

Inê Barroso

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

112
papers

32,397
citations

59
h-index

140
g-index

140
ext. papers

38,336
ext. citations

18.9
avg, IF

5.23
L-index

#	Paper	IF	Citations
112	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
111	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
110	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
109	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
108	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
107	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
106	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010 , 42, 579-89	36.3	1449
105	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
104	Dominant negative mutations in human PPARgamma associated with severe insulin resistance, diabetes mellitus and hypertension. <i>Nature</i> , 1999 , 402, 880-3	50.4	1129
103	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
102	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
101	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
100	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
99	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
98	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
97	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012 , 44, 659-69	36.3	615
96	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597

95	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009 , 41, 77-81	36.3	584
94	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010 , 42, 142-8	36.3	527
93	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
92	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	36.3	414
91	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. <i>PLoS Genetics</i> , 2012 , 8, e1002793	6	395
90	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. <i>PLoS Genetics</i> , 2009 , 5, e1000508	6	393
89	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. <i>PLoS Genetics</i> , 2011 , 7, e1002003	6	336
88	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
87	Common variants at 10 genomic loci influence hemoglobin A1C levels via glycemic and nonglycemic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314
86	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. <i>Nature Genetics</i> , 2017 , 49, 17-26	36.3	312
85	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
84	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. <i>Diabetes</i> , 2011 , 60, 2624-34	0.9	285
83	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
82	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011 , 43, 753-60	36.3	237
81	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. <i>Diabetes</i> , 2014 , 63, 2158-71	0.9	235
80	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. <i>Nature Genetics</i> , 2013 , 45, 513-7	36.3	231
79	Candidate gene association study in type 2 diabetes indicates a role for genes involved in beta-cell function as well as insulin action. <i>PLoS Biology</i> , 2003 , 1, E20	9.7	225
78	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. <i>JAMA - Journal of the American Medical Association</i> , 2016 , 316, 1383-1391	37.4	225

77	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. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
76	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
75	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
74	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. <i>PLoS Medicine</i> , 2016 , 13, e1002179	11.6	214
73	Detailed physiologic characterization reveals diverse mechanisms for novel genetic Loci regulating glucose and insulin metabolism in humans. <i>Diabetes</i> , 2010 , 59, 1266-75	0.9	211
72	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
71	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. <i>Diabetologia</i> , 2011 , 54, 2272-82	10.3	155
70	Genetics of Type 2 diabetes. <i>Diabetic Medicine</i> , 2005 , 22, 517-35	3.5	151
69	Prospective functional classification of all possible missense variants in PPARG. <i>Nature Genetics</i> , 2016 , 48, 1570-1575	36.3	149
68	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. <i>PLoS Medicine</i> , 2014 , 11, e1001647	11.6	149
67	Non-DNA binding, dominant-negative, human PPARGgamma mutations cause lipodystrophic insulin resistance. <i>Cell Metabolism</i> , 2006 , 4, 303-11	24.6	143
66	Common genetic variants highlight the role of insulin resistance and body fat distribution in type 2 diabetes, independent of obesity. <i>Diabetes</i> , 2014 , 63, 4378-4387	0.9	127
65	Genomics of disease risk in globally diverse populations. <i>Nature Reviews Genetics</i> , 2019 , 20, 520-535	30.1	105
64	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
63	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. <i>Cell</i> , 2014 , 156, 343-58	56.2	96
62	Mutations disrupting the Kennedy phosphatidylcholine pathway in humans with congenital lipodystrophy and fatty liver disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8901-6	11.5	88
61	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
60	Meta-analysis of the Gly482Ser variant in PPARGC1A in type 2 diabetes and related phenotypes. <i>Diabetologia</i> , 2006 , 49, 501-5	10.3	88

59	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016 , 8, 341ra76	17.5	77
58	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. <i>Cell</i> , 2019 , 179, 984-1002.e36	56.2	76
57	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 865-884	11	74
56	Gene × dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. <i>Human Molecular Genetics</i> , 2015 , 24, 4728-38	5.6	68
55	Hypomorphism in human NSMCE2 linked to primordial dwarfism and insulin resistance. <i>Journal of Clinical Investigation</i> , 2014 , 124, 4028-38	15.9	63
54	A linear mixed-model approach to study multivariate gene-environment interactions. <i>Nature Genetics</i> , 2019 , 51, 180-186	36.3	63
53	Common genetic variation in the melatonin receptor 1B gene (MTNR1B) is associated with decreased early-phase insulin response. <i>Diabetologia</i> , 2009 , 52, 1537-42	10.3	58
52	Genetic architecture of human thinness compared to severe obesity. <i>PLoS Genetics</i> , 2019 , 15, e1007603	6	51
51	The Genetic Basis of Metabolic Disease. <i>Cell</i> , 2019 , 177, 146-161	56.2	51
50	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
49	Human biallelic MFN2 mutations induce mitochondrial dysfunction, upper body adipose hyperplasia, and suppression of leptin expression. <i>ELife</i> , 2017 , 6,	8.9	42
48	Sugar-sweetened beverage consumption and genetic predisposition to obesity in 2 Swedish cohorts. <i>American Journal of Clinical Nutrition</i> , 2016 , 104, 809-15	7	42
47	Human Semaphorin 3 Variants Link Melanocortin Circuit Development and Energy Balance. <i>Cell</i> , 2019 , 176, 729-742.e18	56.2	38
46	Genome-wide association study of type 2 diabetes in Africa. <i>Diabetologia</i> , 2019 , 62, 1204-1211	10.3	36
45	Population-specific risk of type 2 diabetes conferred by HNF4A P2 promoter variants: a lesson for replication studies. <i>Diabetes</i> , 2008 , 57, 3161-5	0.9	33
44	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021 , 5, 59-70	12.8	33
43	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. <i>Scientific Reports</i> , 2017 , 7, 4394	4.9	31
42	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30

41	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
40	Adiponectin receptor genes: mutation screening in syndromes of insulin resistance and association studies for type 2 diabetes and metabolic traits in UK populations. <i>Diabetologia</i> , 2007 , 50, 555-62	10.3	26
39	Genetic determinants of long-term changes in blood lipid concentrations: 10-year follow-up of the GLACIER study. <i>PLoS Genetics</i> , 2014 , 10, e1004388	6	25
38	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
37	Loss of FTO antagonises Wnt signaling and leads to developmental defects associated with ciliopathies. <i>PLoS ONE</i> , 2014 , 9, e87662	3.7	22
36	Steroid receptor coactivator-1 modulates the function of Pomc neurons and energy homeostasis. <i>Nature Communications</i> , 2019 , 10, 1718	17.4	20
35	Polymorphisms in the gene encoding sterol regulatory element-binding factor-1c are associated with type 2 diabetes. <i>Diabetologia</i> , 2006 , 49, 2642-8	10.3	19
34	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018 , 9, 4674	17.4	19
33	Mendelian Randomization Analysis of Hemoglobin A as a Risk Factor for Coronary Artery Disease. <i>Diabetes Care</i> , 2019 , 42, 1202-1208	14.6	17
32	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. <i>Cell Metabolism</i> , 2020 , 31, 1107-1119.e12	24.6	16
31	Established BMI-associated genetic variants and their prospective associations with BMI and other cardiometabolic traits: the GLACIER Study. <i>International Journal of Obesity</i> , 2016 , 40, 1346-52	5.5	16
30	Gene-Lifestyle Interactions in Complex Diseases: Design and Description of the GLACIER and VIKING Studies. <i>Current Nutrition Reports</i> , 2014 , 3, 400-411	6	15
29	The metabolic syndrome- associated small G protein ARL15 plays a role in adipocyte differentiation and adiponectin secretion. <i>Scientific Reports</i> , 2017 , 7, 17593	4.9	14
28	PARL Leu262Val is not associated with fasting insulin levels in UK populations. <i>Diabetologia</i> , 2006 , 49, 2649-52	10.3	14
27	Innate biology versus lifestyle behaviour in the aetiology of obesity and type 2 diabetes: the GLACIER Study. <i>Diabetologia</i> , 2016 , 59, 462-71	10.3	13
26	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. <i>PLoS Genetics</i> , 2018 , 14, e1007591	6	13
25	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. <i>Journal of Infectious Diseases</i> , 2018 , 218, 1700-1710	7	13
24	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. <i>International Journal of Epidemiology</i> , 2017 , 46, 1211-1222	7.8	12

23	Human BDNF/TrkB variants impair hippocampal synaptogenesis and associate with neurobehavioural abnormalities. <i>Scientific Reports</i> , 2020 , 10, 9028	4.9	11
22	Distinct genetic architectures and environmental factors associate with host response to the \varnothing -herpesvirus infections. <i>Nature Communications</i> , 2020 , 11, 3849	17.4	9
21	Genetic aetiology of glycaemic traits: approaches and insights. <i>Human Molecular Genetics</i> , 2017 , 26, R173-R1848	3.8	8
20	A linear mixed model approach to study multivariate gene-environment interactions		8
19	Whole-genome association study of antibody response to Epstein-Barr virus in an African population: a pilot. <i>Global Health, Epidemiology and Genomics</i> , 2017 , 2, e18	2.9	7
18	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. <i>Scientific Data</i> , 2020 , 7, 393	8.2	7
17	IRS2 variants and syndromes of severe insulin resistance. <i>Diabetologia</i> , 2009 , 52, 1208-11	10.3	6
16	Crucial Role of the SH2B1 PH Domain for the Control of Energy Balance. <i>Diabetes</i> , 2019 , 68, 2049-2062	0.9	6
15	is dispensable for normal fat deposition in mice. <i>DMM Disease Models and Mechanisms</i> , 2017 , 10, 1481-1488	4.8	5
14	ADCY3, neuronal primary cilia and obesity. <i>Nature Genetics</i> , 2018 , 50, 166-167	36.3	4
13	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
12	The influence of rare variants in circulating metabolic biomarkers. <i>PLoS Genetics</i> , 2020 , 16, e1008605	6	3
11	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. <i>Scientific Reports</i> , 2019 , 9, 9439	4.9	3
10	Associations Between Glycemic Traits and Colorectal Cancer: A Mendelian Randomization Analysis.. <i>Journal of the National Cancer Institute</i> , 2022 ,	9.7	3
9	Obesity-Associated Mutations and the Melanocortin Pathway. <i>New England Journal of Medicine</i> , 2021 , 385, 1581-1592	59.2	2
8	Genome-wide scale analyses identify novel BMI genotype-environment interactions using a conditional false discovery rate		2
7	Genome-wide scan and fine-mapping of rare nonsynonymous associations implicates intracellular lipolysis genes in fat distribution and cardio-metabolic risk		2
6	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits		1

5	Identification of rare loss of function genetic variation regulating body fat distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	1
4	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations.. <i>Scientific Reports</i> , 2022 , 12, 1131	4.9	0
3	Predicting novel candidate human obesity genes and their site of action by systematic functional screening in <i>Drosophila</i> . <i>PLoS Biology</i> , 2021 , 19, e3001255	9.7	0
2	The flashfm approach for fine-mapping multiple quantitative traits. <i>Nature Communications</i> , 2021 , 12, 6147	17.4	0
1	The importance of increasing population diversity in genetic studies of type 2 diabetes and related glycaemic traits. <i>Diabetologia</i> , 2021 , 64, 2653-2664	10.3	0