Jason Flannick

List of Publications by Year
in descending order

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42 papers	14,073 citations	212478 28 h-index	325983 40 g-index
54 all docs	54 docs citations	54 times ranked	38748 citing authors

#	Article	IF	Citations
1	Data-driven type 2 diabetes patient clusters predict metabolic surgery outcomes. Lancet Diabetes and Endocrinology,the, 2022, , .	5.5	1
2	The Lipid Droplet Knowledge Portal: A resource for systematic analyses of lipid droplet biology. Developmental Cell, 2022, 57, 387-397.e4.	3.1	22
3	Evaluating human genetic support for hypothesized metabolic disease genes. Cell Metabolism, 2022, 34, 661-666.	7.2	14
4	An Open-Access Platform for Translating Diabetes and Cardiometabolic Disease Genetics Into Accessible Knowledge. Journal of the Endocrine Society, 2021, 5, A406-A406.	0.1	0
5	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
6	Monogenic Diabetes in Youth With Presumed Type 2 Diabetes: Results From the Progress in Diabetes Genetics in Youth (ProDiGY) Collaboration. Diabetes Care, 2021, 44, 2312-2319.	4.3	21
7	The First Genome-Wide Association Study for Type 2 Diabetes in Youth: The Progress in Diabetes Genetics in Youth (ProDiGY) Consortium. Diabetes, 2021, 70, 996-1005.	0.3	37
8	A glomerular transcriptomic landscape of apolipoprotein L1 in Black patients with focal segmental glomerulosclerosis. Kidney International, 2021, , .	2.6	8
9	The Musculoskeletal Knowledge Portal: Making Omics Data Useful to the Broader Scientific Community. Journal of Bone and Mineral Research, 2020, 35, 1626-1633.	3.1	25
10	Loss of ZnT8 function protects against diabetes by enhanced insulin secretion. Nature Genetics, 2019, 51, 1596-1606.	9.4	96
11	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
12	MON-186 An Evaluation of the Ability of Current Exome Sequence Datasets to Retrospectively Validate Drugs for T2D or Related Metabolic Traits. Journal of the Endocrine Society, 2019, 3, .	0.1	0
13	Translocon Declogger Ste24 Protects against IAPP Oligomer-Induced Proteotoxicity. Cell, 2018, 173, 62-73.e9.	13.5	48
14	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
15	Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. Diabetologia, 2018, 61, 1315-1324.	2.9	93
16	Cerebrovascular Disease Knowledge Portal. Stroke, 2018, 49, 470-475.	1.0	39
17	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	5.8	85
18	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102

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19	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
20	Abstract TP161: The Cerebrovascular Disease Knowledge Portal: an Open Access Data Resource to Accelerate Genomic Discoveries in Stroke. Stroke, 2018, 49, .	1.0	0
21	Functional Investigations of HNF1A Identify Rare Variants as Risk Factors for Type 2 Diabetes in the General Population. Diabetes, 2017, 66, 335-346.	0.3	54
22	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
23	A Loss-of-Function Splice Acceptor Variant in IGF2 Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.3	52
24	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
25	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
26	Type 2 diabetes: genetic data sharing to advance complex disease research. Nature Reviews Genetics, 2016, 17, 535-549.	7.7	128
27	Common and rare forms of diabetes mellitus: towards a continuum of diabetes subtypes. Nature Reviews Endocrinology, 2016, 12, 394-406.	4.3	112
28	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
29	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. BMC Endocrine Disorders, 2016, 16, 7.	0.9	9
30	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	5.8	149
31	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	1.5	124
32	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
33	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. Science Translational Medicine, 2015, 7, 270ra6.	5.8	375
34	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
35	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	3.3	152
36	Association of a Low-Frequency Variant inHNF1AWith Type 2 Diabetes in a Latino Population. JAMA - Journal of the American Medical Association, 2014, 311, 2305.	3.8	230

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37	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
38	A Novel Test for Recessive Contributions to Complex Diseases Implicates Bardet-Biedl Syndrome Gene BBS10 in Idiopathic Type 2 Diabetes and Obesity. American Journal of Human Genetics, 2014, 95, 509-520.	2.6	29
39	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
40	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	2.6	24
41	Assessing the phenotypic effects in the general population of rare variants in genes for a dominant Mendelian form of diabetes. Nature Genetics, 2013, 45, 1380-1385.	9.4	129
42	Using multiple alignments to improve seeded local alignment algorithms. Nucleic Acids Research, 2005, 33, 4563-4577.	6.5	8