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	The fat-derived hormone adiponectin reverses insulin resistance associated with both lipoatrophy and obesity. Nature Medicine, 2001, 7, 941-946.	30.7	4,370
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Adiponectin stimulates glucose utilization and fatty-acid oxidation by activating AMP-activated protein kinase. Nature Medicine, 2002, 8, 1288-1295.	30.7	3,692
4	Cloning of adiponectin receptors that mediate antidiabetic metabolic effects. Nature, 2003, 423, 762-769.	27.8	2,804
5	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	27.8	2,651
6	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
7	A mutation in the human leptin receptor gene causes obesity and pituitary dysfunction. Nature, 1998, 392, 398-401.	27.8	2,112
8	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
9	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
10	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
11	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
12	Variation in FTO contributes to childhood obesity and severe adult obesity. Nature Genetics, 2007, 39, 724-726.	21.4	1,390
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	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
16	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
17	Targeted disruption of AdipoR1 and AdipoR2 causes abrogation of adiponectin binding and metabolic actions. Nature Medicine, 2007, 13, 332-339.	30.7	1,177
18	Disruption of Adiponectin Causes Insulin Resistance and Neointimal Formation. Journal of Biological Chemistry, 2002, 277, 25863-25866.	3.4	1,149

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19	Genetic associations with human longevity at the APOE and ACE loci. Nature Genetics, 1994, 6, 29-32.	21.4	1,052
20	A frameshift mutation in human MC4R is associated with a dominant form of obesity. Nature Genetics, 1998, 20, 113-114.	21.4	975
21	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
22	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
23	Impaired Multimerization of Human Adiponectin Mutants Associated with Diabetes. Journal of Biological Chemistry, 2003, 278, 40352-40363.	3.4	871
24	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
25	The Lin28/let-7 Axis Regulates Glucose Metabolism. Cell, 2011, 147, 81-94.	28.9	812
26	Adipose Tissue in Obesity-Related Inflammation and Insulin Resistance: Cells, Cytokines, and Chemokines. ISRN Inflammation, 2013, 2013, 1-12.	4.9	807
27	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
28	Globular Adiponectin Protected ob/ob Mice from Diabetes and ApoE-deficient Mice from Atherosclerosis. Journal of Biological Chemistry, 2003, 278, 2461-2468.	3.4	783
29	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
30	Melanocortin-4 receptor mutations are a frequent and heterogeneous cause of morbid obesity. Journal of Clinical Investigation, 2000, 106, 253-262.	8.2	760
31	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	8.4	753
32	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
33	Genomic insights into the origin of farming in the ancient Near East. Nature, 2016, 536, 419-424.	27.8	733
34	Familial Hyperglycemia Due to Mutations in Glucokinase -- Definition of a Subtype of Diabetes Mellitus. New England Journal of Medicine, 1993, 328, 697-702.	27.0	721
35	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
36	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675

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37	Genetic Variation in the Gene Encoding Adiponectin Is Associated With an Increased Risk of Type 2 Diabetes in the Japanese Population. Diabetes, 2002, 51, 536-540.	0.6	668
38	A genome-wide association study in Europeans and South Asians identifies five new loci for coronary artery disease. Nature Genetics, 2011, 43, 339-344.	21.4	643
39	Close linkage of glucokinase locus on chromosome 7p to early-onset non-insulin-dependent diabetes mellitus. Nature, 1992, 356, 162-164.	27.8	637
40	Nonsense mutation in the glucokinase gene causes early-onset non-insulin-dependent diabetes mellitus. Nature, 1992, 356, 721-722.	27.8	636
41	Genomewide Search for Type 2 Diabetesâ€“Susceptibility Genes in French Whites: Evidence for a Novel Susceptibility Locus for Early-Onset Diabetes on Chromosome 3q27-qter and Independent Replication of a Type 2â€“Diabetes Locus on Chromosome 1q21â€“q24. American Journal of Human Genetics, 2000, 67, 1470-1480.	6.2	630
42	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
43	Genetic Variation in the Î²3-Adrenergic Receptor and an Increased Capacity to Gain Weight in Patients with Morbid Obesity. New England Journal of Medicine, 1995, 333, 352-354.	27.0	614
44	Activating Mutations in theABCC8Gene in Neonatal Diabetes Mellitus. New England Journal of Medicine, 2006, 355, 456-466.	27.0	591
45	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
46	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. Nature Genetics, 2009, 41, 157-159.	21.4	585
47	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
48	Dysfunction of lipid sensor GPR120 leads to obesity in both mouse and human. Nature, 2012, 483, 350-354.	27.8	572
49	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
50	The genetics of human obesity. Nature Reviews Genetics, 2005, 6, 221-234.	16.3	546
51	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	21.4	545
52	Genetic Loci Associated With C-Reactive Protein Levels and Risk of Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2009, 302, 37.	7.4	544
53	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
54	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521

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55	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
56	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
57	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	21.4	481
58	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. Nature, 2010, 463, 671-675.	27.8	476
59	Insulin/Foxo1 Pathway Regulates Expression Levels of Adiponectin Receptors and Adiponectin Sensitivity. Journal of Biological Chemistry, 2004, 279, 30817-30822.	3.4	470
60	Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. Nature Genetics, 2013, 45, 1044-1049.	21.4	467
61	Common genetic variation near MC4R is associated with waist circumference and insulin resistance. Nature Genetics, 2008, 40, 716-718.	21.4	456
62	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. PLoS Medicine, 2011, 8, e1001116.	8.4	446
63	Single-nucleotide polymorphism haplotypes in the both proximal promoter and exon 3 of the APM1 gene modulate adipocyte-secreted adiponectin hormone levels and contribute to the genetic risk for type 2 diabetes in French Caucasians. Human Molecular Genetics, 2002, 11, 2607-2614.	2.9	433
64	Paraoxonase polymorphism Met-Leu54 is associated with modified serum concentrations of the enzyme. A possible link between the paraoxonase gene and increased risk of cardiovascular disease in diabetes.. Journal of Clinical Investigation, 1997, 99, 62-66.	8.2	433
65	FCGR3B copy number variation is associated with susceptibility to systemic, but not organ-specific, autoimmunity. Nature Genetics, 2007, 39, 721-723.	21.4	421
66	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
67	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. Nature Genetics, 2009, 41, 1110-1115.	21.4	418
68	Genetic mapping of a susceptibility locus for insulin-dependent diabetes mellitus on chromosome llq. Nature, 1994, 371, 161-164.	27.8	412
69	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
70	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
71	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
72	Quality control and conduct of genome-wide association meta-analyses. Nature Protocols, 2014, 9, 1192-1212.	12.0	398

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73	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
74	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
75	Insulin-IGF2 region on chromosome 11p encodes a gene implicated in HLA-DR4-dependent diabetes susceptibility. Nature, 1991, 354, 155-159.	27.8	388
76	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
77	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
78	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
79	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
80	A genome-wide scan for human obesity genes reveals a major susceptibility locus on chromosome 10. Nature Genetics, 1998, 20, 304-308.	21.4	356
81	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
82	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	21.4	352
83	Insulin Storage and Glucose Homeostasis in Mice Null for the Granule Zinc Transporter ZnT8 and Studies of the Type 2 Diabetesâ€“Associated Variants. Diabetes, 2009, 58, 2070-2083.	0.6	347
84	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
85	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
86	Loss-of-Function Mutation in the Dioxygenase-Encoding FTO Gene Causes Severe Growth Retardation and Multiple Malformations. American Journal of Human Genetics, 2009, 85, 106-111.	6.2	340
87	The genetic contribution to non-syndromic human obesity. Nature Reviews Genetics, 2009, 10, 431-442.	16.3	338
88	Gln-Arg192 polymorphism of paraoxonase and coronary heart disease in type 2 diabetes. Lancet, The, 1995, 346, 869-872.	13.7	337
89	Detection of human adaptation during the past 2000 years. Science, 2016, 354, 760-764.	12.6	336
90	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335

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91	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
92	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
93	TCF7L2 is reproducibly associated with type 2 diabetes in various ethnic groups: a global meta-analysis. Journal of Molecular Medicine, 2007, 85, 777-782.	3.9	321
94	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
95	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. Nature Genetics, 2012, 44, 297-301.	21.4	319
96	Transcription Factor TCF7L2 Genetic Study in the French Population: Expression in Human Â-Cells and Adipose Tissue and Strong Association With Type 2 Diabetes. Diabetes, 2006, 55, 2903-2908.	0.6	300
97	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
98	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
99	Chromosomal mapping of genetic loci associated with non-insulin dependent diabetes in the GK rat. Nature Genetics, 1996, 12, 38-43.	21.4	296
100	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
101	Variants of ENPP1 are associated with childhood and adult obesity and increase the risk of glucose intolerance and type 2 diabetes. Nature Genetics, 2005, 37, 863-867.	21.4	290
102	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. Nature Genetics, 2011, 43, 561-564.	21.4	289
103	Two New Loci for Body-Weight Regulation Identified in a Joint Analysis of Genome-Wide Association Studies for Early-Onset Extreme Obesity in French and German Study Groups. PLoS Genetics, 2010, 6, e1000916.	3.5	287
104	Defective insulin secretion in hepatocyte nuclear factor 1alpha-deficient mice.. Journal of Clinical Investigation, 1998, 101, 2215-2222.	8.2	286
105	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
106	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
107	KLHL3 mutations cause familial hyperkalemic hypertension by impairing ion transport in the distal nephron. Nature Genetics, 2012, 44, 456-460.	21.4	281
108	Common nonsynonymous variants in PCSK1 confer risk of obesity. Nature Genetics, 2008, 40, 943-945.	21.4	275

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109	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
110	Glucokinase as pancreatic beta cell glucose sensor and diabetes gene.. Journal of Clinical Investigation, 1993, 92, 2092-2098.	8.2	258
111	Defective mutations in the insulin promoter factor-1 (IPF-1) gene in late-onset type 2 diabetes mellitus. Journal of Clinical Investigation, 1999, 104, R41-R48.	8.2	256
112	Missense mutations in the pancreatic islet beta cell inwardly rectifying K + channel gene (KIR6.2/BIR): a meta-analysis suggests a role in the polygenic basis of Type II diabetes mellitus in Caucasians. Diabetologia, 1998, 41, 1511-1515.	6.3	254
113	Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment of DNA spanning the insulin gene and associated VNTR. Nature Genetics, 1993, 4, 305-310.	21.4	253
114	A deletion of the HBII-85 class of small nucleolar RNAs (snoRNAs) is associated with hyperphagia, obesity and hypogonadism. Human Molecular Genetics, 2009, 18, 3257-3265.	2.9	253
115	Identification of 14 new glucokinase mutations and description of the clinical profile of 42 MODY-2 families. Diabetologia, 1997, 40, 217-224.	6.3	252
116	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
117	A missense mutation disrupting a dibasic prohormone processing site in pro-opiomelanocortin (POMC) increases susceptibility to early-onset obesity through a novel molecular mechanism. Human Molecular Genetics, 2002, 11, 1997-2004.	2.9	249
118	Genetic Interaction of BBS1 Mutations with Alleles at Other BBS Loci Can Result in Non-Mendelian Bardet-Biedl Syndrome. American Journal of Human Genetics, 2003, 72, 1187-1199.	6.2	246
119	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. Nature Genetics, 2010, 42, 864-868.	21.4	245
120	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
121	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
122	The genetic abnormality in the beta cell determines the response to an oral glucose load. Diabetologia, 2002, 45, 427-435.	6.3	235
123	A genome-wide scan for coronary heart disease suggests in Indo-Mauritians a susceptibility locus on chromosome 16p13 and replicates linkage with the metabolic syndrome on 3q27. Human Molecular Genetics, 2001, 10, 2751-2765.	2.9	233
124	Role of transcription factor KLF11 and its diabetes-associated gene variants in pancreatic beta cell function. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4807-4812.	7.1	231
125	Genome-Wide Search for Type 2 Diabetes in Japanese Affected Sib-Pairs Confirms Susceptibility Genes on 3q, 15q, and 20q and Identifies Two New Candidate Loci on 7p and 11p. Diabetes, 2002, 51, 1247-1255.	0.6	229
126	Prevalence of Melanocortin-4 Receptor Deficiency in Europeans and Their Age-Dependent Penetrance in Multigenerational Pedigrees. Diabetes, 2008, 57, 2511-2518.	0.6	229

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127	Primary pancreatic beta-cell secretory defect caused by mutations in glucokinase gene in kindreds of maturity onset diabetes of the young. Lancet, The, 1992, 340, 444-448.	13.7	228
128	A Polymorphism Within the G6PC2 Gene Is Associated with Fasting Plasma Glucose Levels. Science, 2008, 320, 1085-1088.	12.6	227
129	Human glucokinase gene: isolation, characterization, and identification of two missense mutations linked to early-onset non-insulin-dependent (type 2) diabetes mellitus.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 7698-7702.	7.1	226
130	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	21.4	223
131	Genomewide Association Study of an AIDSâ€Nonprogression Cohort Emphasizes the Role Played byHLAGenes (ANRS Genomewide Association Study 02). Journal of Infectious Diseases, 2009, 199, 419-426.	4.0	220
132	Integration of clinical data with a genomeâ€scale metabolic model of the human adipocyte. Molecular Systems Biology, 2013, 9, 649.	7.2	217
133	Insertion/deletion polymorphism of the angiotensin-converting enzyme gene is strongly associated with coronary heart disease in non-insulin-dependent diabetes mellitus.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 3662-3665.	7.1	216
134	Predicting Diabetes: Clinical, Biological, and Genetic Approaches. Diabetes Care, 2008, 31, 2056-2061.	8.6	215
135	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	21.4	214
136	Glucokinase mutations associated with non-insulin-dependent (type 2) diabetes mellitus have decreased enzymatic activity: implications for structure/function relationships.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1932-1936.	7.1	211
137	Intracellular retention is a common characteristic of childhood obesity-associated MC4R mutations. Human Molecular Genetics, 2003, 12, 145-153.	2.9	209
138	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
139	A POMC variant implicates Î²-melanocyte-stimulating hormone in the control of human energy balance. Cell Metabolism, 2006, 3, 135-140.	16.2	207
140	A gene for maturity onset diabetes of the young (MODY) maps to chromosome 12q. Nature Genetics, 1995, 9, 418-423.	21.4	205
141	Blood Microbiota Dysbiosis Is Associated with the Onset of Cardiovascular Events in a Large General Population: The D.E.S.I.R. Study. PLoS ONE, 2013, 8, e54461.	2.5	201
142	Array CGH analysis of copy number variation identifies 1284 new genes variant in healthy white males: implications for association studies of complex diseases. Human Molecular Genetics, 2007, 16, 2783-2794.	2.9	200
143	Variations in the HHEX gene are associated with increased risk of type 2 diabetes in the Japanese population. Diabetologia, 2007, 50, 2461-2466.	6.3	199
144	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197

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145	The kynurenine pathway is activated in human obesity and shifted toward kynurenine monooxygenase activation. Obesity, 2015, 23, 2066-2074.	3.0	196
146	HNF1Î± controls renal glucose reabsorption in mouse and man. EMBO Reports, 2000, 1, 359-365.	4.5	192
147	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
148	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
149	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
150	Adiponectin Gene Polymorphisms and Adiponectin Levels Are Independently Associated With the Development of Hyperglycemia During a 3-Year Period: The Epidemiologic Data on the Insulin Resistance Syndrome Prospective Study. Diabetes, 2004, 53, 1150-1157.	0.6	185
151	Impaired hepatic glycogen synthesis in glucokinase-deficient (MODY-2) subjects.. Journal of Clinical Investigation, 1996, 98, 1755-1761.	8.2	183
152	The gene MAPK8IP1, encoding islet-brain-1, is a candidate for type 2 diabetes. Nature Genetics, 2000, 24, 291-295.	21.4	182
153	Mutational analysis of melanocortin-4 receptor, agouti-related protein, and Î±-melanocyte-stimulating hormone genes in severely obese children. Journal of Pediatrics, 2001, 139, 204-209.	1.8	182
154	Systems medicine and integrated care to combat chronic noncommunicable diseases. Genome Medicine, 2011, 3, 43.	8.2	181
155	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
156	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	8.4	180
157	A missense mutation in the glucagon receptor gene is associated with nonâ€“insulinâ€“dependent diabetes mellitus. Nature Genetics, 1995, 9, 299-304.	21.4	177
158	The Common P446L Polymorphism in GCKR Inversely Modulates Fasting Glucose and Triglyceride Levels and Reduces Type 2 Diabetes Risk in the DESIR Prospective General French Population. Diabetes, 2008, 57, 2253-2257.	0.6	177
159	Non-synonymous polymorphisms in melanocortin-4 receptor protect against obesity: the two facets of a Janus obesity gene. Human Molecular Genetics, 2007, 16, 1837-1844.	2.9	174
160	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
161	Genetic Susceptibility for Human Familial Essential Hypertension in a Region of Homology with Blood Pressure Linkage on Rat Chromosome 10. Human Molecular Genetics, 1997, 6, 2077-2085.	2.9	172
162	Type 2 Diabetes Whole-Genome Association Study in Four Populations: The DiaGen Consortium. American Journal of Human Genetics, 2007, 81, 338-345.	6.2	172

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163	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
164	Design and cohort description of the InterAct Project: an examination of the interaction of genetic and lifestyle factors on the incidence of type 2 diabetes in the EPIC Study. Diabetologia, 2011, 54, 2272-2282.	6.3	169
165	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
166	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	2.9	168
167	Genome-Wide Association Study Identifies a Novel Locus Contributing to Type 2 Diabetes Susceptibility in Sikhs of Punjabi Origin From India. Diabetes, 2013, 62, 1746-1755.	0.6	167
168	Dynamic hydroxymethylation of deoxyribonucleic acid marks differentiation-associated enhancers. Nucleic Acids Research, 2012, 40, 8255-8265.	14.5	166
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