Michael L Stitzel

List of Publications by Year
in descending order

39 papers	4,139 citations	304743 22 h-index	302126 39 g-index
55 all docs	55 docs citations	55 times ranked	8916 citing authors

#	Article	IF	Citations
1	Single Cell Analysis of Blood Mononuclear Cells Stimulated Through Either LPS or Anti-CD3 and Anti-CD28. Frontiers in Immunology, 2021, 12, 636720.	4.8	32
2	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. Diabetes, 2021, 70, 1581-1591.	0.6	7
3	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCRâ€“FlowFISH. Nature Genetics, 2021, 53, 1166-1176.	21.4	36
4	Tet2 Controls the Responses of Î² cells to Inflammation in Autoimmune Diabetes. Nature Communications, 2021, 12, 5074.	12.8	11
5	AMULET: a novel read count-based method for effective multiplet detection from single nucleus ATAC-seq data. Genome Biology, 2021, 22, 252.	8.8	36
6	Functional characterization of T2D-associated SNP effects on baseline and ER stress-responsive Î² cell transcriptional activation. Nature Communications, 2021, 12, 5242.	12.8	13
7	A new graph-based clustering method with application to single-cell RNA-seq data from human pancreatic islets. NAR Genomics and Bioinformatics, 2021, 3, lqaa087.	3.2	2
8	CoRE-ATAC: A deep learning model for the functional classification of regulatory elements from single cell and bulk ATAC-seq data. PLoS Computational Biology, 2021, 17, e1009670.	3.2	7
9	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	12.8	89
10	From GWAS Association to Function. Circulation Research, 2020, 126, 347-349.	4.5	3
11	(Epi)genomic heterogeneity of pancreatic islet function and failure in type 2 diabetes. Molecular Metabolism, 2019, 27, S15-S24.	6.5	12
12	Cell Specificity of Human Regulatory Annotations and Their Genetic Effects on Gene Expression. Genetics, 2019, 211, 549-562.	2.9	16
13	BiFET: sequencing <u>Bi</u>as-free transcription factor <u>F</u>ootprint <u>E</u>nrichment <u>T</u>est. Nucleic Acids Research, 2019, 47, e11-e11.	14.5	9
14	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic Î² Cell Identity and Function. Cell Reports, 2019, 26, 788-801.e6.	6.4	68
15	Two-phase differential expression analysis for single cell RNA-seq. Bioinformatics, 2018, 34, 3340-3348.	4.1	34
16	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	6.2	47
17	A neural network based model effectively predicts enhancers from clinical ATAC-seq samples. Scientific Reports, 2018, 8, 16048.	3.3	23
18	Type 2 Diabetesâ€“Associated Genetic Variants Regulate Chromatin Accessibility in Human Islets. Diabetes, 2018, 67, 2466-2477.	0.6	44

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19	Genomics of Islet (Dys)function and Type 2 Diabetes. Trends in Genetics, 2017, 33, 244-255.	6.7	55
20	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	7.1	189
21	The chromatin accessibility signature of human immune aging stems from CD8+ T cells. Journal of Experimental Medicine, 2017, 214, 3123-3144.	8.5	150
22	Alpha TC1 and Beta-TC-6 genomic profiling uncovers both shared and distinct transcriptional regulatory features with their primary islet counterparts. Scientific Reports, 2017, 7, 11959.	3.3	41
23	A Type 2 Diabetesâ€“Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. Diabetes, 2017, 66, 2521-2530.	0.6	54
24	Single-cell transcriptomes identify human islet cell signatures and reveal cell-typeâ€“specific expression changes in type 2 diabetes. Genome Research, 2017, 27, 208-222.	5.5	440
25	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
26	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
27	QuIN: A Web Server for Querying and Visualizing Chromatin Interaction Networks. PLoS Computational Biology, 2016, 12, e1004809.	3.2	10
28	Computational inference of H3K4me3 and H3K27ac domain length. PeerJ, 2016, 4, e1750.	2.0	7
29	Transcriptional Regulation of the Pancreatic Islet: Implications for Islet Function. Current Diabetes Reports, 2015, 15, 66.	4.2	11
30	A Common Functional Regulatory Variant at a Type 2 Diabetes Locus Upregulates ARAP1 Expression in the Pancreatic Beta Cell. American Journal of Human Genetics, 2014, 94, 186-197.	6.2	67
31	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
32	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	7.1	147
33	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17921-17926.	7.1	606
34	Autosomal Dominant Diabetes Arising From a Wolfram Syndrome 1 Mutation. Diabetes, 2013, 62, 3943-3950.	0.6	100
35	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	16.2	190
36	Regulation of the Oocyte-to-Zygote Transition. Science, 2007, 316, 407-408.	12.6	235

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37	Regulation of MBK-2/Dyrk Kinase by Dynamic Cortical Anchoring during the Oocyte-to-Zygote Transition. Current Biology, 2007, 17, 1545-1554.	3.9	58
38	The C. elegans DYRK Kinase MBK-2 Marks Oocyte Proteins for Degradation in Response to Meiotic Maturation. Current Biology, 2006, 16, 56-62.	3.9	102
39	Targeted Disruption of the Methionine Synthase Gene in Mice. Molecular and Cellular Biology, 2001, 21, 1058-1065.	2.3	145