## Jason Flannick

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4128413/publications.pdf

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42 papers

14,073 citations

28 h-index 289244 40 g-index

54 all docs

54 docs citations

54 times ranked

35677 citing authors

#	Article	IF	CITATIONS
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	27.8	9,051
2	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
3	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
4	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. Science Translational Medicine, 2015, 7, 270ra6.	12.4	375
5	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
6	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
7	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
8	Association of a Low-Frequency Variant in <i>HNF1A</i> With Type 2 Diabetes in a Latino Population. JAMA - Journal of the American Medical Association, 2014, 311, 2305.	7.4	230
9	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
10	Rare variants in <i>PPARG</i> 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.	7.1	152
11	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	12.8	149
12	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.	21.4	129
13	Type 2 diabetes: genetic data sharing to advance complex disease research. Nature Reviews Genetics, 2016, 17, 535-549.	16.3	128
14	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	3.5	124
15	Common and rare forms of diabetes mellitus: towards a continuum of diabetes subtypes. Nature Reviews Endocrinology, 2016, 12, 394-406.	9.6	112
16	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	6.2	102
17	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99
18	Loss of ZnT8 function protects against diabetes by enhanced insulin secretion. Nature Genetics, 2019, 51, 1596-1606.	21.4	96

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19	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.	3.5	95
20	Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. Diabetologia, 2018, 61, 1315-1324.	6.3	93
21	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	12.8	85
22	Functional Investigations of <i>HNF1A</i> Identify Rare Variants as Risk Factors for Type 2 Diabetes in the General Population. Diabetes, 2017, 66, 335-346.	0.6	54
23	A Loss-of-Function Splice Acceptor Variant in <i>IGF2</i> Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.6	52
24	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
25	Translocon Declogger Ste24 Protects against IAPP Oligomer-Induced Proteotoxicity. Cell, 2018, 173, 62-73.e9.	28.9	48
26	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
27	Cerebrovascular Disease Knowledge Portal. Stroke, 2018, 49, 470-475.	2.0	39
28	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.	0.6	37
29	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
30	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.	6.2	29
31	The Musculoskeletal Knowledge Portal: Making Omics Data Useful to the Broader Scientific Community. Journal of Bone and Mineral Research, 2020, 35, 1626-1633.	2.8	25
32	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.	6.2	24
33	The Lipid Droplet Knowledge Portal: A resource for systematic analyses of lipid droplet biology. Developmental Cell, 2022, 57, 387-397.e4.	7.0	22
34	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.	8.6	21
35	Evaluating human genetic support for hypothesized metabolic disease genes. Cell Metabolism, 2022, 34, 661-666.	16.2	14
36	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. BMC Endocrine Disorders, 2016, 16, 7.	2.2	9

#	Article	lF	CITATIONS
37	Using multiple alignments to improve seeded local alignment algorithms. Nucleic Acids Research, 2005, 33, 4563-4577.	14.5	8
38	A glomerular transcriptomic landscape of apolipoprotein L1 in Black patients with focal segmental glomerulosclerosis. Kidney International, 2021, , .	5.2	8
39	Data-driven type 2 diabetes patient clusters predict metabolic surgery outcomes. Lancet Diabetes and Endocrinology,the, 2022, , .	11.4	1
40	An Open-Access Platform for Translating Diabetes and Cardiometabolic Disease Genetics Into Accessible Knowledge. Journal of the Endocrine Society, 2021, 5, A406-A406.	0.2	0
41	Abstract TP161: The Cerebrovascular Disease Knowledge Portal: an Open Access Data Resource to Accelerate Genomic Discoveries in Stroke. Stroke, 2018, 49, .	2.0	O
42	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, .	0.2	0