Jonathan Schug

List of Publications by Year
in descending order

41 papers	2,711 citations	201575 27 h-index	276775 41 g-index
42 all docs	42 docs citations	42 times ranked	5131 citing authors

#	Article	IF	Citations
1	Single-Cell Transcriptomics of the Human Endocrine Pancreas. Diabetes, 2016, 65, 3028-3038.	0.3	346
2	Epigenetic Regulation of the DLK1-MEG3 MicroRNA Cluster in Human Type 2 Diabetic Islets. Cell Metabolism, 2014, 19, 135-145.	7.2	304
3	Integration of ATAC-seq and RNA-seq identifies human alpha cell and beta cell signature genes. Molecular Metabolism, 2016, 5, 233-244.	3.0	233
4	Aging-Dependent Demethylation of Regulatory Elements Correlates with Chromatin State and Improved Î² Cell Function. Cell Metabolism, 2015, 22, 619-632.	7.2	172
5	Multiplexed In Situ Imaging Mass Cytometry Analysis of the Human Endocrine Pancreas and Immune System in Type 1 Diabetes. Cell Metabolism, 2019, 29, 769-783.e4.	7.2	151
6	Single-Cell Mass Cytometry Analysis of the Human Endocrine Pancreas. Cell Metabolism, 2016, 24, 616-626.	7.2	126
7	Genome-Wide Alteration of Histone H3K9 Acetylation Pattern in Mouse Offspring Prenatally Exposed to Arsenic. PLoS ONE, 2013, 8, e53478.	1.1	85
8	Genome-wide approaches reveal EGR1-controlled regulatory networks associated with neurodegeneration. Neurobiology of Disease, 2014, 63, 107-114.	2.1	70
9	Effect of high fat diet on phenotype, brain transcriptome and lipidome in Alzheimerâ€™s model mice. Scientific Reports, 2017, 7, 4307.	1.6	69
10	Islet-1 Is Essential for Pancreatic Î²-Cell Function. Diabetes, 2014, 63, 4206-4217.	0.3	67
11	Single-cell transcriptomics of human islet ontogeny defines the molecular basis of Î²-cell dedifferentiation in T2D. Molecular Metabolism, 2020, 42, 101057.	3.0	63
12	The next generation of target capture technologies - large DNA fragment enrichment and sequencing determines regional genomic variation of high complexity. BMC Genomics, 2016, 17, 486.	1.2	61
13	Dnmt1 is essential to maintain progenitors in the perinatal intestinal epithelium. Development (Cambridge), 2015, 142, 2163-2172.	1.2	60
14	Dynamic recruitment of microRNAs to their mRNA targets in the regenerating liver. BMC Genomics, 2013, 14, 264.	1.2	59
15	A comparison of Illumina and Ion Torrent sequencing platforms in the context of differential gene expression. BMC Genomics, 2017, 18, 602.	1.2	57
16	Genome-wide Identification of Structure-Forming Repeats as Principal Sites of Fork Collapse upon ATR Inhibition. Molecular Cell, 2018, 72, 222-238.e11.	4.5	55
17	Paternal Exercise Improves the Metabolic Health of Offspring via Epigenetic Modulation of the Germline. International Journal of Molecular Sciences, 2022, 23, 1.	1.8	53
18	Bexarotene-Activated Retinoid X Receptors Regulate Neuronal Differentiation and Dendritic Complexity. Journal of Neuroscience, 2015, 35, 11862-11876.	1.7	52

#	Article	IF	Citations
19	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. Nature Metabolism, 2022, 4, 284-299.	5.1	52
20	A miRNA181a/NFAT5 axis links impaired T cell tolerance induction with autoimmune type 1 diabetes. Science Translational Medicine, 2018, 10, .	5.8	49
21	miRNA142-3p targets Tet2 and impairs Treg differentiation and stability in models of type 1 diabetes. Nature Communications, 2019, 10, 5697.	5.8	48
22	Sleeve Gastrectomy Improves Glycemia Independent of Weight Loss by Restoring Hepatic Insulin Sensitivity. Diabetes, 2018, 67, 1079-1085.	0.3	42
23	APOE2 orchestrated differences in transcriptomic and lipidomic profiles of postmortem AD brain. Alzheimer's Research and Therapy, 2019, 11, 113.	3.0	42
24	Gene co-expression networks identify Trem2 and Tyrobp as major hubs in human APOE expressing mice following traumatic brain injury. Neurobiology of Disease, 2017, 105, 1-14.	2.1	39
25	RXR controlled regulatory networks identified in mouse brain counteract deleterious effects of AÎ² oligomers. Scientific Reports, 2016, 6, 24048.	1.6	37
26	Functional and Metabolomic Consequences of KATP Channel Inactivation in Human Islets. Diabetes, 2017, 66, 1901-1913.	0.3	35
27	Reprogramming human gallbladder cells into insulin-producing Î²-like cells. PLoS ONE, 2017, 12, e0181812.	1.1	35
28	A negative reciprocal regulatory axis between cyclin D1 and HNF4Î± modulates cell cycle progression and metabolism in the liver. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17177-17186.	3.3	34
29	Single-cell analysis of the human pancreas in type 2 diabetes using multi-spectral imaging mass cytometry. Cell Reports, 2021, 37, 109919.	2.9	33
30	FoxA-dependent demethylation of DNA initiates epigenetic memory of cellular identity. Developmental Cell, 2021, 56, 602-612.e4.	3.1	30
31	Defiant: (DMRs: easy, fast, identification and ANnoTation) identifies differentially Methylated regions from iron-deficient rat hippocampus. BMC Bioinformatics, 2018, 19, 31.	1.2	29
32	RNA-sequencing reveals transcriptional up-regulation of Trem2 in response to bexarotene treatment. Neurobiology of Disease, 2015, 82, 132-140.	2.1	27
33	Integrated approach reveals diet, APOE genotype and sex affect immune response in APP mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 152-161.	1.8	23
34	Highly Multiplexed Image Analysis of Intestinal Tissue Sections in Patients With Inflammatory Bowel Disease. Gastroenterology, 2021, 161, 1940-1952.	0.6	18
35	Two novel type 2 diabetes loci revealed through integration of TCF7L2 DNA occupancy and SNP association data. BMJ Open Diabetes Research and Care, 2014, 2, e000052.	1.2	17
36	Highly multiplexed 2-dimensional imaging mass cytometry analysis of HBV-infected liver. JCI Insight, 2021, 6, .	2.3	15

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37	A High-Content Screen Identifies MicroRNAs That Regulate Liver Repopulation After Injury in Mice. Gastroenterology, 2020, 158, 1044-1057.e17.	0.6	8
38	A LAMP sequencing approach for high-throughput co-detection of SARS-CoV-2 and influenza virus in human saliva. ELife, 2022, 11, .	2.8	6
39	Evaluating whole-genome expression differences in idiopathic and diabetic adhesive capsulitis. Journal of Shoulder and Elbow Surgery, 2022, 31, e1-e13.	1.2	4
40	ChIP-Seq: Library Preparation and Sequencing. Methods in Molecular Biology, 2016, 1402, 101-117.	0.4	3
41	CAMPAREE: a robust and configurable RNA expression simulator. BMC Genomics, 2021, 22, 692.	1.2	2