MickaÃ«l Canouil

List of Publications by Year
in descending order

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	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. Cell Reports Medicine, 2022, 3, 100477.	6.5	39
2	Rare Variant Analysis of Obesity-Associated Genes in Young Adults With Severe Obesity From a Consanguineous Population of Pakistan. Diabetes, 2022, 71, 694-705.	0.6	7
3	Maternal Glycemic Dysregulation During Pregnancy and Neonatal Blood DNA Methylation: Meta-analyses of Epigenome-Wide Association Studies. Diabetes Care, 2022, 45, 614-623.	8.6	19
4	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	2.9	47
5	Epigenetic changes associated with hyperglycaemia exposure in the longitudinal D.E.S.I.R. cohort. Diabetes and Metabolism, 2022, 48, 101347.	2.9	0
6	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
7	Epigenetic and Transcriptomic Programming of HSC Quiescence Signaling in Large for Gestational Age Neonates. International Journal of Molecular Sciences, 2022, 23, 7323.	4.1	2
8	Monogenic diabetes characteristics in a transnational multicenter study from Mediterranean countries. Diabetes Research and Clinical Practice, 2021, 171, 108553.	2.8	7
9	Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a regulator of insulin secretion. Cell Reports, 2021, 34, 108703.	6.4	4
10	SHP2 drives inflammation-triggered insulin resistance by reshaping tissue macrophage populations. Science Translational Medicine, 2021, 13, .	12.4	26
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	Epigenome-Wide Association Study Reveals Methylation Loci Associated With Offspring Gestational Diabetes Mellitus Exposure and Maternal Methylome. Diabetes Care, 2021, 44, 1992-1999.	8.6	17
13	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2021, 4, 1614-1627.	4.9	4
14	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	8.6	16
15	Elevated circulating follistatin associates with an increased risk of type 2 diabetes. Nature Communications, 2021, 12, 6486.	12.8	31
16	*NACHO:* an R package for quality control of NanoString nCounter data. Bioinformatics, 2020, 36, 970-971.	4.1	13
17	The expression of genes in top obesity-associated loci is enriched in insula and substantia nigra brain regions involved in addiction and reward. International Journal of Obesity, 2020, 44, 539-543.	3.4	38
18	General regression model: A "model"free"association test for quantitative traits allowing to test for the underlying genetic model. Annals of Human Genetics, 2020, 84, 280-290.	0.8	0

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19	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. Nature Metabolism, 2020, 2, 1126-1134.	11.9	43
20	Persistent or Transient Human β Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. Cell Reports, 2020, 33, 108466.	6.4	65
21	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
22	Histone deacetylase 9 promoter hypomethylation associated with adipocyte dysfunction is a statin-related metabolic effect. Clinical Epigenetics, 2020, 12, 68.	4.1	10
23	1901-P: Individual and Longitudinal Effects of Gastric Bypass Surgery on the Circulating Proteome. Diabetes, 2020, 69, 1901-P.	0.6	0
24	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
25	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
26	Loss-of-function mutations in MRAP2 are pathogenic in hyperphagic obesity with hyperglycemia and hypertension. Nature Medicine, 2019, 25, 1733-1738.	30.7	54
27	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
28	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
29	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
30	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. Molecular Metabolism, 2019, 24, 98-107.	6.5	26
31	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
32	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
33	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
34	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
35	Increased Hepatic PDGF-AA Signaling Mediates Liver Insulin Resistance in Obesity-Associated Type 2 Diabetes. Diabetes, 2018, 67, 1310-1321.	0.6	64
36	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331

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37	Jointly Modelling Single Nucleotide Polymorphisms With Longitudinal and Time-to-Event Trait: An Application to Type 2 Diabetes and Fasting Plasma Glucose. Frontiers in Genetics, 2018, 9, 210.	2.3	1
38	Type 2 diabetes–associated variants of the MT$_2$ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, .	3.6	45
39	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
40	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	6.2	60
41	Expression and functional assessment of candidate type 2 diabetes susceptibility genes identify four new genes contributing to human insulin secretion. Molecular Metabolism, 2017, 6, 459-470.	6.5	55
42	Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. BMC Medicine, 2017, 15, 37.	5.5	47
43	Hepatic *DPP4* DNA Methylation Associates With Fatty Liver. Diabetes, 2017, 66, 25-35.	0.6	59
44	Low-dose exposure to bisphenols A, F and S of human primary adipocyte impacts coding and non-coding RNA profiles. PLoS ONE, 2017, 12, e0179583.	2.5	64
45	Variable Clustering in High-Dimensional Linear Regression: The R Package clere. R Journal, 2016, 8, 92.	1.8	1