Nathan Salomonis

List of Publications by Year
in descending order

97 papers	5,762 citations	94433 37 h-index	91884 69 g-index
116 all docs	116 docs citations	116 times ranked	11274 citing authors

#	Article	IF	Citations
1	LAMP-5 is an essential inflammatory-signaling regulator and novel immunotherapy target for mixed lineage leukemia-rearranged acute leukemia. Haematologica, 2022, 107, 803-815.	3.5	9
2	Ontogeny and function of the circadian clock in intestinal organoids. EMBO Journal, 2022, 41, e106973.	7.8	24
3	Induced cell-autonomous neutropenia systemically perturbs hematopoiesis in Cebpa enhancer-null mice. Blood Advances, 2022, 6, 1406-1419.	5.2	2
4	A census of the lung: CellCards from LungMAP. Developmental Cell, 2022, 57, 112-145.e2.	7.0	67
5	Inflammatory blockade prevents injury to the developing pulmonary gas exchange surface in preterm primates. Science Translational Medicine, 2022, 14, eabl8574.	12.4	10
6	A potent myeloid response is rapidly activated in the lungs of premature Rhesus macaques exposed to intra-uterine inflammation. Mucosal Immunology, 2022, 15, 730-744.	6.0	2
7	The balance between protective and pathogenic immune responses to pneumonia in the neonatal lung is enforced by gut microbiota. Science Translational Medicine, 2022, 14, .	12.4	17
8	Cannabidiol Treatment Results in a Common Gene Expression Response Across Aggressive Cancer Cells from Various Origins. Cannabis and Cannabinoid Research, 2021, 6, 148-155.	2.9	11
9	Monocyte and bone marrow macrophage transcriptional phenotypes in systemic juvenile idiopathic arthritis reveal TRIM8 as a mediator of IFN-Î³ hyper-responsiveness and risk for macrophage activation syndrome. Annals of the Rheumatic Diseases, 2021, 80, 617-625.	0.9	31
10	Differential transcriptome response to proton versus X-ray radiation reveals novel candidate targets for combinatorial PT therapy in lymphoma. Radiotherapy and Oncology, 2021, 155, 293-303.	0.6	5
11	In situ mapping identifies distinct vascular niches for myelopoiesis. Nature, 2021, 590, 457-462.	27.8	74
12	Short-term exposure to intermittent hypoxia leads to changes in gene expression seen in chronic pulmonary disease. ELife, 2021, 10, .	6.0	22
13	The Rhesus Macaque Serves As a Model for Human Lateral Branch Nephrogenesis. Journal of the American Society of Nephrology: JASN, 2021, 32, 1097-1112.	6.1	12
14	Coupled analysis of transcriptome and BCR mutations reveals role of OXPHOS in affinity maturation. Nature Immunology, 2021, 22, 904-913.	14.5	62
15	Pseudocell Tracerâ€"A method for inferring dynamic trajectories using scRNAseq and its application to B cells undergoing immunoglobulin class switch recombination. PLoS Computational Biology, 2021, 17, e1008094.	3.2	5
16	PKM2-dependent metabolic skewing of hepatic Th17 cells regulates pathogenesis of non-alcoholic fatty liver disease. Cell Metabolism, 2021, 33, 1187-1204.e9.	16.2	60
17	DeepImmuno: deep learning-empowered prediction and generation of immunogenic peptides for T-cell immunity. Briefings in Bioinformatics, 2021, 22, .	6.5	48
18	Prevalence of Homologous Recombination Pathway Gene Mutations in Melanoma: Rationale for a New Targeted Therapeutic Approach. Journal of Investigative Dermatology, 2021, 141, 2028-2036.e2.	0.7	17

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19	IFN-Î³ is essential for alveolar macrophageâ€“driven pulmonary inflammation in macrophage activation syndrome. JCI Insight, 2021, 6, .	5.0	18
20	Gain-of-function cardiomyopathic mutations in RBM20 rewire splicing regulation and re-distribute ribonucleoprotein granules within processing bodies. Nature Communications, 2021, 12, 6324.	12.8	23
21	Progenitor translatome changes coordinated by Tsc1 increase perception of Wnt signals to end nephrogenesis. Nature Communications, 2021, 12, 6332.	12.8	10
22	Divisional Memory Drives Hematopoietic Stem Cell Functional Diversity. Blood, 2021, 138, 20-20.	1.4	0
23	GM-CSF Programs Hematopoietic Stem and Progenitor Cells During Candida albicans Vaccination for Protection Against Reinfection. Frontiers in Immunology, 2021, 12, 790309.	4.8	5
24	Unraveling bone marrow architecture. Nature Cell Biology, 2020, 22, 5-6.	10.3	7
25	FOXO activity adaptation safeguards the hematopoietic stem cell compartment in hyperglycemia. Blood Advances, 2020, 4, 5512-5526.	5.2	7
26	Single-nucleus RNA-seq identifies transcriptional heterogeneity in multinucleated skeletal myofibers. Nature Communications, 2020, 11, 6374.	12.8	187
27	Protocol for Identification and Removal of Doublets with DoubletDecon. STAR Protocols, 2020, 1, 100085.	1.2	6
28	MBNL1 regulates essential alternative RNA splicing patterns in MLL-rearranged leukemia. Nature Communications, 2020, 11, 2369.	12.8	40
29	Combinatorial Single-Cell Analyses of Granulocyte-Monocyte Progenitor Heterogeneity Reveals an Early Uni-potent Neutrophil Progenitor. Immunity, 2020, 53, 303-318.e5.	14.3	153
30	Resolving single-cell heterogeneity from hundreds of thousands of cells through sequential hybrid clustering and NMF. Bioinformatics, 2020, 36, 3773-3780.	4.1	42
31	Pbx4 limits heart size and fosters arch artery formation through partitioning second heart field progenitors and restricting proliferation. Development (Cambridge), 2020, 147, .	2.5	10
32	Asymmetrically Segregated Mitochondria Provide Cellular Memory of Hematopoietic Stem Cell Replicative History and Drive HSC Attrition. Cell Stem Cell, 2020, 26, 420-430.e6.	11.1	108
33	PHIP drives glioblastoma motility and invasion by regulating the focal adhesion complex. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9064-9073.	7.1	27
34	Mouse models of neutropenia reveal progenitor-stage-specific defects. Nature, 2020, 582, 109-114.	27.8	79
35	In Situ Fate Mapping of Native and Stress Myelopoiesis Reveals a Unique Niche for Mono- and Dendritic Cell -Poiesis. Blood, 2020, 136, 38-39.	1.4	0
36	DoubletDecon: Deconvoluting Doublets from Single-Cell RNA-Sequencing Data. Cell Reports, 2019, 29, 1718-1727.e8.	6.4	134

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37	cellHarmony: cell-level matching and holistic comparison of single-cell transcriptomes. Nucleic Acids Research, 2019, 47, e138-e138.	14.5	57
38	Investigating Cell Fate Decisions with ICGS Analysis of Single Cells. Methods in Molecular Biology, 2019, 1975, 251-275.	0.9	3
39	Aging Human Hematopoietic Stem Cells Manifest Profound Epigenetic Reprogramming of Enhancers That May Predispose to Leukemia. Cancer Discovery, 2019, 9, 1080-1101.	9.4	119
40	U2AF1 mutations induce oncogenic IRAK4 isoforms and activate innate immune pathways in myeloid malignancies. Nature Cell Biology, 2019, 21, 640-650.	10.3	165
41	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
42	Maturation of heart valve cell populations during postnatal remodeling. Development (Cambridge), 2019, 146, .	2.5	78
43	Rational targeting Cdc42 restrains Th2 cell differentiation and prevents allergic airway inflammation. Clinical and Experimental Allergy, 2019, 49, 92-107.	2.9	28
44	Cxcr3-expressing leukocytes are necessary for neurofibroma formation in mice. JCI Insight, 2019, 4, .	5.0	21
45	Autism-Associated Chromatin Remodeler CHD8 Governs the Survival and Differentiation of Hematopoietic Stem/Progenitor Cells. Blood, 2019, 134, 1191-1191.	1.4	0
46	The Molecular Basis of Long First Remissions in Normal Karyotype AML Patients. Blood, 2019, 134, 3827-3827.	1.4	0
47	Transcription factors operate across disease loci, with EBNA2 implicated in autoimmunity. Nature Genetics, 2018, 50, 699-707.	21.4	286
48	Synthetic Gene Network with Positive Feedback Loop Amplifies Cellulase Gene Expression in Neurospora crassa. ACS Synthetic Biology, 2018, 7, 1395-1405.	3.8	12
49	TRAF6 Mediates Basal Activation of NF-ÎºB Necessary for Hematopoietic Stem Cell Homeostasis. Cell Reports, 2018, 22, 1250-1262.	6.4	62
50	Obesity alters the long-term fitness of the hematopoietic stem cell compartment through modulation of Gfi1 expression. Journal of Experimental Medicine, 2018, 215, 627-644.	8.5	62
51	Cross-platform single cell analysis of kidney development shows stromal cells express Gdnf. Developmental Biology, 2018, 434, 36-47.	2.0	88
52	The Molecular Signature of Megakaryocyte-Erythroid Progenitors Reveals a Role for the Cell Cycle in Fate Specification. Cell Reports, 2018, 25, 2083-2093.e4.	6.4	64
53	Defining human cardiac transcription factor hierarchies using integrated single-cell heterogeneity analysis. Nature Communications, 2018, 9, 4906.	12.8	147
54	SKI controls MDS-associated chronic TGF-Î² signaling, aberrant splicing, and stem cell fitness. Blood, 2018, 132, e24-e34.	1.4	21

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55	The Human Cell Atlas bone marrow single-cell interactive web portal. Experimental Hematology, 2018, 68, 51-61.	0.4	168
56	miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. Journal of Experimental Medicine, 2018, 215, 2115-2136.	8.5	20
57	Pathobiological Pseudohypoxia as a Putative Mechanism Underlying Myelodysplastic Syndromes. Cancer Discovery, 2018, 8, 1438-1457.	9.4	38
58	PHIP as a therapeutic target for driver-negative subtypes of melanoma, breast, and lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5766-E5775.	7.1	17
59	IL-1 signaling mediates intrauterine inflammation and chorio-decidua neutrophil recruitment and activation. JCI Insight, 2018, 3, .	5.0	86
60	A Prognostic Human Splicing Signature That Precurses Leukemia. Blood, 2018, 132, 877-877.	1.4	2
61	MLL-Fusion Leukemia Dependence on MBNL1 Is Associated with Alternative Splicing of Oncogenic Proteins. Blood, 2018, 132, 3883-3883.	1.4	0
62	SKI Controls MDS-Associated Chronic TGFb Signaling, Aberrant Splicing, and Stem Cell Fitness. Blood, 2018, 132, 4350-4350.	1.4	0
63	The Erythro-Myeloblastic Island (EMBI): A Hematopoietic Niche Balancing Erythropoiesis and Myelopoiesis. Blood, 2018, 132, 842-842.	1.4	0
64	Neutropenia-Associated Mutations Differentially Impact Developmental Cell-States. Blood, 2018, 132, 18-18.	1.4	0
65	Molecular Signature of Megakaryocyte-Erythroid Progenitors Reveals Role of Cell Cycle in Fate Specification. Blood, 2018, 132, 3828-3828.	1.4	0
66	Molecular Characterization of Pediatric Restrictive Cardiomyopathy from Integrative Genomics. Scientific Reports, 2017, 7, 39276.	3.3	19
67	KIF3A genetic variation is associated with pediatric asthma in the presence of eczema independent of allergic rhinitis. Journal of Allergy and Clinical Immunology, 2017, 140, 595-598.e5.	2.9	18
68	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. Scientific Data, 2017, 4, 170030.	5.3	48
69	Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods. Nature Biomedical Engineering, 2017, 1, 826-837.	22.5	38
70	Integrative Analysis of Proteomics Data to Obtain Clinically Relevant Markers. Methods in Molecular Biology, 2017, 1788, 89-111.	0.9	1
71	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. Immunity, 2017, 47, 890-902.e4.	14.3	297
72	An Unbiased High-Throughput Screen to Identify Novel Effectors That Impact on Cardiomyocyte Aggregate Levels. Circulation Research, 2017, 121, 604-616.	4.5	13

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73	Loaded, locked, drawn: kSORT validated for patient samples. Nature Reviews Nephrology, 2017, 13, 60-60.	9.6	2
74	Splicesome Mutant MDS and AML Cells Activate Innate Immune Signaling By Regulating the Expression of Therapeutically Targetable IRAK4 Isoforms. Blood, 2017, 130, 785-785.	1.4	0
75	Integrative Epigenetic and Single-Cell RNA-Seq Profiling of Human Hematopoietic Stem Cells Reveals Epigenetic Reprogramming of Enhancer and Regulatory Elements during Normal Aging. Blood, 2017, 130, 770-770.	1.4	0
76	Mitochondrial Morphology Controls Hematopoietic Stem Cell Self-Renewal and Confers Them Divisional Memory. Blood, 2017, 130, 633-633.	1.4	1
77	DNMT3A Haploinsufficiency Transforms FLT3ITD Myeloproliferative Disease into a Rapid, Spontaneous, and Fully Penetrant Acute Myeloid Leukemia. Cancer Discovery, 2016, 6, 501-515.	9.4	73
78	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. Stem Cell Reports, 2016, 7, 110-125.	4.8	101
79	Single-cell analysis of mixed-lineage states leading to a binary cell fate choice. Nature, 2016, 537, 698-702.	27.8	444
80	Systems biology evaluation of cell-free amniotic fluid transcriptome of term and preterm infants to detect fetal maturity. BMC Medical Genomics, 2015, 8, 67.	1.5	25
81	MBNL1-mediated regulation of differentiation RNAs promotes myofibroblast transformation and the fibrotic response. Nature Communications, 2015, 6, 10084.	12.8	72
82	Analyzing alternative splicing data of splice junction arrays from Parkinson patients' leukocytes before and after deep brain stimulation as compared with control donors. Genomics Data, 2015, 5, 340-343.	1.3	9
83	Intrinsic Age-Dependent Changes and Cell-Cell Contacts Regulate Nephron Progenitor Lifespan. Developmental Cell, 2015, 35, 49-62.	7.0	88
84	Whole transcriptome RNA sequencing data from blood leukocytes derived from Parkinson's disease patients prior to and following deep brain stimulation treatment. Genomics Data, 2015, 3, 57-60.	1.3	35
85	Long-Lasting Dysregulation of the Hematopoietic Stem Cell Compartment in Obesity. Blood, 2015, 126, 245-245.	1.4	0
86	Single Cell RNA seq for Analysis of Cell Fate Decisions. Blood, 2015, 126, SCI-20-SCI-20.	1.4	0
87	The kSORT Assay to Detect Renal Transplant Patients at High Risk for Acute Rejection: Results of the Multicenter AART Study. PLoS Medicine, 2014, 11, e1001759.	8.4	153
88	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. PLoS Computational Biology, 2014, 10, e1003517.	3.2	167
89	Systems-level perspective of sudden infant death syndrome. Pediatric Research, 2014, 76, 220-229.	2.3	10
90	Alternative Splicing of MBD2 Supports Self-Renewal in Human Pluripotent Stem Cells. Cell Stem Cell, 2014, 15, 92-101.	11.1	93

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91	MAAMD: a workflow to standardize meta-analyses and comparison of affymetrix microarray data. BMC Bioinformatics, 2014, 15, 69.	2.6	14
92	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 621-631.	3.8	73
93	A robust method to derive functional neural crest cells from human pluripotent stem cells. American Journal of Stem Cells, 2013, 2, 119-31.	0.4	83
94	GO-Elite: a flexible solution for pathway and ontology over-representation. Bioinformatics, 2012, 28, 2209-2210.	4.1	268
95	Alternative splicing regulates mouse embryonic stem cell pluripotency and differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10514-10519.	7.1	222
96	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. Nucleic Acids Research, 2010, 38, W755-W762.	14.5	310
97	Alternative Splicing in the Differentiation of Human Embryonic Stem Cells into Cardiac Precursors. PLoS Computational Biology, 2009, 5, e1000553.	3.2	86