Philippe Froguel

List of Publications by Year
in descending order

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696	119,621	124	176
papers	citations	162 h-index	320 g-index

751	751	751	82788
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gain of Function of Malate Dehydrogenase 2 and Familial Hyperglycemia. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 668-684.	3.6	4
2	Glucose Regulates m6A Methylation of RNA in Pancreatic Islets. Cells, 2022, 11, 291.	4.1	16
3	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
4	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
5	Maternal Glycemic Dysregulation During Pregnancy and Neonatal Blood DNA Methylation: Meta-analyses of Epigenome-Wide Association Studies. Diabetes Care, 2022, 45, 614-623.	8.6	19
6	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
7	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
8	Epigenetic changes associated with hyperglycaemia exposure in the longitudinal D.E.S.I.R. cohort. Diabetes and Metabolism, 2022, 48, 101347.	2.9	0
9	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
10	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
11	Monogenic diabetes characteristics in a transnational multicenter study from Mediterranean countries. Diabetes Research and Clinical Practice, 2021, 171, 108553.	2.8	7
12	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
13	Clustering for a better prediction of type 2 diabetes mellitus. Nature Reviews Endocrinology, 2021, 17, 193-194.	9.6	9
14	Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a regulator of insulin secretion. Cell Reports, 2021, 34, 108703.	6.4	4
15	Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes. Scientific Reports, 2021, 11, 6197.	3.3	18
16	SHP2 drives inflammation-triggered insulin resistance by reshaping tissue macrophage populations. Science Translational Medicine, 2021, 13, .	12.4	26
17	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
18	Metaâ€analysis of genomeâ€wide DNA methylation and integrative omics of age in human skeletal muscle. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 1064-1078.	7.3	37

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19	Epigenome-Wide Association Study Reveals Methylation Loci Associated With Offspring Gestational Diabetes Mellitus Exposure and Maternal Methylome. Diabetes Care, 2021, 44, 1992-1999.	8.6	17
20	Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. IScience, 2021, 24, 102893.	4.1	5
21	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
22	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	8.6	16
23	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
24	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
25	Genetic Discrimination Between LADA and Childhood-Onset Type 1 Diabetes Within the MHC. Diabetes Care, 2020, 43, 418-425.	8.6	23
26	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. Nature Metabolism, 2020, 2, 1126-1134.	11.9	43
27	Emerging Roles for the INK4a/ARF (CDKN2A) Locus in Adipose Tissue: Implications for Obesity and Type 2 Diabetes. Biomolecules, 2020, 10, 1350.	4.0	16
28	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	3.5	95
29	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
30	Persistent or Transient Human Î² Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. Cell Reports, 2020, 33, 108466.	6.4	65
31	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
32	Genetic Causes of Severe Childhood Obesity: A Remarkably High Prevalence in an Inbred Population of Pakistan. Diabetes, 2020, 69, 1424-1438.	0.6	16
33	The Case | Hypokalemia and severe renal loss of sodium. Kidney International, 2020, 97, 1305-1306.	5.2	8
34	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. European Journal of Epidemiology, 2020, 35, 685-697.	5.7	9
35	Histone deacetylase 9 promoter hypomethylation associated with adipocyte dysfunction is a statin-related metabolic effect. Clinical Epigenetics, 2020, 12, 68.	4.1	10
36	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

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37	Fostering improved human islet research: a European perspective. Diabetologia, 2019, 62, 1514-1516.	6.3	13
38	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
39	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
40	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
41	Loss-of-function mutations in MRAP2 are pathogenic in hyperphagic obesity with hyperglycemia and hypertension. Nature Medicine, 2019, 25, 1733-1738.	30.7	54
42	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
43	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
44	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
45	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
46	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
47	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
48	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. Molecular Metabolism, 2019, 24, 98-107.	6.5	26
49	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
50	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
51	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
52	Contribution of rare coding mutations in CD36 to type 2 diabetes and cardio-metabolic complications. Scientific Reports, 2019, 9, 17123.	3.3	8
53	Effect of Sex and Underlying Disease on the Genetic Association of QT Interval and Sudden Cardiac Death. Journal of the American Heart Association, 2019, 8, e013751.	3.7	6
54	Genetics of Obesity in Consanguineous Populations: Toward Precision Medicine and the Discovery of Novel Obesity Genes. Obesity, 2018, 26, 474-484.	3.0	35

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55	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
56	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
57	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
58	Loss-of-function mutations in ADCY3 cause monogenic severe obesity. Nature Genetics, 2018, 50, 175-179.	21.4	122
59	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. Diabetes, 2018, 67, 1310-1321.	0.6	64
60	Physiopathologie du diabÃ¨te. Revue Francophone Des Laboratoires, 2018, 2018, 26-32.	0.0	4
61	Epigenome-wide association study of adiposity and future risk of obesity-related diseases. International Journal of Obesity, 2018, 42, 2022-2035.	3.4	43
62	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
63	The unique clinical spectrum of maturity onset diabetes of the young type 3. Diabetes Research and Clinical Practice, 2018, 135, 18-22.	2.8	7
64	A novel <scp>NEUROG3</scp> mutation in neonatal diabetes associated with a neuroâ€intestinal syndrome. Pediatric Diabetes, 2018, 19, 381-387.	2.9	17
65	Systems biology of the IMIDIA biobank from organ donors and pancreatectomised patients defines a novel transcriptomic signature of islets from individuals with type 2 diabetes. Diabetologia, 2018, 61, 641-657.	6.3	131
66	Cdkn2a deficiency promotes adipose tissue browning. Molecular Metabolism, 2018, 8, 65-76.	6.5	35
67	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
68	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
69	First Genome-Wide Association Study of Latent Autoimmune Diabetes in Adults Reveals Novel Insights Linking Immune and Metabolic Diabetes. Diabetes Care, 2018, 41, 2396-2403.	8.6	99
70	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
71	Distinct virulence ranges for infection of mice by Bordetella pertussis revealed by engineering of the sensor-kinase BvgS. PLoS ONE, 2018, 13, e0204861.	2.5	4
72	ALDH2 Polymorphism rs671, but Not ADH1B Polymorphism rs1229984, Increases Risk for Hypoâ€HDLâ€Cholesterolemia in a/a Carriers Compared to the G/G Carriers. Lipids, 2018, 53, 797-807.	1.7	7

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73	MFN2-associated lipomatosis: Clinical spectrum and impact on adipose tissue. Journal of Clinical Lipidology, 2018, 12, 1420-1435.	1.5	47
74	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
75	Jointly Modelling Single Nucleotide Polymorphisms With Longitudinal and Time-to-Event Trait: An Application to Type 2 Diabetes and Fasting Plasma Glucose. Frontiers in Genetics, 2018, 9, 210.	2.3	1
76	Type 2 diabetesâ€“associated variants of the MT ₂ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, .	3.6	45
77	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
78	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	7.9	63
79	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	6.2	60
80	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
81	Shared genetic predisposition in rheumatoid arthritis-interstitial lung disease and familial pulmonary fibrosis. European Respiratory Journal, 2017, 49, 1602314.	6.7	154
82	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
83	Maturity-Onset Diabetes of the Young: From Genetics to Translational Biology and Personalized Medicine. Frontiers in Diabetes, 2017, , 26-48.	0.4	1
84	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
85	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. Diabetologia, 2017, 60, 1740-1750.	6.3	96
86	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
87	The case for too little melatonin signalling in increased diabetes risk. Diabetologia, 2017, 60, 823-825.	6.3	22
88	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
89	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
90	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

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91	Variants gÃ©nÃ©tiques associÃ©s Ã la trajectoire de la glycÃ©mie Ã jeun et Ã lâ€™incidence du diabÃ¨te de type 2 : Une approche par modÃ¨le joint. Diabetes and Metabolism, 2017, 43, A76.	2.9	0
92	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
93	Transmission of Type 2 diabetes to sons and daughters: the D.E.S.I.R. cohort. Diabetic Medicine, 2017, 34, 1615-1622.	2.3	5
94	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. BMC Medicine, 2017, 15, 37.	5.5	47
95	Hepatic DPP4 DNA Methylation Associates With Fatty Liver. Diabetes, 2017, 66, 25-35.	0.6	59
96	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
97	Cofactors As Metabolic Sensors Driving Cell Adaptation in Physiology and Disease. Frontiers in Endocrinology, 2017, 8, 304.	3.5	19
98	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
99	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
100	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
101	Characterization of a Bvg-regulated fatty acid methyl-transferase in Bordetella pertussis. PLoS ONE, 2017, 12, e0176396.	2.5	4
102	Low-dose exposure to bisphenols A, F and S of human primary adipocyte impacts coding and non-coding RNA profiles. PLoS ONE, 2017, 12, e0179583.	2.5	64
103	Post-Bariatric Surgery Changes in Quinolinic and Xanthurenic Acid Concentrations Are Associated with Glucose Homeostasis. PLoS ONE, 2016, 11, e0158051.	2.5	21
104	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
105	DNA Damage and the Activation of the p53 Pathway Mediate Alterations in Metabolic and Secretory Functions of Adipocytes. Diabetes, 2016, 65, 3062-3074.	0.6	92
106	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
107	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
108	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

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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	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
111	Detection of human adaptation during the past 2000 years. Science, 2016, 354, 760-764.	12.6	336
112	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
113	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
114	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
115	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
116	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
117	Genomic insights into the origin of farming in the ancient Near East. Nature, 2016, 536, 419-424.	27.8	733
118	Monogenic diabetes: Implementation of translational genomic research towards precision medicine. Journal of Diabetes, 2016, 8, 782-795.	1.8	36
119	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
120	Historical Overview of Gene Discovery Methodologies in Type 2 Diabetes. , 2016, , 3-12.		1
121	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
122	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
123	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
124	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
125	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
126	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

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127	The kynurenine pathway is activated in human obesity and shifted toward kynurenine monooxygenase activation. Obesity, 2015, 23, 2066-2074.	3.0	196
128	What Is the Best NGS Enrichment Method for the Molecular Diagnosis of Monogenic Diabetes and Obesity?. PLoS ONE, 2015, 10, e0143373.	2.5	16
129	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
130	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
131	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
132	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
133	Rare and Common Genetic Events in Type 2 Diabetes: What Should Biologists Know?. Cell Metabolism, 2015, 21, 357-368.	16.2	128
134	Fine-scale human genetic structure in Western France. European Journal of Human Genetics, 2015, 23, 831-836.	2.8	31
135	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
136	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
137	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 526-534.	11.4	396
138	The loss-of-function PCSK9 p.R46L genetic variant does not alter glucose homeostasis. Diabetologia, 2015, 58, 2051-2055.	6.3	49
139	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
140	Reflections on the Field of Metabolism. Cell Metabolism, 2015, 21, 505-506.	16.2	0
141	Genetic Determinants of Leucocyte Telomere Length in Children: a Neglected and Challenging Field. Paediatric and Perinatal Epidemiology, 2015, 29, 146-150.	1.7	10
142	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
143	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nature Genetics, 2015, 47, 1206-1211.	21.4	103
144	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365

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145	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
146	Les gÃ¨nes de lâ€™obÃ©sitÃ© et leur contribution Ã la balance Ã©nergÃ©tique. Bulletin De L'Academie Nationale De Medecine, 2015, 199, 1269-1279.	0.0	4
147	Association of gene variants with susceptibility to type 2 diabetes among Omanis. World Journal of Diabetes, 2015, 6, 358.	3.5	39
148	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
149	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	8.4	180
150	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
151	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
152	Role of the Unfolded Protein Response inÎ²Cell Compensation and Failure during Diabetes. Journal of Diabetes Research, 2014, 2014, 1-11.	2.3	31
153	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
154	Characterization of human variants in obesity-related SIM1 protein identifies a hot-spot for dimerization with the partner protein ARNT2. Biochemical Journal, 2014, 461, 403-412.	3.7	10
155	RFX6 Regulates Insulin Secretion by Modulating Ca2+ Homeostasis in Human Î² Cells. Cell Reports, 2014, 9, 2206-2218.	6.4	73
156	Coffee and tea consumption, genotype-basedCYP1A2andNAT2activity and colorectal cancer risk-Results from the EPIC cohort study. International Journal of Cancer, 2014, 135, 401-412.	5.1	35
157	Copy Number Variants and Their Contribution to the Risk of Obesity. , 2014, , 55-70.		1
158	Role of Ink4a/Arf Locus in Beta Cell Mass Expansion under Physiological and Pathological Conditions. Journal of Diabetes Research, 2014, 2014, 1-7.	2.3	13
159	Weight loss independent association of TCF7 L2 gene polymorphism with fasting blood glucose after Roux-en-Y gastric bypass in type 2 diabetic patients. Surgery for Obesity and Related Diseases, 2014, 10, 679-683.	1.2	5
160	Changes in levels of peripheral hormones controlling appetite are inconsistent with hyperphagia in leptin-deficient subjects. Endocrine, 2014, 45, 401-408.	2.3	19
161	Genome-wide association study identifies three novel loci for type 2 diabetes. Human Molecular Genetics, 2014, 23, 239-246.	2.9	158
162	Alternative human liver transcripts of TCF7L2 bind to the gluconeogenesis regulator HNF4Î± at the protein level. Diabetologia, 2014, 57, 785-796.	6.3	33

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163	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
164	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	21.4	214
165	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
166	Novel LEPR mutations in obese Pakistani children identified by PCRâ€based enrichment and next generation sequencing. Obesity, 2014, 22, 1112-1117.	3.0	51
167	Multi-ethnic fine-mapping of 14 central adiposity loci. Human Molecular Genetics, 2014, 23, 4738-4744.	2.9	41
168	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
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