Amelie Bonnefond

List of Publications by Year
in descending order

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139 papers	15,432 citations	38742 50 h-index	19190 118 g-index
176 all docs	176 docs citations	176 times ranked	25092 citing authors

#	Article	IF	Citations
1	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
2	The Lin28/let-7 Axis Regulates Glucose Metabolism. Cell, 2011, 147, 81-94.	28.9	812
3	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	3.5	796
4	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
5	Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human. Nature, 2012, 483, 350-354.	27.8	572
6	A variant near MTNR1B is associated with increased fasting plasma glucose levels and type 2 diabetes risk. Nature Genetics, 2009, 41, 89-94.	21.4	540
7	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
8	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
9	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
10	Quality control and conduct of genome-wide association meta-analyses. Nature Protocols, 2014, 9, 1192-1212.	12.0	398
11	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
12	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
13	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
14	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
15	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. Nature Genetics, 2012, 44, 297-301.	21.4	319
16	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
17	KLHL3 mutations cause familial hyperkalemic hypertension by impairing ion transport in the distal nephron. Nature Genetics, 2012, 44, 456-460.	21.4	281
18	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275

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19	Genome-Wide Association for Abdominal Subcutaneous and Visceral Adipose Reveals a Novel Locus for Visceral Fat in Women. PLoS Genetics, 2012, 8, e1002695.	3.5	245
20	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
21	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	21.4	214
22	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
23	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907.	10.2	191
24	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
25	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
26	Whole-Exome Sequencing and High Throughput Genotyping Identified KCNJ11 as the Thirteenth MODY Gene. PLoS ONE, 2012, 7, e37423.	2.5	161
27	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
28	Shared genetic predisposition in rheumatoid arthritis-interstitial lung disease and familial pulmonary fibrosis. European Respiratory Journal, 2017, 49, 1602314.	6.7	154
29	Insulin Gene Mutations Resulting in Early-Onset Diabetes: Marked Differences in Clinical Presentation, Metabolic Status, and Pathogenic Effect Through Endoplasmic Reticulum Retention. Diabetes, 2010, 59, 653-661.	0.6	132
30	Rare and Common Genetic Events in Type 2 Diabetes: What Should Biologists Know?. Cell Metabolism, 2015, 21, 357-368.	16.2	128
31	Interactions of Dietary Whole-Grain Intake With Fasting Glucose- and Insulin-Related Genetic Loci in Individuals of European Descent: A meta-analysis of 14 cohort studies. Diabetes Care, 2010, 33, 2684-2691.	8.6	127
32	The emerging genetics of type 2 diabetes. Trends in Molecular Medicine, 2010, 16, 407-416.	6.7	127
33	G-allele of Intronic rs10830963 in MTNR1B Confers Increased Risk of Impaired Fasting Glycemia and Type 2 Diabetes Through an Impaired Glucose-Stimulated Insulin Release. Diabetes, 2009, 58, 1450-1456.	0.6	125
34	Loss-of-function mutations in ADCY3 cause monogenic severe obesity. Nature Genetics, 2018, 50, 175-179.	21.4	122
35	Association between large detectable clonal mosaicism and type 2 diabetes with vascular complications. Nature Genetics, 2013, 45, 1040-1043.	21.4	106
36	Loss-of-function mutations in SIM1 contribute to obesity and Prader-Williâ€“like features. Journal of Clinical Investigation, 2013, 123, 3037-3041.	8.2	105

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37	Molecular Diagnosis of Neonatal Diabetes Mellitus Using Next-Generation Sequencing of the Whole Exome. PLoS ONE, 2010, 5, e13630.	2.5	102
38	Beneficial effect of a high number of copies of salivary amylase AMY1 gene on obesity risk in Mexican children. Diabetologia, 2015, 58, 290-294.	6.3	89
39	Neuropsychological dysfunction and developmental defects associated with genetic changes in infants with neonatal diabetes mellitus: a prospective cohort study. Lancet Diabetes and Endocrinology,the, 2013, 1, 199-207.	11.4	87
40	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
41	Genetic variants in LEP, LEPR, and <scp>MC4R</scp> explain 30% of severe obesity in children from a consanguineous population. Obesity, 2015, 23, 1687-1695.	3.0	82
42	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
43	Endoplasmic Reticulum Stress Links Oxidative Stress to Impaired Pancreatic Beta-Cell Function Caused by Human Oxidized LDL. PLoS ONE, 2016, 11, e0163046.	2.5	75
44	Disruption of a Novel KrÃ¼ppel-like Transcription Factor p300-regulated Pathway for Insulin Biosynthesis Revealed by Studies of the c.-331 INS Mutation Found in Neonatal Diabetes Mellitus. Journal of Biological Chemistry, 2011, 286, 28414-28424.	3.4	72
45	Highly Sensitive Diagnosis of 43 Monogenic Forms of Diabetes or Obesity Through One-Step PCR-Based Enrichment in Combination With Next-Generation Sequencing. Diabetes Care, 2014, 37, 460-467.	8.6	69
46	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. Diabetes, 2018, 67, 1310-1321.	0.6	64
47	The lessons of early-onset monogenic diabetes for the understanding of diabetes pathogenesis. Best Practice and Research in Clinical Endocrinology and Metabolism, 2012, 26, 171-187.	4.7	55
48	Analysis of the contribution of FTO, NPC1, ENPP1, NEGR1, GNPDA2 and MC4Rgenes to obesity in Mexican children. BMC Medical Genetics, 2013, 14, 21.	2.1	55
49	Expression and functional assessment of candidate type 2 diabetes susceptibility genes identify four new genes contributing to human insulin secretion. Molecular Metabolism, 2017, 6, 459-470.	6.5	55
50	A nonsense loss-of-function mutation in PCSK1 contributes to dominantly inherited human obesity. International Journal of Obesity, 2015, 39, 295-302.	3.4	54
51	Loss-of-function mutations in MRAP2 are pathogenic in hyperphagic obesity with hyperglycemia and hypertension. Nature Medicine, 2019, 25, 1733-1738.	30.7	54
52	GATA6 inactivating mutations are associated with heart defects and, inconsistently, with pancreatic agenesis and diabetes. Diabetologia, 2012, 55, 2845-2847.	6.3	53
53	Contribution of 24 obesity-associated genetic variants to insulin resistance, pancreatic beta-cell function and type 2 diabetes risk in the French population. International Journal of Obesity, 2013, 37, 980-985.	3.4	52
54	Novel LEPR mutations in obese Pakistani children identified by PCRâ€based enrichment and next generation sequencing. Obesity, 2014, 22, 1112-1117.	3.0	51

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55	Pluripotent Stem Cells as a Potential Tool for Disease Modelling and Cell Therapy in Diabetes. Stem Cell Reviews and Reports, 2014, 10, 327-337.	5.6	49
56	The loss-of-function PCSK9 p.R46L genetic variant does not alter glucose homeostasis. Diabetologia, 2015, 58, 2051-2055.	6.3	49
57	Transcription factor gene MNX1 is a novel cause of permanent neonatal diabetes in a consanguineous family. Diabetes and Metabolism, 2013, 39, 276-280.	2.9	48
58	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. BMC Medicine, 2017, 15, 37.	5.5	47
59	MFN2-associated lipomatosis: Clinical spectrum and impact on adipose tissue. Journal of Clinical Lipidology, 2018, 12, 1420-1435.	1.5	47
60	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	2.9	47
61	Eating Behavior, Low-Frequency Functional Mutations in the Melanocortin-4 Receptor (MC4R) Gene, and Outcomes of Bariatric Operations: A 6-Year Prospective Study. Diabetes Care, 2016, 39, 1384-1392.	8.6	46
62	Type 2 diabetesâ€“associated variants of the MT ₂ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, .	3.6	45
63	A GWAS sequence variant for platelet volume marks an alternative DNM3 promoter in megakaryocytes near a MEIS1 binding site. Blood, 2012, 120, 4859-4868.	1.4	44
64	MTNR1B G24E Variant Associates With BMI and Fasting Plasma Glucose in the General Population in Studies of 22,142 Europeans. Diabetes, 2010, 59, 1539-1548.	0.6	43
65	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
66	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. Nature Metabolism, 2020, 2, 1126-1134.	11.9	43
67	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. International Journal of Obesity, 2012, 36, 137-147.	3.4	42
68	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
69	Type 2 diabetes-related genetic risk scores associated with variations in fasting plasma glucose and development of impaired glucose homeostasis in the prospective DESIR study. Diabetologia, 2014, 57, 1601-1610.	6.3	38
70	The expression of genes in top obesity-associated loci is enriched in insula and substantia nigra brain regions involved in addiction and reward. International Journal of Obesity, 2020, 44, 539-543.	3.4	38
71	What Is the Contribution of Two Genetic Variants Regulating VEGF Levels to Type 2 Diabetes Risk and to Microvascular Complications?. PLoS ONE, 2013, 8, e55921.	2.5	35
72	Cdkn2a deficiency promotes adipose tissue browning. Molecular Metabolism, 2018, 8, 65-76.	6.5	35

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73	Genetic Variant in HK1 Is Associated With a Proanemic State and A1C but Not Other Glycemic Control-Related Traits. Diabetes, 2009, 58, 2687-2697.	0.6	34
74	Maps of open chromatin highlight cell typeâ€“restricted patterns of regulatory sequence variation at hematological trait loci. Genome Research, 2013, 23, 1130-1141.	5.5	34
75	A Genome-Wide Association Study Identifies rs2000999 as a Strong Genetic Determinant of Circulating Haptoglobin Levels. PLoS ONE, 2012, 7, e32327.	2.5	34
76	Multiple functional polymorphisms in the G6PC2 gene contribute to the association with higher fasting plasma glucose levels. Diabetologia, 2013, 56, 1306-1316.	6.3	33
77	Reassessment of the putative role of BLK-p.A71T loss-of-function mutation in MODY and type 2 diabetes. Diabetologia, 2013, 56, 492-496.	6.3	32
78	Genetic and Functional Assessment of the Role of the rs13431652-A and rs573225-A Alleles in the G6PC2 Promoter That Are Strongly Associated With Elevated Fasting Glucose Levels. Diabetes, 2010, 59, 2662-2671.	0.6	31
79	Contribution of the low-frequency, loss-of-function p.R270H mutation inFFAR4(GPR120) to increased fasting plasma glucose levels. Journal of Medical Genetics, 2015, 52, 595-598.	3.2	29
80	A common variant highly associated with plasma VEGFA levels also contributes to the variation of both LDL-C and HDL-C. Journal of Lipid Research, 2013, 54, 535-541.	4.2	28
81	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. Molecular Metabolism, 2019, 24, 98-107.	6.5	26
82	Impaired histone deacetylases 5 and 6 expression mimics the effects of obesity and hypoxia on adipocyte function. Molecular Metabolism, 2016, 5, 1200-1207.	6.5	25
83	Breakthroughs in monogenic diabetes genetics: from pediatric forms to young adulthood diabetes. Pediatric Endocrinology Reviews, 2009, 6, 405-17.	1.2	25
84	Associations of vascular endothelial growth factor (VEGF) with adhesion and inflammation molecules in a healthy population. Cytokine, 2013, 61, 602-607.	3.2	24
85	Identification of two novel loss-of-function SIM1 mutations in two overweight children with developmental delay. Obesity, 2014, 22, 2621-2624.	3.0	22
86	KAT2B Is Required for Pancreatic Beta Cell Adaptation to Metabolic Stress by Controlling the Unfolded Protein Response. Cell Reports, 2016, 15, 1051-1061.	6.4	22
87	The case for too little melatonin signalling in increased diabetes risk. Diabetologia, 2017, 60, 823-825.	6.3	22
88	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
89	Human Mutation within Per-Arnt-Sim (PAS) Domain-containing Protein Kinase (PASK) Causes Basal Insulin Hypersecretion*. Journal of Biological Chemistry, 2011, 286, 44005-44014.	3.4	21
90	Disentangling the Role of Melatonin and its Receptor MTNR1B in Type 2 Diabetes: Still a Long Way to Go?. Current Diabetes Reports, 2017, 17, 122.	4.2	21

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91	MYEOV is a prognostic factor in multiple myeloma. Experimental Hematology, 2010, 38, 1189-1198.e3.	0.4	20
92	High Prevalence of Rare Monogenic Forms of Obesity in Obese Guadeloupean Afro-Caribbean Children. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 539-545.	3.6	20
93	Impact of statistical models on the prediction of type 2 diabetes using non-targeted metabolomics profiling. Molecular Metabolism, 2016, 5, 918-925.	6.5	18
94	The Difficult Journey from Genome-wide Association Studies to Pathophysiology: The Melatonin Receptor 1B (MT2) Paradigm. Cell Metabolism, 2016, 24, 345-347.	16.2	17
95	Generation of an induced pluripotent stem cell (iPSC) line from a patient with maturity-onset diabetes of the young type 3 (MODY3) carrying a hepatocyte nuclear factor 1-alpha (HNF1A) mutation. Stem Cell Research, 2018, 29, 56-59.	0.7	17
96	A novel <scp>NEUROG3</scp> mutation in neonatal diabetes associated with a neuroâ€intestinal syndrome. Pediatric Diabetes, 2018, 19, 381-387.	2.9	17
97	What Is the Best NGS Enrichment Method for the Molecular Diagnosis of Monogenic Diabetes and Obesity?. PLoS ONE, 2015, 10, e0143373.	2.5	16
98	Genetic Causes of Severe Childhood Obesity: A Remarkably High Prevalence in an Inbred Population of Pakistan. Diabetes, 2020, 69, 1424-1438.	0.6	16
99	Glucose Regulates m6A Methylation of RNA in Pancreatic Islets. Cells, 2022, 11, 291.	4.1	16
100	CoDE-seq, an augmented whole-exome sequencing, enables the accurate detection of CNVs and mutations in Mendelian obesity and intellectual disability. Molecular Metabolism, 2018, 13, 1-9.	6.5	13
101	How Recent Advances in Genomics Improve Precision Diagnosis and Personalized Care of Maturity-Onset Diabetes of the Young. Current Diabetes Reports, 2019, 19, 79.	4.2	13
102	NACHO: an R package for quality control of NanoString nCounter data. Bioinformatics, 2020, 36, 970-971.	4.1	13
103	Associations Between Type 2 Diabetes-Related Genetic Scores and Metabolic Traits, in Obese and Normal-Weight Youths. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4244-4250.	3.6	11
104	Generation of an induced pluripotent stem cell (iPSC) line from a patient with maturity-onset diabetes of the young type 13 (MODY13) with a the potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11) mutation. Stem Cell Research, 2017, 23, 178-181.	0.7	11
105	The Map3k12 (Dlk)/JNK3 signaling pathway is required for pancreatic beta-cell proliferation during postnatal development. Cellular and Molecular Life Sciences, 2021, 78, 287-298.	5.4	11
106	Achievements, prospects and challenges in precision care for monogenic insulin-deficient and insulin-resistant diabetes. Diabetologia, 2022, 65, 1782-1795.	6.3	11
107	A girl with incomplete Praderâ€“Willi syndrome and negative MSâ€PCR, found to have mosaic maternal UPDâ€15 at SNP array. American Journal of Medical Genetics, Part A, 2015, 167, 2720-2726.	1.2	10
108	Combined RNAseq and ChIPseq Analyses of the BvgA Virulence Regulator of Bordetella pertussis. MSystems, 2020, 5, .	3.8	10

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109	Interaction between GPR120 p.R270H loss-of-function variant and dietary fat intake on incident type 2 diabetes risk in the D.E.S.I.R. study. Nutrition, Metabolism and Cardiovascular Diseases, 2016, 26, 931-936.	2.6	9
110	Circadian, Sleep and Caloric Intake Phenotyping in Type 2 Diabetes Patients With Rare Melatonin Receptor 2 Mutations and Controls: A Pilot Study. Frontiers in Physiology, 2020, 11, 564140.	2.8	9
111	Clustering for a better prediction of type 2 diabetes mellitus. Nature Reviews Endocrinology, 2021, 17, 193-194.	9.6	9
112	Copy Number Variations in Candidate Genes and Intergenic Regions Affect Body Mass Index and Abdominal Obesity in Mexican Children. BioMed Research International, 2017, 2017, 1-10.	1.9	8
113	The Relationship Between Vascular Endothelial Growth Factor Cis- and Trans-Acting Genetic Variants and Metabolic Syndrome. American Journal of the Medical Sciences, 2018, 355, 559-565.	1.1	8
114	The Case | Hypokalemia and severe renal loss of sodium. Kidney International, 2020, 97, 1305-1306.	5.2	8
115	Neonatal diabetes mellitus because of pancreatic agenesis with dysmorphic features and recurrent bacterial infections. Pediatric Diabetes, 2008, 9, 240-244.	2.9	7
116	Studies of a genetic variant in HK1 in relation to quantitative metabolic traits and to the prevalence of type 2 diabetes. BMC Medical Genetics, 2011, 12, 99.	2.1	7
117	Transcriptomic Analysis of Breast Cancer Stem Cells and Development of a pALDH1A1:mNeptune Reporter System for Live Tracking. Proteomics, 2019, 19, e1800454.	2.2	7
118	A Novel Rare Missense Variation of the NOD2 Gene: Evidencesof Implication in Crohnâ€™s Disease. International Journal of Molecular Sciences, 2019, 20, 835.	4.1	7
119	Monogenic diabetes characteristics in a transnational multicenter study from Mediterranean countries. Diabetes Research and Clinical Practice, 2021, 171, 108553.	2.8	7
120	Rare Variant Analysis of Obesity-Associated Genes in Young Adults With Severe Obesity From a Consanguineous Population of Pakistan. Diabetes, 2022, 71, 694-705.	0.6	7
121	Mutations in G6PC2 do not contribute to monogenic forms of early infancy diabetes and beta cell dysfunction. Diabetologia, 2009, 52, 982-985.	6.3	5
122	Physiopathologie du diabÃ¨te. Revue Francophone Des Laboratoires, 2018, 2018, 26-32.	0.0	4
123	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2021, 4, 1614-1627.	4.9	4
124	Obesity status modifies the association between rs7556897T>C in the intergenic region SLC19A3-CCL20 and blood pressure in French children. Clinical Chemistry and Laboratory Medicine, 2020, 58, 1819-1827.	2.3	3
125	Does TypeÂ2 diabetes increase the risk of developing cancer?. Diabetes Management, 2013, 3, 439-441.	0.5	2
126	From Association to Function: MTNR1B. , 2016, , 403-421.		2

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127	Structural Elements Directing G Proteins and Î²-Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2022, 5, 89-101.	4.9	2
128	Epigenetic and Transcriptomic Programming of HSC Quiescence Signaling in Large for Gestational Age Neonates. International Journal of Molecular Sciences, 2022, 23, 7323.	4.1	2
129	Comment on Beltrand et al. Sulfonylurea Therapy Benefits Neurological and Psychomotor Functions in Patients With Neonatal Diabetes Owing to Potassium Channel Mutations. Diabetes Care 2015;38:2033â€“2041. Diabetes Care, 2016, 39, e153-e154.	8.6	1
130	Historical Overview of Gene Discovery Methodologies in Type 2 Diabetes. , 2016, , 3-12.		1
131	GÃ©nÃ©tique du diabÃ¨te de typeÂ2 et de lâ€™obÃ©sitÃ©Â: oÃ¹ en sommes-nousÂ? Que pouvons-nous en attendreÂ?. Medecine Des Maladies Metaboliques, 2011, 5, 477-488.	0.1	0
132	O53 Lâ€™altÃ©ration du rÃ©cepteur des acides gras insaturÃ©s de type omega-3 GPR120 entraÃ®ne une obÃ©sitÃ© chez lâ€™Homme et la Souris. Diabetes and Metabolism, 2012, 38, A13.	2.9	0
133	Women in Metabolism: The Next Generation. Cell Metabolism, 2017, 26, 449-453.	16.2	0
134	General regression model: A â€œmodelâ€•freeâ€•association test for quantitative traits allowing to test for the underlying genetic model. Annals of Human Genetics, 2020, 84, 280-290.	0.8	0
135	GÃ©nÃ©tique. , 2021, , 123-127.		0
136	29-OR: High Prevalence of Pathogenic Mutations in Genes Causing Monogenic Diabetes among Patients with Common Type 2 Diabetes. Diabetes, 2019, 68, .	0.6	0
137	Design of a prospective, longitudinal cohort of people living with type 1 diabetes exploring factors associated with the residual cardiovascular risk and other diabetes-related complications: the SFDT1 study. Diabetes and Metabolism, 2021, 48, 101306.	2.9	0
138	Compound genetic etiology in a patient with a syndrome including diabetes, intellectual deficiency and distichiasis. Orphanet Journal of Rare Diseases, 2022, 17, 86.	2.7	0
139	Epigenetic changes associated with hyperglycaemia exposure in the longitudinal D.E.S.I.R. cohort. Diabetes and Metabolism, 2022, 48, 101347.	2.9	0