

Lukas M Simon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/549812/publications.pdf>

Version: 2024-02-01

33
papers

4,764
citations

394286

19
h-index

434063

31
g-index

43
all docs

43
docs citations

43
times ranked

9459
citing authors

#	ARTICLE	IF	CITATIONS
1	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , 2019, 20, 59.	3.8	911
2	Single-cell RNA-seq denoising using a deep count autoencoder. <i>Nature Communications</i> , 2019, 10, 390.	5.8	668
3	A cellular census of human lungs identifies novel cell states in health and in asthma. <i>Nature Medicine</i> , 2019, 25, 1153-1163.	15.2	631
4	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , 2019, 10, 963.	5.8	408
5	The spliceosome is a therapeutic vulnerability in MYC-driven cancer. <i>Nature</i> , 2015, 525, 384-388.	13.7	392
6	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. <i>Nature Communications</i> , 2020, 11, 3559.	5.8	378
7	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 31-41.	1.4	178
8	Single cells make big data: New challenges and opportunities in transcriptomics. <i>Current Opinion in Systems Biology</i> , 2017, 4, 85-91.	1.3	171
9	IRE1 α -XBP1s pathway promotes prostate cancer by activating c-MYC signaling. <i>Nature Communications</i> , 2019, 10, 323.	5.8	158
10	EMT cells increase breast cancer metastasis via paracrine Gli activation in neighbouring tumour cells. <i>Nature Communications</i> , 2017, 8, 15773.	5.8	126
11	A paradox of transcriptional and functional innate interferon responses of human intestinal enteroids to enteric virus infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E570-E579.	3.3	112
12	Common variants in the human platelet PAR4 thrombin receptor alter platelet function and differ by race. <i>Blood</i> , 2014, 124, 3450-3458.	0.6	107
13	Spliceosome-targeted therapies trigger an antiviral immune response in triple-negative breast cancer. <i>Cell</i> , 2021, 184, 384-403.e21.	13.5	94
14	CELF1 is a central node in post-transcriptional regulatory programmes underlying EMT. <i>Nature Communications</i> , 2016, 7, 13362.	5.8	53
15	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. <i>EMBO Molecular Medicine</i> , 2021, 13, e12871.	3.3	53
16	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. <i>Cell Reports</i> , 2020, 33, 108552.	2.9	50
17	Targeting the Mevalonate Pathway to Overcome Acquired Anti-HER2 Treatment Resistance in Breast Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 2318-2330.	1.5	41
18	Longitudinal RNA-Seq Analysis of the Repeatability of Gene Expression and Splicing in Human Platelets Identifies a Platelet <i>SELP</i> Splice QTL. <i>Circulation Research</i> , 2020, 126, 501-516.	2.0	39

#	ARTICLE	IF	CITATIONS
19	Integrative Multi-omic Analysis of Human Platelet eQTLs Reveals Alternative Start Site in Mitofusin 2. <i>American Journal of Human Genetics</i> , 2016, 98, 883-897.	2.6	27
20	MetaMap: an atlas of metatranscriptomic reads in human disease-related RNA-seq data. <i>GigaScience</i> , 2018, 7, .	3.3	22
21	Integration of millions of transcriptomes using batch-aware triplet neural networks. <i>Nature Machine Intelligence</i> , 2021, 3, 705-715.	8.3	19
22	Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches. <i>Genes</i> , 2021, 12, 635.	1.0	13
23	Identification of a Racially Dimorphic Variant in the Human Platelet PAR4 Thrombin Receptor Altering Platelet Function and Pharmacologic Inhibition. <i>Blood</i> , 2014, 124, 1434-1434.	0.6	11
24	<i>deCS</i> : A Tool for Systematic Cell Type Annotations of Single-Cell RNA Sequencing Data Among Human Tissues. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 370-384.	3.0	11
25	Effects of genetic variation in protease activated receptor 4 after an acute coronary syndrome: Analysis from the TRACER trial. <i>Blood Cells, Molecules, and Diseases</i> , 2018, 72, 37-43.	0.6	10
26	DrivAER: Identification of driving transcriptional programs in single-cell RNA sequencing data. <i>GigaScience</i> , 2020, 9, .	3.3	10
27	Gene expression imputation and cell-type deconvolution in human brain with spatiotemporal precision and its implications for brain-related disorders. <i>Genome Research</i> , 2021, 31, 146-158.	2.4	10
28	EmptyNN: A neural network based on positive and unlabeled learning to remove cell-free droplets and recover lost cells in scRNA-seq data. <i>Patterns</i> , 2021, 2, 100311.	3.1	9
29	Identification of the Genetic Mechanism Responsible for Racially-Dimorphic Expression of the Thrombin-Receptor Regulator, Pctp. <i>Blood</i> , 2015, 126, 415-415.	0.6	7
30	A Large Cluster of Micrnas At 14q32 Defines an RNA Expression Module That Accounts for Racial Differences in Protease Activated Receptor 4-Mediated Platelet Reactivity. <i>Blood</i> , 2012, 120, 380-380.	0.6	1
31	Racial Differences In Thrombin-Induced Human Platelet PAR4 Reactivity. <i>Blood</i> , 2013, 122, 1054-1054.	0.6	0
32	Effect Of Age and Gender On Human Platelet mRNA and Micro-RNA Levels. <i>Blood</i> , 2013, 122, 3518-3518.	0.6	0
33	Abstract 015: PAR4 Ala120Thr Variant Alters PAR4 Desensitization, Sensitivity to Platelet Antagonists and Risk of Large Vessel Stroke. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, .	1.1	0