InÃªs Barroso

List of Publications by Year
in descending order

108 papers	41,943 citations	15466 65 h-index	23472 111 g-index
140 all docs	140 docs citations	140 times ranked	41079 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
7	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
8	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
10	Dominant negative mutations in human PPARÎ³ associated with severe insulin resistance, diabetes mellitus and hypertension. Nature, 1999, 402, 880-883.	13.7	1,286
11	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
12	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
13	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
14	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
15	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.	9.4	762
16	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
17	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
18	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662

#	Article	IF	Citations
19	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
20	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
21	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
22	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
23	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	9.4	452
24	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	1.5	448
25	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
26	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	1.5	392
27	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
28	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
29	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
30	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
31	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.	3.9	341
32	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
33	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.3	335
34	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.	1.5	331
35	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. PLoS Medicine, 2016, 13, e1002179.	3.9	324
36	Association Between Low-Density Lipoprotein Cholesterolâ€“Lowering Genetic Variants and Risk of Type 2 Diabetes. JAMA - Journal of the American Medical Association, 2016, 316, 1383.	3.8	310

#	Article	IF	Citations
37	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.3	297
38	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
39	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
40	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. Nature Genetics, 2013, 45, 513-517.	9.4	278
41	Candidate Gene Association Study in Type 2 Diabetes Indicates a Role for Genes Involved in Î²-Cell Function as Well as Insulin Action. PLoS Biology, 2003, 1, e20.	2.6	262
42	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.3	237
43	Genomics of disease risk in globally diverse populations. Nature Reviews Genetics, 2019, 20, 520-535.	7.7	217
44	Prospective functional classification of all possible missense variants in PPARG. Nature Genetics, 2016, 48, 1570-1575.	9.4	210
45	Genetics of Type 2 diabetes. Diabetic Medicine, 2005, 22, 517-535.	1.2	193
46	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	3.9	180
47	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.	2.9	169
48	Non-DNA binding, dominant-negative, human PPARÎ³ mutations cause lipodystrophic insulin resistance. Cell Metabolism, 2006, 4, 303-311.	7.2	164
49	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
50	Common Genetic Variants Highlight the Role of Insulin Resistance and Body Fat Distribution in Type 2 Diabetes, Independent of Obesity. Diabetes, 2014, 63, 4378-4387.	0.3	153
51	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
52	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
53	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
54	Mutations disrupting the Kennedy phosphatidylcholine pathway in humans with congenital lipodystrophy and fatty liver disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8901-8906.	3.3	125

#	Article	IF	Citations
55	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
56	A linear mixed-model approach to study multivariate geneâ€“environment interactions. Nature Genetics, 2019, 51, 180-186.	9.4	112
57	The Genetic Basis of Metabolic Disease. Cell, 2019, 177, 146-161.	13.5	104
58	Meta-analysis of the Gly482Ser variant in PPARGC1A in type 2 diabetes and related phenotypes. Diabetologia, 2006, 49, 501-505.	2.9	102
59	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
60	Genetic architecture of human thinness compared to severe obesity. PLoS Genetics, 2019, 15, e1007603.	1.5	98
61	Hypomorphism in human NSMCE2 linked to primordial dwarfism and insulin resistance. Journal of Clinical Investigation, 2014, 124, 4028-4038.	3.9	90
62	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
63	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	1.4	84
64	Human Semaphorin 3 Variants Link Melanocortin Circuit Development and Energy Balance. Cell, 2019, 176, 729-742.e18.	13.5	80
65	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
66	Common genetic variation in the melatonin receptor 1B gene (MTNR1B) is associated with decreased early-phase insulin response. Diabetologia, 2009, 52, 1537-1542.	2.9	70
67	Sugar-sweetened beverage consumption and genetic predisposition to obesity in 2 Swedish cohorts. American Journal of Clinical Nutrition, 2016, 104, 809-815.	2.2	61
68	Human biallelic MFN2 mutations induce mitochondrial dysfunction, upper body adipose hyperplasia, and suppression of leptin expression. ELife, 2017, 6, .	2.8	60
69	Genome-wide association study of type 2 diabetes in Africa. Diabetologia, 2019, 62, 1204-1211.	2.9	56
70	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
71	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.	0.3	47
72	Steroid receptor coactivator-1 modulates the function of Pomc neurons and energy homeostasis. Nature Communications, 2019, 10, 1718.	5.8	45

#	Article	IF	Citations
73	Obesity-Associated GNAS Mutations and the Melanocortin Pathway. New England Journal of Medicine, 2021, 385, 1581-1592.	13.9	44
74	Human BDNF/TrkB variants impair hippocampal synaptogenesis and associate with neurobehavioural abnormalities. Scientific Reports, 2020, 10, 9028.	1.6	40
75	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. Cell Metabolism, 2020, 31, 1107-1119.e12.	7.2	38
76	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.3	37
77	Associations Between Glycemic Traits and Colorectal Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2022, 114, 740-752.	3.0	35
78	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	5.8	33
79	Mendelian Randomization Analysis of Hemoglobin A1c as a Risk Factor for Coronary Artery Disease. Diabetes Care, 2019, 42, 1202-1208.	4.3	33
80	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
81	Adiponectin receptor genes: mutation screening in syndromes of insulin resistance and association studies for type 2 diabetes and metabolic traits in UK populations. Diabetologia, 2007, 50, 555-562.	2.9	29
82	Loss of FTO Antagonises Wnt Signaling and Leads to Developmental Defects Associated with Ciliopathies. PLoS ONE, 2014, 9, e87662.	1.1	25
83	Genetic Determinants of Long-Term Changes in Blood Lipid Concentrations: 10-Year Follow-Up of the GLACIER Study. PLoS Genetics, 2014, 10, e1004388.	1.5	25
84	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. Journal of Infectious Diseases, 2018, 218, 1700-1710.	1.9	25
85	The metabolic syndrome- associated small G protein ARL15 plays a role in adipocyte differentiation and adiponectin secretion. Scientific Reports, 2017, 7, 17593.	1.6	24
86	Distinct genetic architectures and environmental factors associate with host response to the Î³2-herpesvirus infections. Nature Communications, 2020, 11, 3849.	5.8	24
87	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. PLoS Genetics, 2018, 14, e1007591.	1.5	23
88	Polymorphisms in the gene encoding sterol regulatory element-binding factor-1c are associated with type 2 diabetes. Diabetologia, 2006, 49, 2642-2648.	2.9	22
89	Established BMI-associated genetic variants and their prospective associations with BMI and other cardiometabolic traits: the GLACIER Study. International Journal of Obesity, 2016, 40, 1346-1352.	1.6	22
90	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. Scientific Data, 2020, 7, 393.	2.4	19

#	Article	IF	Citations
91	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. International Journal of Epidemiology, 2016, 46, dyw245.	0.9	17
92	PARL Leu262Val is not associated with fasting insulin levels in UK populations. Diabetologia, 2006, 49, 2649-2652.	2.9	16
93	Crucial Role of the SH2B1 PH Domain for the Control of Energy Balance. Diabetes, 2019, 68, 2049-2062.	0.3	16
94	Gene-Lifestyle Interactions in Complex Diseases: Design and Description of the GLACIER and VIKING Studies. Current Nutrition Reports, 2014, 3, 400-411.	2.1	15
95	The flashfm approach for fine-mapping multiple quantitative traits. Nature Communications, 2021, 12, 6147.	5.8	14
96	Innate biology versus lifestyle behaviour in the aetiology of obesity and type 2 diabetes: the GLACIER Study. Diabetologia, 2016, 59, 462-471.	2.9	13
97	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1065-1077.	1.8	12
98	Whole-genome association study of antibody response to Epstein-Barr virus in an African population: a pilot. Global Health, Epidemiology and Genomics, 2017, 2, e18.	0.2	11
99	The importance of increasing population diversity in genetic studies of type 2 diabetes and related glycaemic traits. Diabetologia, 2021, 64, 2653-2664.	2.9	10
100	Genetic aetiology of glycaemic traits: approaches and insights. Human Molecular Genetics, 2017, 26, R172-R184.	1.4	9
101	ADCY3, neuronal primary cilia and obesity. Nature Genetics, 2018, 50, 166-167.	9.4	9
102	The influence of rare variants in circulating metabolic biomarkers. PLoS Genetics, 2020, 16, e1008605.	1.5	9
103	IRS2 variants and syndromes of severe insulin resistance. Diabetologia, 2009, 52, 1208-1211.	2.9	8
104	Predicting novel candidate human obesity genes and their site of action by systematic functional screening in Drosophila. PLoS Biology, 2021, 19, e3001255.	2.6	7
105	Lyplal1 is dispensable for normal fat deposition in mice. DMM Disease Models and Mechanisms, 2017, 10, 1481-1488.	1.2	6
106	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	1.6	5
107	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. Scientific Reports, 2022, 12, 1131.	1.6	2
108	An Expanded Genome-Wide Association Study of Fructosamine Levels Identifies RCN3 as a Replicating Locus and Implicates FCGRT as the Effector Transcript. Diabetes, 2022, 71, 359-364.	0.3	1