Partial Lipodystrophy (Dunnigan-Kobberling Syndrome). Nephron Clinical Practice, 2004, 96, c35-c38.	2.3	21
501	Assessing newborn body composition using principal components analysis: differences in the determinants of fat and skeletal size. BMC Pediatrics, 2006, 6, 24.	1.7	21
502	Epistasis Between Type 2 Diabetes Susceptibility Loci on Chromosomes 1q21-25 and 10q23-26 in Northern Europeans. Annals of Human Genetics, 2006, 70, 726-737.	0.8	20
503	Glibenclamide unresponsiveness in a Brazilian child with permanent neonatal diabetes mellitus and DEND syndrome due to a C166Y mutation in KCNJ11 (Kir6.2) gene. Arquivos Brasileiros De Endocrinologia E Metabologia, 2008, 52, 1350-1355.	1.3	20
504	In celebration of a century with insulin â€“ Update of insulin gene mutations in diabetes. Molecular Metabolism, 2021, 52, 101280.	6.5	20

#	Article	IF	Citations
505	The Role of Inflammatory Pathway Genetic Variation on Maternal Metabolic Phenotypes during Pregnancy. PLoS ONE, 2012, 7, e32958.	2.5	20
506	The transcription factor 7â€like 2 (TCF7L2) gene is associated with TypeÂ2 diabetes in UK communityâ€based cases, but the risk allele frequency is reduced compared with UK cases selected for genetic studies. Diabetic Medicine, 2007, 24, 1067-1072.	2.3	19
507	A conserved tryptophan at the membraneâ€“water interface acts as a gatekeeper for Kir6.2/SUR1 channels and causes neonatal diabetes when mutated. Journal of Physiology, 2011, 589, 3071-3083.	2.9	19
508	The impact of insulin administration during the mixed meal tolerance test. Diabetic Medicine, 2012, 29, 1279-1284.	2.3	19
509	Fetal Macrosomia and Neonatal Hyperinsulinemic Hypoglycemia Associated With Transplacental Transfer of Sulfonylurea in a Mother With KCNJ11-Related Neonatal Diabetes. Diabetes Care, 2014, 37, 3333-3335.	8.6	19
510	PLIN1 Haploinsufficiency Is Not Associated With Lipodystrophy. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3225-3230.	3.6	19
511	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.	8.6	19
512	A Non-Coding Disease Modifier of Pancreatic Agenesis Identified by Genetic Correction in a Patient-Derived iPSC Line. Cell Stem Cell, 2020, 27, 137-146.e6.	11.1	19
513	Skin microvascular vasodilatory capacity in offspring of two parents with Type 2 diabetes. Diabetic Medicine, 2001, 18, 541-545.	2.3	18
514	Human calcium/calmodulin-dependent protein kinase II gamma gene (CAMK2G): cloning, genomic structure and detection of variants in subjects with Type II diabetes. Diabetologia, 2002, 45, 580-583.	6.3	18
515	Apolipoprotein E genotype, islet amyloid deposition and severity of Type 2 diabetes. Diabetes Research and Clinical Practice, 2003, 60, 105-110.	2.8	18
516	GAD antibodies in probands and their relatives in a cohort clinically selected for Type 2 diabetes. Diabetic Medicine, 2006, 23, 834-838.	2.3	18
517	Paternal insulin resistance and its association with umbilical cord insulin concentrations. Diabetologia, 2006, 49, 2668-2674.	6.3	18
518	Conditional expression of hepatocyte nuclear factor-1Î², the maturity-onset diabetes of the young-5 gene product, influences the viability and functional competence of pancreatic Î²-cells. Journal of Endocrinology, 2006, 190, 171-181.	2.6	18
519	Reduced peripheral blood mitochondrial DNA content is not a risk factor for TypeÂ2 diabetes. Diabetic Medicine, 2007, 24, 784-787.	2.3	18
520	The association between postprandial urinary Câ€peptide creatinine ratio and the treatment response to liraglutide: a multiâ€centre observational study. Diabetic Medicine, 2014, 31, 403-411.	2.3	18
521	Differential regulation of serum microRNA expression by HNF1Î² and HNF1Î± transcription factors. Diabetologia, 2016, 59, 1463-1473.	6.3	18
522	The prevalence of monogenic diabetes in Australia: the Fremantle Diabetes Study Phase II. Medical Journal of Australia, 2017, 207, 344-347.	1.7	18

#	Article	IF	Citations
523	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. Clinical Epigenetics, 2018, 10, 97.	4.1	18
524	The disproportionate excess mortality risk of COVID-19 in younger people with diabetes warrants vaccination prioritisation. Diabetologia, 2021, 64, 1184-1186.	6.3	18
525	No Evidence for Linkage at Candidate Type 2 Diabetes Susceptibility Loci on Chromosomes 12 and 20 in United Kingdom Caucasians. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 853-857.	3.6	17
526	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
527	Neonatal hyperinsulinaemic hypoglycaemia and monogenic diabetes due to a heterozygous mutation of the HNF4A gene. Australian and New Zealand Journal of Obstetrics and Gynaecology, 2009, 49, 328-330.	1.0	17
528	The impact of gender on urine C-peptide creatinine ratio interpretation. Annals of Clinical Biochemistry, 2012, 49, 363-368.	1.6	17
529	Urine C-peptide creatinine ratio can be used to assess insulin resistance and insulin production in people without diabetes: an observational study. BMJ Open, 2013, 3, e003193.	1.9	17
530	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. Diabetes, 2021, 70, 2092-2106.	0.6	17
531	TriMaster: randomised double-blind crossover study of a DPP4 inhibitor, SGLT2 inhibitor and thiazolidinedione as second-line or third-line therapy in patients with type 2 diabetes who have suboptimal glycaemic control on metformin treatment with or without a sulfonylureaâ€”a MASTERMIND study protocol. BMJ Open, 2020, 10, e042784.	1.9	17
532	Improvements in Awareness and Testing Have Led to a Threefold Increase Over 10 Years in the Identification of Monogenic Diabetes in the U.K.. Diabetes Care, 2022, 45, 642-649.	8.6	17
533	Increased Risk of Diabetes in First-Degree Relatives of Young-Onset Type 2 Diabetic Patients Compared With Relatives of Those Diagnosed Later. Diabetes Care, 2002, 25, 636-637.	8.6	16
534	Rare variants identified in the HNF-4Î± Î²-cell-specific promoter and alternative exon 1 lack biological significance in maturity onset diabetes of the young and young onset Type II diabetes. Diabetologia, 2002, 45, 1344-1348.	6.3	16
535	Preserved insulin response to tolbutamide in hepatocyte nuclear factor-1Î± mutation carriers. Diabetic Medicine, 2005, 22, 406-409.	2.3	16
536	A genetic syndrome of chronic renal failure with multiple renal cysts and early onset diabetes. Kidney International, 2008, 74, 1094-1099.	5.2	16
537	Ten years of the national genetic diabetes nurse network: a model for the translation of genetic information into clinical care. Clinical Medicine, 2014, 14, 117-121.	1.9	16
538	Genetic mutations associated with neonatal diabetes mellitus in Omani patients. Journal of Pediatric Endocrinology and Metabolism, 2018, 31, 195-204.	0.9	16
539	A genome-wide association study implicates multiple mechanisms influencing raised urinary albuminâ€“creatinine ratio. Human Molecular Genetics, 2019, 28, 4197-4207.	2.9	16
540	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	8.6	16

#	Article	IF	Citations
541	Understanding the pathogenesis of lean non-autoimmune diabetes in an African population with newly diagnosed diabetes. Diabetologia, 2022, 65, 675-683.	6.3	16
542	Candidate gene studies in pedigrees with maturity-onset diabetes of the young not linked with glucokinase. Diabetologia, 1995, 38, 1055-1060.	6.3	15
543	The mitochondrial tRNALeu(UUR) A to G 3243 mutation is associated with insulin-dependent and non-insulin-dependent diabetes in a Chinese population. , 1997, 14, 1026-1031.		15
544	Non-penetrance in a MODY 3 family with a mutation in the hepatic nuclear factor 1Î± gene: implications for predictive testing. European Journal of Human Genetics, 1999, 7, 729-732.	2.8	15
545	The role of the HNF4Î± enhancer in type 2 diabetes. Molecular Genetics and Metabolism, 2002, 76, 148-151.	1.1	15
546	Interaction between mutations in the slide helix of Kir6.2 associated with neonatal diabetes and neurological symptoms. Human Molecular Genetics, 2010, 19, 963-972.	2.9	15
547	The previously reported T342P GCK missense variant is not a pathogenic mutation causing MODY. Diabetologia, 2011, 54, 2202-2205.	6.3	15
548	Assessment of the HNF1B Score as a Tool to Select Patients for <i>HNF1B</i> Genetic Testing. Nephron, 2015, 130, 134-140.	1.8	15
549	Failure to detect cytomegalovirus DNA in pancreas in type 2 diabetes. Lancet, The, 1992, 339, 459-460.	13.7	14
550	Loss of HNF1? function in human renal cell carcinoma: Frequent mutations in theVHL gene but not theHNF1? gene. , 1999, 24, 305-314.		14
551	A severe clinical phenotype results from the co-inheritance of type 2 susceptibility genes and a hepatocyte nuclear factor-1alpha mutation. Diabetes Care, 2000, 23, 424-425.	8.6	14
552	Kidney disease in hypomelanosis of Ito. Nephrology Dialysis Transplantation, 2001, 16, 1267-1269.	0.7	14
553	Adult height and proteinuria in type 2 diabetes. Nephrology Dialysis Transplantation, 2001, 16, 525-528.	0.7	14
554	Quantitative traits associated with the Type 2 diabetes susceptibility allele in Kir6.2. Diabetologia, 2003, 46, 1021-1023.	6.3	14
555	Maternal glucose levels influence birthweight and 'catch-up' and 'catch-down' growth in a large contemporary cohort. Diabetic Medicine, 2006, 23, 1207-1212.	2.3	14
556	Offspring birthweight is not associated with paternal insulin resistance. Diabetologia, 2006, 49, 2675-2678.	6.3	14
557	Assessment of endogenous insulin secretion in insulin treated diabetes predicts postprandial glucose and treatment response to prandial insulin. BMC Endocrine Disorders, 2012, 12, 6.	2.2	14
558	Neuropsychological impairments in children with <scp>KCNJ</scp>11 neonatal diabetes. Diabetic Medicine, 2017, 34, 1171-1173.	2.3	14

#	Article	IF	Citations
559	Evaluating associations between the benefits and risks of drug therapy in type 2 diabetes: a joint modeling approach. Clinical Epidemiology, 2018, Volume 10, 1869-1877.	3.0	14
560	Beyond the beta cell in diabetes. Nature Genetics, 2006, 38, 12-13.	21.4	13
561	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.	0.6	13
562	Future Roadmaps for Precision Medicine Applied to Diabetes: Rising to the Challenge of Heterogeneity. Journal of Diabetes Research, 2018, 2018, 1-12.	2.3	13
563	Type 1 diabetes genetic risk score discriminates between monogenic and Type 1 diabetes in children diagnosed at the age of <5 years in the Iranian population. Diabetic Medicine, 2019, 36, 1694-1702.	2.3	13
564	Common maternal and fetal genetic variants show expected polygenic effects on risk of small- or large-for-gestational-age (SGA or LGA), except in the smallest 3% of babies. PLoS Genetics, 2020, 16, e1009191.	3.5	13
565	Genes versus environment in insulindependent diabetes: the phoney war. Lancet, The, 1997, 349, 147-148.	13.7	12
566	Diagnosis of Maturity-Onset Diabetes of the Young in the Pediatric Diabetes Clinic. Journal of Pediatric Endocrinology and Metabolism, 2000, 13, 1411-1418.	0.9	12
567	Allelic drop-out may occur with a primer binding site polymorphism for the commonly used RFLP assay for the -1131T>C polymorphism of the Apolipoprotein AV gene. Lipids in Health and Disease, 2006, 5, 11.	3.0	12
568	Determinants of insulin concentrations in healthy 1-week-old babies in the community: Applications of a bloodspot assay. Early Human Development, 2006, 82, 143-148.	1.8	12
569	Digenic heterozygousHNF1AandHNF4Amutations in two siblings with childhood-onset diabetes. Pediatric Diabetes, 2013, 14, 535-538.	2.9	12
570	Screening for neonatal diabetes at day 5 of life using dried blood spot glucose measurement. Diabetologia, 2017, 60, 2168-2173.	6.3	12
571	The Common HNF1A Variant I27L Is a Modifier of Age at Diabetes Diagnosis in Individuals With HNF1A-MODY. Diabetes, 2018, 67, 1903-1907.	0.6	12
572	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. Diabetologia, 2020, 63, 744-756.	6.3	12
573	Identifying Good Responders to Glucose Lowering Therapy in Type 2 Diabetes: Implications for Stratified Medicine. PLoS ONE, 2014, 9, e111235.	2.5	12
574	Linkage analysis of glucokinase gene with NIDDM in Caucasian pedigrees. Diabetes, 1992, 41, 1496-1500.	0.6	12
575	Systematic genetic testing for recessively inherited monogenic diabetes: a cross-sectional study in paediatric diabetes clinics. Diabetologia, 2022, 65, 336-342.	6.3	12
576	An HNF1Î± truncation associated with maturity-onset diabetes of the young impairs pancreatic progenitor differentiation by antagonizing HNF1Î² function. Cell Reports, 2022, 38, 110425.	6.4	12

#	Article	IF	Citations
577	Association of Thyroid Peroxidase Antibodies and Thyroglobulin Antibodies with Thyroid Function in Pregnancy: An Individual Participant Data Meta-Analysis. Thyroid, 2022, 32, 828-840.	4.5	12
578	Beta-cell secretory defect caused by mutations in glucokinase gene. Lancet, The, 1992, 340, 1162-1163.	13.7	11
579	Conflicting results on variation in the IGFI gene highlight methodological considerations in the design of genetic association studies. Diabetologia, 2002, 45, 1605-1606.	6.3	11
580	Sequencing PDX1 (insulin promoter factorâ€ƒ1) in 1788 UK individuals found 5% had a low frequency coding variant, but these variants are not associated with Typeâ€ƒ2 diabetes. Diabetic Medicine, 2011, 28, 681-684.	2.3	11
581	Reappearance of C-Peptide During the Third Trimester of Pregnancy in Type 1 Diabetes: Pancreatic Regeneration or Fetal Hyperinsulinism?. Diabetes Care, 2021, 44, 1826-1834.	8.6	11
582	Genetic Disorders of the Pancreatic Beta Cell and Diabetes (Permanent Neonatal Diabetes and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54		11
583	The Impact of the Angiotensin-Converting Enzyme Insertion/Deletion Polymorphism on Severe Hypoglycemia in Type 2 Diabetes. Review of Diabetic Studies, 2006, 3, 76-76.	1.3	11
584	Unlocking the secrets of the pancreatic Î² cell: man and mouse provide the key. Journal of Clinical Investigation, 2004, 114, 314-316.	8.2	11
585	Impaired maximum microvascular hyperaemia in patients with MODY 3 (hepatocyte nuclear) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.3	10
586	Genetic association analysis of LARS2 with type 2 diabetes. Diabetologia, 2010, 53, 103-110.	6.3	10
587	Exocrine pancreatic dysfunction is common in hepatocyte nuclear factor 1Î²-associated renal disease and can be symptomatic. CKJ: Clinical Kidney Journal, 2018, 11, 453-458.	2.9	10
588	What to do with diabetes therapies when HbA1c lowering is inadequate: add, switch, or continue? A MASTERMIND study. BMC Medicine, 2019, 17, 79.	5.5	10
589	Identifying routine clinical predictors of nonâ€adherence to secondâ€line therapies in type 2 diabetes: A retrospective cohort analysis in a large primary care database. Diabetes, Obesity and Metabolism, 2020, 22, 59-65.	4.4	10
590	Clinical Characteristics and Long-term Follow-up of Patients with Diabetes Due To PTF1A Enhancer Mutations. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e4351-e4359.	3.6	10
591	Prior event rate ratio adjustment produced estimates consistent with randomized trial: a diabetes case study. Journal of Clinical Epidemiology, 2020, 122, 78-86.	5.0	10
592	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
593	Type II Diabetes: Search for Primary Defects. Annals of Medicine, 1992, 24, 511-516.	3.8	9
594	Phenotypic Multiple Endocrine Neoplasia Type 2B, Without Endocrinopathy or RET Gene Mutation: Implications for Management. Thyroid, 2006, 16, 605-608.	4.5	9

#	Article	IF	Citations
595	Effect of the Holiday Season in Patients With Diabetes: Glycemia and Lipids Increase Postholiday, but the Effect Is Small and Transient. Diabetes Care, 2014, 37, e98-e99.	8.6	9
596	Costs and Treatment Pathways for Type 2 Diabetes in the UK: A Mastermind Cohort Study. Diabetes Therapy, 2017, 8, 1031-1045.	2.5	9
597	Patterns of postmeal insulin secretion in individuals with sulfonylurea-treated KCNJ11 neonatal diabetes show predominance of non-KATP-channel pathways. BMJ Open Diabetes Research and Care, 2019, 7, e000721.	2.8	9
598	Neonatal diabetes mutations disrupt a chromatin pioneering function that activates the human insulin gene. Cell Reports, 2021, 35, 108981.	6.4	9
599	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	6.3	9
600	Microsatellite Polymorphisms at the Glucokinase Locus: a Population Association Study in Caucasian Type 2 Diabetic Subjects. Diabetic Medicine, 1993, 10, 694-698.	2.3	8
601	Glucokinase deficiency results in a beta-cell disorder characterised by normal fasting plasma proinsulin concentrations. Diabetologia, 1997, 40, 1367-1368.	6.3	8
602	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
603	Adolescent onset Type 2 diabetes in a non-obese Caucasian patient with an unbalanced translocation. Diabetic Medicine, 2003, 20, 483-485.	2.3	8
604	Variants in the aromatase gene and on the Y-chromosome are not associated with adult height or insulin resistance in a UK population. Clinical Endocrinology, 2003, 59, 175-179.	2.4	8
605	KCNJ11 activating mutation in an Indian family with remitting and relapsing diabetes. Indian Journal of Pediatrics, 2010, 77, 551-554.	0.8	8
606	Genetic influences on the association between fetal growth and susceptibility to type 2 diabetes. Journal of Developmental Origins of Health and Disease, 2010, 1, 96-105.	1.4	8
607	Cystatin C is not a good candidate biomarker for HNF1A-MODY. Acta Diabetologica, 2013, 50, 815-820.	2.5	8
608	Hyperglycaemiaâ€related complications at the time of diagnosis can cause permanent neurological disability in children with neonatal diabetes. Diabetic Medicine, 2017, 34, 1000-1004.	2.3	8
609	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. Genome Medicine, 2020, 12, 109.	8.2	8
610	Strategies to identify individuals with monogenic diabetes: results of an economic evaluation. BMJ Open, 2020, 10, e034716.	1.9	8
611	Associations between low HDL, sex and cardiovascular risk markers are substantially different in sub-Saharan Africa and the UK: analysis of four population studies. BMJ Global Health, 2021, 6, e005222.	4.7	8
612	Identification of<scp>GCKâ€</scp>maturityâ€onset diabetes of the young in cases of neonatal hyperglycemia: A case series and review of clinical features. Pediatric Diabetes, 2021, 22, 876-881.	2.9	8

#	Article	IF	Citations
613	Loss of HNF1alpha function in human renal cell carcinoma: frequent mutations in the VHL gene but not the HNF1alpha gene. Molecular Carcinogenesis, 1999, 24, 305-14.	2.7	8
614	Sequencing of candidate genes selected by beta cell experts in monogenic diabetes of unknown aetiology. JOP: Journal of the Pancreas, 2010, 11, 14-7.	1.5	8
615	Necrobiosis Lipodica Is a Clinical Feature of Maturity-Onset Diabetes of the Young. Diabetes Care, 2002, 25, 1249-1250.	8.6	7
616	Examining the Candidacy of Ghrelin as a Gene Responsible for Variation in Adult Stature in a United Kingdom Population with Type 2 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2201-2204.	3.6	7
617	Hypoplastic Glomerulocystic Kidney Disease and Hepatoblastoma. Journal of Pediatric Hematology/Oncology, 2009, 31, 527-529.	0.6	7
618	Reevaluation of a case of type 1 diabetes mellitus diagnosed before 6 months of age. Nature Reviews Endocrinology, 2010, 6, 347-351.	9.6	7
619	Permanent neonatal diabetes in siblings with novel C109YINSmutation transmitted by an unaffected parent with somatic mosaicism. Pediatric Diabetes, 2014, 15, 324-328.	2.9	7
620	Hypogonadotropic Hypogonadism and Short Stature in Patients with Diabetes Due to Neurogenin 3 Deficiency. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 3555-3558.	3.6	7
621	Permanent neonatal diabetes: combining sulfonylureas with insulin may be an effective treatment. Diabetic Medicine, 2018, 35, 1291-1296.	2.3	7
622	Monogenic Diabetes and Integrated Stress Response Genes Display Altered Gene Expression in Type 1 Diabetes. Diabetes, 2021, 70, 1885-1897.	0.6	7
623	Gain-of-Function Mutations in the KATP Channel (KCNJ11) Impair Coordinated Hand-Eye Tracking. PLoS ONE, 2013, 8, e62646.	2.5	7
624	PLIN1 Haploinsufficiency Causes a Favorable Metabolic Profile. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2318-e2323.	3.6	7
625	The HOPE study and diabetes. Lancet, The, 2000, 355, 1182-1183.	13.7	6
626	Serum amino acids in patients with mutations in the hepatocyte nuclear factor-1 alpha gene. Diabetic Medicine, 2004, 21, 928-930.	2.3	6
627	Role of the D76N polymorphism of insulin promoter factor-1 in predisposing to Type 2 diabetes. Diabetologia, 2004, 47, 957-958.	6.3	6
628	A successful transition to sulfonylurea treatment in male infant with neonatal diabetes caused by the novel abcc8 gene mutation and three years follow-up. Diabetes Research and Clinical Practice, 2017, 129, 59-61.	2.8	6
629	No Evidence for Linkage at Candidate Type 2 Diabetes Susceptibility Loci on Chromosomes 12 and 20 in United Kingdom Caucasians. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 853-857.	3.6	6
630	Distribution of type II diabetes in nuclear families. Diabetes, 1993, 42, 106-112.	0.6	6

#	Article	IF	Citations
631	Availability of type II diabetic families for detection of diabetes susceptibility genes. Diabetes, 1993, 42, 1536-1543.	0.6	6
632	Estimating disease prevalence in large datasets using genetic risk scores. Nature Communications, 2021, 12, 6441.	12.8	6
633	Intermediate expansions of a X25/frataxin gene GAA repeat and Type II diabetes: assessment using parent-offspring trios. Diabetologia, 2000, 43, 384-385.	6.3	5
634	R127W in HNF4? is a loss-of-function mutation causing maturity-onset diabetes of the young (MODY) in a UK Caucasian family. Diabetologia, 2000, 43, 1203-1203.	6.3	5
635	Weight differences in Plymouth toddlers compared to the British Growth Reference Population. Archives of Disease in Childhood, 2004, 89, 843-844.	1.9	5
636	The accuracy of birth weight. Journal of Clinical Nursing, 2004, 13, 767-768.	3.0	5
637	Mutations in HHEX are not a common cause of monogenic forms of beta cell dysfunction. Diabetologia, 2007, 50, 2019-2022.	6.3	5
638	KCNJ11 activating mutations cause both transient and permanent neonatal diabetes mellitus in Cypriot patients. Pediatric Diabetes, 2011, 12, 133-137.	2.9	5
639	Home Urine C-Peptide Creatinine Ratio Can Be Used to Monitor Islet Transplant Function: Figure 1. Diabetes Care, 2014, 37, 1737-1740.	8.6	5
640	Physiology Helps GWAS Take a Step Closer to Mechanism. Diabetes, 2014, 63, 1836-1837.	0.6	5
641	Low IgE Is a Useful Tool to Identify STAT3 Gain-of-Function Mutations. Clinical Chemistry, 2016, 62, 1536-1538.	3.2	5
642	Pancreas and gallbladder agenesis in a newborn with semilobar holoprosencephaly, a case report. BMC Medical Genetics, 2017, 18, 57.	2.1	5
643	The challenge of diagnosing type 1 diabetes in older adults. Diabetic Medicine, 2020, 37, 1781-1782.	2.3	5
644	Choice of HbA1c threshold for identifying individuals at high risk of type 2 diabetes and implications for diabetes prevention programmes: a cohort study. BMC Medicine, 2021, 19, 184.	5.5	5
645	HbA1c performs well in monitoring glucose control even in populations with high prevalence of medical conditions that may alter its reliability: the OPTIMAL observational multicenter study. BMJ Open Diabetes Research and Care, 2021, 9, e002350.	2.8	5
646	Non-linkage of the glucagon-like peptide 1 receptor gene with maturity onset diabetes of the young. Diabetologia, 1994, 37, 721-724.	6.3	5
647	Low Frequency Variants in the Exons Only Encoding Isoform A of HNF1A Do Not Contribute to Susceptibility to Type 2 Diabetes. PLoS ONE, 2009, 4, e6615.	2.5	5
648	Dimensions of Personal Loss and Gain Associated with a Rare Genetic Type of Diabetes. Illness Crisis and Loss, 2003, 11, 362-376.	0.7	4

#	Article	IF	Citations
649	Amino acid properties may be useful in predicting clinical outcome in patients with Kir6.2 neonatal diabetes. European Journal of Endocrinology, 2012, 167, 417-421.	3.7	4
650	Continue with long term sulfonylureas in patients with mutations in the KCNJ11 gene when there is evidence of response even if insulin treatment is still required. Diabetes Research and Clinical Practice, 2013, 100, e63.	2.8	4
651	The value of inÂvitro studies in a case of neonatal diabetes with a novel Kir6.2â€W68G mutation. Clinical Case Reports (discontinued), 2015, 3, 884-887.	0.5	4
652	Genetic risk scores in adult-onset type 1 diabetes â€“ Authors' reply. Lancet Diabetes and Endocrinology,the, 2018, 6, 169.	11.4	4
653	Comment on Dubois-Laforgue et al. Diabetes, Associated Clinical Spectrum, Long-term Prognosis, and Genotype/Phenotype Correlations in 201 Adult Patients With Hepatocyte Nuclear Factor 1B (HNF1B) Molecular Defects. Diabetes Care 2017;40:1436â€“1443. Diabetes Care, 2018, 41, e7-e7.	8.6	4
654	Understanding cystic-fibrosis-related diabetes: best thought of as insulin deficiency?. Journal of the Royal Society of Medicine, 2004, 97 Suppl 44, 26-35.	2.0	4
655	How well do midwives estimate the date of delivery?. Midwifery, 2003, 19, 125-131.	2.3	3
656	Genetic Testing in Diabetes Mellitus. , 2010, , 17-25.		3
657	Identifying clinical criteria to predict Type 1 diabetes, as defined by absolute insulin deficiency: a systematic review protocol. BMJ Open, 2012, 2, e002309.	1.9	3
658	Early-onset, severe lipoatrophy in a patient with permanent neonatal diabetes mellitus secondary to a recessive mutation in the INS gene. Pediatric Diabetes, 2012, 13, e26-e29.	2.9	3
659	Response to Comment on: Chakera et al. Antenatal Diagnosis of Fetal Genotype Determines if Maternal Hyperglycemia due to a Glucokinase Mutation Requires Treatment. Diabetes Care 2012;35:1832â€“1834. Diabetes Care, 2013, 36, e15-e15.	8.6	3
660	Comment on: Khurana et al. The Diagnosis of Neonatal Diabetes in a Mother at 25 Years of Age. Diabetes Care 2012;35:e59. Diabetes Care, 2013, 36, e31-e31.	8.6	3
661	Screening of monogenic autoimmune diabetes among children with type 1 diabetes and multiple autoimmune diseases: is it worth doing?. Journal of Pediatric Endocrinology and Metabolism, 2019, 32, 1147-1153.	0.9	3
662	Clusters provide a better holistic view of type 2 diabetes than simple clinical features â€“ Authors' reply. Lancet Diabetes and Endocrinology,the, 2019, 7, 669.	11.4	3
663	Predicting post one-year durability of glucose-lowering monotherapies in patients with newly-diagnosed type 2 diabetes mellitus â€“ A MASTERMIND precision medicine approach (UKPDS 87). Diabetes Research and Clinical Practice, 2020, 166, 108333.	2.8	3
664	Linkage of maturity-onset diabetes of the young to the glucokinase gene-evidence of genetic heterogeneity. Biochemical Society Transactions, 1993, 21, 24S-24S.	3.4	2
665	Heterogeneity in the clinical course of patients with Type 2 diabetes on dialysis - the need for different preventative strategies. Diabetic Medicine, 2000, 17, 685-686.	2.3	2
666	Chapter 1 Transcription factor genes in type 2 diabetes. Advances in Molecular and Cellular Endocrinology, 2006, 5, 1-14.	0.1	2

#	Article	IF	Citations
667	Coincidence of a Novel KCNJ11 Missense Variant R365H With a Paternally Inherited 6q24 Duplication in a Patient With Transient Neonatal Diabetes. Diabetes Care, 2008, 31, 1736-1737.	8.6	2
668	Mutations in the third gene shown to alter fasting glucose levels in the population (G6PC2) are not a common cause of monogenic forms of pancreatic Bâ€cell dysfunction. Diabetic Medicine, 2009, 26, 113-114.	2.3	2
669	Lifecourse: management of type 1 diabetes. Lancet Diabetes and Endocrinology,the, 2014, 2, 194-195.	11.4	2
670	More on STAT1 Gain of Function, Type 1 Diabetes, and JAK Inhibition. New England Journal of Medicine, 2021, 384, 93-94.	27.0	2
671	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. Wellcome Open Research, 2020, 5, 175.	1.8	2
672	Segregation analysis of NIDDM in Caucasian families. Diabetologia, 1994, 37, 1231-1240.	6.3	2
673	Association of birthweight and penetrance of diabetes in individuals with HNF4A-MODY: a cohort study. Diabetologia, 2022, 65, 246-249.	6.3	2
674	Using highly sensitive C-reactive protein measurement to diagnose MODY in a family with suspected type 2 diabetes. BMJ Case Reports, 2012, 2012, bcr0120125612-bcr0120125612.	0.5	2
675	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. Human Molecular Genetics, 2022, 31, 1762-1775.	2.9	2
676	Continuous glucose monitoring demonstrates low risk of clinically significant hypoglycemia associated with sulphonylurea treatment in an African type 2 diabetes population: results from the OPTIMAL observational multicenter study. BMJ Open Diabetes Research and Care, 2022, 10, e002714.	2.8	2
677	Mild MDPL in a patient with a novel de novo missense variant in the Cys-B region of POLD1. European Journal of Human Genetics, 2022, 30, 960-966.	2.8	2
678	Genetic Factors in the Aetiology of Non-Insulin-Dependent Diabetes. Frontiers of Hormone Research, 1997, 22, 157-178.	1.0	1
679	A study of association between common variation in the growth hormone-chorionic somatomammotropin hormone gene cluster and adult fasting insulin in a UK Caucasian population. Journal of Negative Results in BioMedicine, 2006, 5, 18.	1.4	1
680	A pathway to insulin independence in newborns and infants with diabetes. Journal of Perinatology, 2011, 31, 567-570.	2.0	1
681	A diagnostic approach for defining idiopathic remitting diabetes: a retrospective cohort study. BMC Endocrine Disorders, 2014, 14, 45.	2.2	1
682	Permanent neonatal diabetes misdiagnosed as type 1 diabetes in a 28-year-old female: A life-changing diagnosis. Diabetes Research and Clinical Practice, 2014, 106, e22-e24.	2.8	1
683	Type 1 diabetes phenotype in white and South Asian people with young onset diabetes in the UK: results from the MY DIABETES study. Lancet, The, 2017, 389, S69.	13.7	1
684	The Absence of Islet Autoantibodies in Clinically Diagnosed Older-Adult Onset Type 1 Diabetes Suggests an Alternative Pathology, Advocating for Routine Testing in This Age Group. SSRN Electronic Journal, 0, , .	0.4	1

#	Article	IF	Citations
685	Candidate gene studies in pedigrees with maturity-onset diabetes of the young not linked with glucokinase. Diabetologia, 1995, 38, 1055-1060.	6.3	1
686	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. Wellcome Open Research, 2020, 5, 175.	1.8	1
687	Congenital beta cell defects are not associated with markers of islet autoimmunity, even in the context of high genetic risk for type 1 diabetes. Diabetologia, 2022, , 1.	6.3	1
688	The effect of long- and short-term corticosteroids on plasma calcitonin and parathyroid hormone. Bone and Mineral, 1990, 10, S289.	1.9	0
689	Tall stories: the fundamental difficulties of genetic association studies. Clinical Endocrinology, 2004, 60, 145-146.	2.4	0
690	Reported parental age of death in type 2 diabetic patients with and without established diabetic nephropathy. European Journal of Internal Medicine, 2005, 16, 482-484.	2.2	0
691	Low prevalence of mitochondrial DNA 3243A>G point mutation in Caucasians with unexplained renal disease. Diabetic Medicine, 2007, 24, 804-806.	2.3	0
692	PREVALENCE AND INCIDENCE OF A NEWLY DEFINED TYPE OF DIABETES IN CHILDREN, ADOLESCENTS, AND ADULTS IN THE LARGEST INTERNATIONAL SERIES TO DATE. Pediatrics, 2008, 121, S115-S116.	2.1	0
693	RET gene mutations are not a common cause of congenital solitary functioning kidney in adults. CKJ: Clinical Kidney Journal, 2009, 2, 183-184.	2.9	0
694	Response to Comment on: McDonald et al. High-Sensitivity CRP Discriminates HNF1A-MODY From Other Subtypes of Diabetes. Diabetes Care 2011;34:1860-1862. Diabetes Care, 2011, 34, e187-e187.	8.6	0
695	Response to Comment on: Besser et al. Lessons From the Mixed-Meal Tolerance Test: Use of 90-Minute and Fasting C-Peptide in Pediatric Diabetes. Diabetes Care 2013;36:195-201. Diabetes Care, 2013, 36, e222-e222.	8.6	0
696	Crossover studies can help the individualisation of care in type 2 diabetes: the MASTERMIND approach. Practical Diabetes, 2016, 33, 115-117.	0.3	0
697	Marked intrafamilial variability of exocrine and endocrine pancreatic phenotypes due to a splice site mutation in GATA6. Biotechnology and Biotechnological Equipment, 2018, 32, 124-129.	1.3	0
698	Clinical Consequences of Defects in Î²-Cell Genes. Growth Hormone, 2001, , 325-336.	0.2	0
699	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. Wellcome Open Research, 0, 5, 175.	1.8	0
700	Response to Comment on Meek et al. Reappearance of C-Peptide During the Third Trimester in Type 1 Diabetes Pregnancy: Pancreatic Regeneration or Fetal Hyperinsulinism? Diabetes Care 2021;44:1826â€“1834. Diabetes Care, 2022, 45, e43-e44.	8.6	0
701	Alternative pre-analytic sample handling techniques for glucose measurement in the absence of fluoride tubes in low resource settings. PLoS ONE, 2022, 17, e0264432.	2.5	0
702	Title is missing!. , 2020, 17, e1003149.		0

#	Article	IF	Citations
703	Title is missing!. , 2020, 17, e1003149.		0
704	Title is missing!. , 2020, 17, e1003149.		0
705	Title is missing!. , 2020, 17, e1003149.		0
706	Title is missing!. , 2020, 17, e1003149.		0
707	Islet autoantibody positivity in an adult population with recently diagnosed diabetes in Uganda. PLoS ONE, 2022, 17, e0268783.	2.5	0
708	A biallelic lossâ€ofâ€function PDIA6 variant in a second patient with polycystic kidney disease, infancyâ€onset diabetes, and microcephaly. Clinical Genetics, 2022, 102, 457-458.	2.0	0