Inês Barroso

List of Publications by Year in Descending Order

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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	Associations Between Glycemic Traits and Colorectal Cancer: A Mendelian Randomization Analysis.. *Journal of the National Cancer Institute*, **2022**,	9.7	3
111	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	4.9	0
110	Predicting novel candidate human obesity genes and their site of action by systematic functional screening in Drosophila. *PLoS Biology*, **2021**, 19, e3001255	9.7	0
109	The flashfm approach for fine-mapping multiple quantitative traits. *Nature Communications*, **2021**, 12, 6147	17.4	0
108	Obesity-Associated Mutations and the Melanocortin Pathway. *New England Journal of Medicine*, **2021**, 385, 1581-1592	59.2	2
107	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
106	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
105	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
104	The importance of increasing population diversity in genetic studies of type 2 diabetes and related glycaemic traits. *Diabetologia*, **2021**, 64, 2653-2664	10.3	0
103	Identification of rare loss of function genetic variation regulating body fat distribution. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	1
102	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	24.6	16
101	Human BDNF/TrkB variants impair hippocampal synaptogenesis and associate with neurobehavioural abnormalities. *Scientific Reports*, **2020**, 10, 9028	4.9	11
100	The influence of rare variants in circulating metabolic biomarkers. *PLoS Genetics*, **2020**, 16, e1008605	6	3
99	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. *Scientific Data*, **2020**, 7, 393	8.2	7
98	Distinct genetic architectures and environmental factors associate with host response to the □-herpesvirus infections. *Nature Communications*, **2020**, 11, 3849	17.4	9
97	Genetic architecture of human thinness compared to severe obesity. *PLoS Genetics*, **2019**, 15, e1007603	6	51
96	Mendelian Randomization Analysis of Hemoglobin A as a Risk Factor for Coronary Artery Disease. *Diabetes Care*, **2019**, 42, 1202-1208	14.6	17

95	Genomics of disease risk in globally diverse populations. *Nature Reviews Genetics*, **2019**, 20, 520-535	30.1	105
94	Genome-wide association study of type 2 diabetes in Africa. *Diabetologia*, **2019**, 62, 1204-1211	10.3	36
93	The Genetic Basis of Metabolic Disease. *Cell*, **2019**, 177, 146-161	56.2	51
92	Steroid receptor coactivator-1 modulates the function of Pomc neurons and energy homeostasis. *Nature Communications*, **2019**, 10, 1718	17.4	20
91	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. *Scientific Reports*, **2019**, 9, 9439	4.9	3
90	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
89	Crucial Role of the SH2B1 PH Domain for the Control of Energy Balance. *Diabetes*, **2019**, 68, 2049-2062	0.9	6
88	A linear mixed-model approach to study multivariate gene-environment interactions. *Nature Genetics*, **2019**, 51, 180-186	36.3	63
87	Human Semaphorin 3 Variants Link Melanocortin Circuit Development and Energy Balance. *Cell*, **2019**, 176, 729-742.e18	56.2	38
86	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
85	ADCY3, neuronal primary cilia and obesity. *Nature Genetics*, **2018**, 50, 166-167	36.3	4
84	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
83	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. *Nature Communications*, **2018**, 9, 4674	17.4	19
82	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	6	13
81	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. *Journal of Infectious Diseases*, **2018**, 218, 1700-1710	7	13
80	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
79	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
78	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29

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. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
76	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. *International Journal of Epidemiology*, **2017**, 46, 1211-1222	7.8	12
75	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
74	The metabolic syndrome- associated small G protein ARL15 plays a role in adipocyte differentiation and adiponectin secretion. *Scientific Reports*, **2017**, 7, 17593	4.9	14
73	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, **2017**, 7, 4394	4.9	31
72	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. *Nature Genetics*, **2017**, 49, 17-26	36.3	312
71	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	2.9	7
70	is dispensable for normal fat deposition in mice. *DMM Disease Models and Mechanisms*, **2017**, 10, 1481-1488	4.8	5
69	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
68	Genetic aetiology of glycaemic traits: approaches and insights. *Human Molecular Genetics*, **2017**, 26, R172-R184	5.8	48
67	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
66	Human biallelic MFN2 mutations induce mitochondrial dysfunction, upper body adipose hyperplasia, and suppression of leptin expression. *ELife*, **2017**, 6,	8.9	42
65	Prospective functional classification of all possible missense variants in PPARG. *Nature Genetics*, **2016**, 48, 1570-1575	36.3	149
64	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
63	Innate biology versus lifestyle behaviour in the aetiology of obesity and type 2 diabetes: the GLACIER Study. *Diabetologia*, **2016**, 59, 462-71	10.3	13
62	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	11.6	214
61	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
60	Established BMI-associated genetic variants and their prospective associations with BMI and other cardiometabolic traits: the GLACIER Study. *International Journal of Obesity*, **2016**, 40, 1346-52	5.5	16

59	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. *JAMA - Journal of the American Medical Association*, **2016**, 316, 1383-1391	27.4	225
58	Sugar-sweetened beverage consumption and genetic predisposition to obesity in 2 Swedish cohorts. *American Journal of Clinical Nutrition*, **2016**, 104, 809-15	7	42
57	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
56	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
55	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	6	220
54	Gene dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. *Human Molecular Genetics*, **2015**, 24, 4728-38	5.6	68
53	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
52	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
51	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96
50	Gene-Lifestyle Interactions in Complex Diseases: Design and Description of the GLACIER and VIKING Studies. *Current Nutrition Reports*, **2014**, 3, 400-411	6	15
49	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
48	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
47	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	0.9	127
46	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, 8901-6	11.5	88
45	Loss of FTO antagonises Wnt signaling and leads to developmental defects associated with ciliopathies. *PLoS ONE*, **2014**, 9, e87662	3.7	22
44	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
43	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. *PLoS Medicine*, **2014**, 11, e1001647	11.6	149
42	Genetic determinants of long-term changes in blood lipid concentrations: 10-year follow-up of the GLACIER study. *PLoS Genetics*, **2014**, 10, e1004388	6	25

41	Hypomorphism in human NSMCE2 linked to primordial dwarfism and insulin resistance. *Journal of Clinical Investigation*, **2014**, 124, 4028-38	15.9	63
40	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
39	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
38	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. *Nature Genetics*, **2013**, 45, 513-7	36.3	231
37	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
36	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
35	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
34	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
33	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
32	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	6	326
31	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
30	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
29	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
28	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, 2624-34	0.9	285
27	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, 2272-82	10.3	155
26	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
25	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
24	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527

23	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
22	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, 949-60	36.3	724
21	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
20	Detailed physiologic characterization reveals diverse mechanisms for novel genetic Loci regulating glucose and insulin metabolism in humans. *Diabetes*, **2010**, 59, 1266-75	0.9	211
19	Common variants at 10 genomic loci influence hemoglobin A[C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
18	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
17	IRS2 variants and syndromes of severe insulin resistance. *Diabetologia*, **2009**, 52, 1208-11	10.3	6
16	Common genetic variation in the melatonin receptor 1B gene (MTNR1B) is associated with decreased early-phase insulin response. *Diabetologia*, **2009**, 52, 1537-42	10.3	58
15	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
14	Population-specific risk of type 2 diabetes conferred by HNF4A P2 promoter variants: a lesson for replication studies. *Diabetes*, **2008**, 57, 3161-5	0.9	33
13	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, 555-62	10.3	26
12	Meta-analysis of the Gly482Ser variant in PPARGC1A in type 2 diabetes and related phenotypes. *Diabetologia*, **2006**, 49, 501-5	10.3	88
11	Polymorphisms in the gene encoding sterol regulatory element-binding factor-1c are associated with type 2 diabetes. *Diabetologia*, **2006**, 49, 2642-8	10.3	19
10	PARL Leu262Val is not associated with fasting insulin levels in UK populations. *Diabetologia*, **2006**, 49, 2649-52	10.3	14
9	Non-DNA binding, dominant-negative, human PPARgamma mutations cause lipodystrophic insulin resistance. *Cell Metabolism*, **2006**, 4, 303-11	24.6	143
8	Genetics of Type 2 diabetes. *Diabetic Medicine*, **2005**, 22, 517-35	3.5	151
7	Candidate gene association study in type 2 diabetes indicates a role for genes involved in beta-cell function as well as insulin action. *PLoS Biology*, **2003**, 1, E20	9.7	225
6	Dominant negative mutations in human PPARgamma associated with severe insulin resistance, diabetes mellitus and hypertension. *Nature*, **1999**, 402, 880-3	50.4	1129

5	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits	1
4	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes	4
3	Genome-wide scale analyses identify novel BMI genotype-environment interactions using a conditional false discovery rate	2
2	A linear mixed model approach to study multivariate gene-environment interactions	8
1	Genome-wide scan and fine-mapping of rare nonsynonymous associations implicates intracellular lipolysis genes in fat distribution and cardio-metabolic risk	2