

Mickaël Canouil

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

4,334
citations

236925

25
h-index

254184

43
g-index

52
all docs

52
docs citations

52
times ranked

7484
citing authors

#	ARTICLE	IF	CITATIONS
1	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
3	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
4	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
5	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
6	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
7	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
8	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
9	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
10	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. <i>Human Molecular Genetics</i> , 2019, 28, 3327-3338.	2.9	76
11	Persistent or Transient Human β^2 Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. <i>Cell Reports</i> , 2020, 33, 108466.	6.4	65
12	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. <i>Diabetes</i> , 2018, 67, 1310-1321.	0.6	64
13	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
14	Low-dose exposure to bisphenols A, F and S of human primary adipocyte impacts coding and non-coding RNA profiles. <i>PLoS ONE</i> , 2017, 12, e0179583.	2.5	64
15	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. <i>American Journal of Human Genetics</i> , 2017, 100, 238-256.	6.2	60
16	Hepatic <i>DPP4</i> DNA Methylation Associates With Fatty Liver. <i>Diabetes</i> , 2017, 66, 25-35.	0.6	59
17	Expression and functional assessment of candidate type 2 diabetes susceptibility genes identify four new genes contributing to human insulin secretion. <i>Molecular Metabolism</i> , 2017, 6, 459-470.	6.5	55
18	Loss-of-function mutations in MRAP2 are pathogenic in hyperphagic obesity with hyperglycemia and hypertension. <i>Nature Medicine</i> , 2019, 25, 1733-1738.	30.7	54

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19	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. <i>BMC Medicine</i> , 2017, 15, 37.	5.5	47
20	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	2.9	47
21	Type 2 diabetes-associated variants of the MT ₂ melatonin receptor affect distinct modes of signaling. <i>Science Signaling</i> , 2018, 11, .	3.6	45
22	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. <i>Nature Metabolism</i> , 2020, 2, 1126-1134.	11.9	43
23	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. <i>Cell Reports Medicine</i> , 2022, 3, 100477.	6.5	39
24	The expression of genes in top obesity-associated loci is enriched in insula and substantia nigra brain regions involved in addiction and reward. <i>International Journal of Obesity</i> , 2020, 44, 539-543.	3.4	38
25	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	2.9	31
26	Elevated circulating follistatin associates with an increased risk of type 2 diabetes. <i>Nature Communications</i> , 2021, 12, 6486.	12.8	31
27	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. <i>Molecular Metabolism</i> , 2019, 24, 98-107.	6.5	26
28	SHP2 drives inflammation-triggered insulin resistance by reshaping tissue macrophage populations. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	26
29	Maternal Glycemic Dysregulation During Pregnancy and Neonatal Blood DNA Methylation: Meta-analyses of Epigenome-Wide Association Studies. <i>Diabetes Care</i> , 2022, 45, 614-623.	8.6	19
30	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
31	Epigenome-Wide Association Study Reveals Methylation Loci Associated With Offspring Gestational Diabetes Mellitus Exposure and Maternal Methylome. <i>Diabetes Care</i> , 2021, 44, 1992-1999.	8.6	17
32	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	8.6	16
33	<i>NACHO</i> : an R package for quality control of NanoString nCounter data. <i>Bioinformatics</i> , 2020, 36, 970-971.	4.1	13
34	Histone deacetylase 9 promoter hypomethylation associated with adipocyte dysfunction is a statin-related metabolic effect. <i>Clinical Epigenetics</i> , 2020, 12, 68.	4.1	10
35	Monogenic diabetes characteristics in a transnational multicenter study from Mediterranean countries. <i>Diabetes Research and Clinical Practice</i> , 2021, 171, 108553.	2.8	7
36	Rare Variant Analysis of Obesity-Associated Genes in Young Adults With Severe Obesity From a Consanguineous Population of Pakistan. <i>Diabetes</i> , 2022, 71, 694-705.	0.6	7

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37	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.	3.3	5
38	Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a regulator of insulin secretion. <i>Cell Reports</i> , 2021, 34, 108703.	6.4	4
39	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 1614-1627.	4.9	4
40	Epigenetic and Transcriptomic Programming of HSC Quiescence Signaling in Large for Gestational Age Neonates. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7323.	4.1	2
41	Jointly Modelling Single Nucleotide Polymorphisms With Longitudinal and Time-to-Event Trait: An Application to Type 2 Diabetes and Fasting Plasma Glucose. <i>Frontiers in Genetics</i> , 2018, 9, 210.	2.3	1
42	Variable Clustering in High-Dimensional Linear Regression: The R Package clere. <i>R Journal</i> , 2016, 8, 92.	1.8	1
43	General regression model: A "model-free" association test for quantitative traits allowing to test for the underlying genetic model. <i>Annals of Human Genetics</i> , 2020, 84, 280-290.	0.8	0
44	1901-P: Individual and Longitudinal Effects of Gastric Bypass Surgery on the Circulating Proteome. <i>Diabetes</i> , 2020, 69, 1901-P.	0.6	0
45	Epigenetic changes associated with hyperglycaemia exposure in the longitudinal D.E.S.I.R. cohort. <i>Diabetes and Metabolism</i> , 2022, 48, 101347.	2.9	0