Josep Maria Mercader

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.

85
papers

5,507
citations

102
ext. papers

7,388
ext. citations

35
h-index

36
g-index

4.98
L-index

#	Paper	IF	Citations
85	Metformin alters the gut microbiome of individuals with treatment-naive type 2 diabetes, contributing to the therapeutic effects of the drug. <i>Nature Medicine</i> , 2017 , 23, 850-858	50.5	732
84	SNPassoc: an R package to perform whole genome association studies. <i>Bioinformatics</i> , 2007 , 23, 644-5	7.2	513
83	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. <i>Nature Genetics</i> , 2014 , 46, 51-5	36.3	376
82	Brain-derived neurotrophic factor Val66Met and psychiatric disorders: meta-analysis of case-control studies confirm association to substance-related disorders, eating disorders, and schizophrenia. <i>Biological Psychiatry</i> , 2007 , 61, 911-22	7.9	338
81	Targeting the circulating microRNA signature of obesity. Clinical Chemistry, 2013, 59, 781-92	5.5	281
80	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016 , 538, 248-	2 5 2.4	266
79	Profiling of circulating microRNAs reveals common microRNAs linked to type 2 diabetes that change with insulin sensitization. <i>Diabetes Care</i> , 2014 , 37, 1375-83	14.6	241
78	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181
77	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. <i>PLoS Medicine</i> , 2018 , 15, e1002654	11.6	180
76	Association of a low-frequency variant in HNF1A with type 2 diabetes in a Latino population. <i>JAMA - Journal of the American Medical Association</i> , 2014 , 311, 2305-14	27.4	164
75	Changes in circulating microRNAs are associated with childhood obesity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013 , 98, E1655-60	5.6	148
74	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
73	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13127-32	11.5	121
72	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. <i>Nature Genetics</i> , 2019 , 51, 1137-1148	36.3	111
71	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016 , 7, 10531	17.4	99
70	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. <i>Cell</i> , 2017 , 170, 199-212.e20	56.2	94
69	Decreased lipid metabolism but increased FA biosynthesis are coupled with changes in liver microRNAs in obese subjects with NAFLD. <i>International Journal of Obesity</i> , 2017 , 41, 620-630	5.5	73

(2017-2015)

68	Inflammation triggers specific microRNA profiles in human adipocytes and macrophages and in their supernatants. <i>Clinical Epigenetics</i> , 2015 , 7, 49	7	71
67	Altered Circulating miRNA Expression Profile in Pregestational and Gestational Obesity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015 , 100, E1446-56	ϵ	58
66	Altered brain-derived neurotrophic factor blood levels and gene variability are associated with anorexia and bulimia. <i>Genes, Brain and Behavior</i> , 2007 , 6, 706-16	6	57
65	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018 , 102, 1204-1211	5	59
64	New insights into the expression profile and function of micro-ribonucleic acid in human spermatozoa. <i>Fertility and Sterility</i> , 2014 , 102, 213-222.e4	5	, 8
63	Circulating profiling reveals the effect of a polyunsaturated fatty acid-enriched diet on common microRNAs. <i>Journal of Nutritional Biochemistry</i> , 2015 , 26, 1095-101	5	57
62	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018 , 50, 1072-1080	5	52
61	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 321	. 5	50
60	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020 , 16, e1008629	4	19
59	Genome-wide association study meta-analysis identifies five new loci for systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2018 , 20, 100	4	17
58	Suicide attempts in bulimia nervosa: personality and psychopathological correlates. <i>European Psychiatry</i> , 2009 , 24, 91-7	4	ļ 6
57	Dysregulation of Placental miRNA in Maternal Obesity Is Associated With Pre- and Postnatal Growth. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017 , 102, 2584-2594	4	15
56	ZNRD1 (zinc ribbon domain-containing 1) is a host cellular factor that influences HIV-1 replication and disease progression. <i>Clinical Infectious Diseases</i> , 2010 , 50, 1022-32	4	ļ 2
55	Association of NTRK3 and its interaction with NGF suggest an altered cross-regulation of the neurotrophin signaling pathway in eating disorders. <i>Human Molecular Genetics</i> , 2008 , 17, 1234-44	4	ļ2
54	Cardiometabolic risk factors for COVID-19 susceptibility and severity: A Mendelian randomization analysis. <i>PLoS Medicine</i> , 2021 , 18, e1003553	3	3 7
53	miRNAs in cerebrospinal fluid identify patients with MS and specifically those with lipid-specific oligoclonal IgM bands. <i>Multiple Sclerosis Journal</i> , 2017 , 23, 1716-1726	3	;6
52	Surgery-Induced Weight Loss Is Associated With the Downregulation of Genes Targeted by MicroRNAs in Adipose Tissue. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015 , 100, E1467-76	3	35
51	A Loss-of-Function Splice Acceptor Variant in Is Protective for Type 2 Diabetes. <i>Diabetes</i> , 2017 , 66, 2903-291	4 3	32

50	Contribution of the serotoninergic system to anxious and depressive traits that may be partially responsible for the phenotypical variability of bulimia nervosa. <i>Journal of Psychiatric Research</i> , 2008 , 42, 50-7	5.2	32
49	A cancer-associated polymorphism in ESCRT-III disrupts the abscission checkpoint and promotes genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8900-E8908	11.5	28
48	Blood levels of brain-derived neurotrophic factor correlate with several psychopathological symptoms in anorexia nervosa patients. <i>Neuropsychobiology</i> , 2007 , 56, 185-90	4	25
47	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
46	Correlation of BDNF blood levels with interoceptive awareness and maturity fears in anorexia and bulimia nervosa patients. <i>Journal of Neural Transmission</i> , 2010 , 117, 505-12	4.3	21
45	A Genome-Wide Association Study Using a Custom Genotyping Array Identifies Variants in Associated With Reduced Energy Expenditure in American Indians. <i>Diabetes</i> , 2017 , 66, 2284-2295	0.9	20
44	Transferrin receptor-1 gene polymorphisms are associated with type 2 diabetes. <i>European Journal of Clinical Investigation</i> , 2010 , 40, 600-7	4.6	19
43	Functional connectivity of the hippocampus in elderly with mild memory dysfunction carrying the APOE epsilon4 allele. <i>Neurobiology of Aging</i> , 2008 , 29, 1644-53	5.6	19
42	Hypothalamus transcriptome profile suggests an anorexia-cachexia syndrome in the anx/anx mouse model. <i>Physiological Genomics</i> , 2008 , 35, 341-50	3.6	19
41	The Genetic Basis of Type 2 Diabetes in Hispanics and Latin Americans: Challenges and Opportunities. <i>Frontiers in Public Health</i> , 2017 , 5, 329	6	18
40	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. <i>PLoS Genetics</i> , 2012 , 8, e1003046	6	17
39	Nucleotide, cytogenetic and expression impact of the human chromosome 8p23.1 inversion polymorphism. <i>PLoS ONE</i> , 2009 , 4, e8269	3.7	15
38	Adaptation to environmental factors shapes the organization of regulatory regions in microbial communities. <i>BMC Genomics</i> , 2014 , 15, 877	4.5	13
37	Thyroid hormone receptor alpha gene variants increase the risk of developing obesity and show gene-diet interactions. <i>International Journal of Obesity</i> , 2013 , 37, 1499-505	5.5	12
36	Common genetic variants of surfactant protein-D (SP-D) are associated with type 2 diabetes. <i>PLoS ONE</i> , 2013 , 8, e60468	3.7	12
35	Targeting the association of calgranulin B (S100A9) with insulin resistance and type 2 diabetes. Journal of Molecular Medicine, 2013 , 91, 523-34	5.5	11
34	Aberrant brain microRNA target and miRISC gene expression in the anx/anx anorexia mouse model. <i>Gene</i> , 2012 , 497, 181-90	3.8	11
33	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. <i>Nucleic Acids Research</i> , 2013 , 41, 7220-30	20.1	11

32	Trans-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation		10
31	The impact of non-additive genetic associations on age-related complex diseases. <i>Nature Communications</i> , 2021 , 12, 2436	17.4	10
30	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. <i>PLoS Computational Biology</i> , 2019 , 15, e1006734	5	9
29	Interaction Between Type 2 Diabetes Prevention Strategies and Genetic Determinants of Coronary Artery Disease on Cardiometabolic Risk Factors. <i>Diabetes</i> , 2020 , 69, 112-120	0.9	9
28	Genomic profiling in advanced stage non-small-cell lung cancer patients with platinum-based chemotherapy identifies germline variants with prognostic value in SMYD2. <i>Cancer Treatment and Research Communications</i> , 2018 , 15, 21-31	2	8
27	MRPS18CP2 alleles and DEFA3 absence as putative chromosome 8p23.1 modifiers of hearing loss due to mtDNA mutation A1555G in the 12S rRNA gene. <i>BMC Medical Genetics</i> , 2007 , 8, 81	2.1	8
26	The First Genome-Wide Association Study for Type 2 Diabetes in Youth: The Progress in Diabetes Genetics in Youth (ProDiGY) Consortium. <i>Diabetes</i> , 2021 , 70, 996-1005	0.9	8
25	Role of the neurotrophin network in eating disorders subphenotypes: body mass index and age at onset of the disease. <i>Journal of Psychiatric Research</i> , 2010 , 44, 834-40	5.2	7
24	Human pancreatic islet 3D chromatin architecture provides insights into the genetics of type 2 diabetes	i	7
23	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation <i>Nature Genetics</i> , 2022 ,	36.3	7
22	A Polygenic Lipodystrophy Genetic Risk Score Characterizes Risk Independent of BMI in the Diabetes Prevention Program. <i>Journal of the Endocrine Society</i> , 2019 , 3, 1663-1677	0.4	6
21	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations. <i>Human Molecular Genetics</i> , 2021 , 30, 1521-1534	5.6	6
20	A functional IFN-A-generating DNA polymorphism could protect older asthmatic women from aeroallergen sensitization and associate with clinical features of asthma. <i>Scientific Reports</i> , 2017 , 7, 105	0b 9	5
19	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. <i>Diabetes Care</i> , 2021 , 44, 2673-2682	14.6	5
18	TIGER: The gene expression regulatory variation landscape of human pancreatic islets. <i>Cell Reports</i> , 2021 , 37, 109807	10.6	5
17	Clustering of Type 2 Diabetes Genetic Loci by Multi-Trait Associations Identifies Disease Mechanisms and Subtypes		5
16	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
15	Integrating untargeted metabolomics, genetically informed causal inference, and pathway enrichment to define the obesity metabolome. <i>International Journal of Obesity</i> , 2020 , 44, 1596-1606	5.5	4

14	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. <i>Diabetes Care</i> , 2021 ,	14.6	4
13	Using metabolite profiling to construct and validate a metabolite risk score for predicting future weight gain. <i>PLoS ONE</i> , 2019 , 14, e0222445	3.7	3
12	Polymorphic Inversions Underlie the Shared Genetic Susceptibility of Obesity-Related Diseases. American Journal of Human Genetics, 2020 , 106, 846-858	11	3
11	Analysis of the multi-copy gene family FAM90A as a copy number variant in different ethnic backgrounds. <i>Gene</i> , 2008 , 420, 113-7	3.8	3
10	The impact of non-additive genetic associations on age-related complex diseases		3
9	Discovering cellular programs of intrinsic and extrinsic drivers of metabolic traits using LipocyteProfiler		3
8	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
7	Analysis of Glucocorticoid-Related Genes Reveal as a New Candidate Gene for Type 2 Diabetes. Journal of the Endocrine Society, 2020 , 4, bvaa121	0.4	2
6	Cytoskeletal transgelin 2 contributes to gender-dependent adipose tissue expandability and immune function. <i>FASEB Journal</i> , 2019 , 33, 9656-9671	0.9	1
5	Predicting diabetes risk in diverse populations: what next?. <i>Lancet Diabetes and Endocrinology,the</i> , 2021 , 9, 808-810	18.1	1
4	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes		1
3	Recessive Genome-wide Meta-analysis Illuminates Genetic Architecture of Type 2 Diabetes. <i>Diabetes</i> , 2021 ,	0.9	О
2	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium <i>Human Genetics and Genomics Advances</i> , 2022 , 3, 100099	0.8	О
1	Response to Comment on Dawed et al. Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. Diabetes Care 2021;44:2673-2682 <i>Diabetes Care</i> , 2022 , 45, e82-e83	14.6	