

Nathan Salomonis

List of Publications by Year in descending order

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Version: 2024-02-01

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	Single-cell analysis of mixed-lineage states leading to a binary cell fate choice. <i>Nature</i> , 2016, 537, 698-702.	27.8	444
2	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762.	14.5	310
3	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. <i>Immunity</i> , 2017, 47, 890-902.e4.	14.3	297
4	Transcription factors operate across disease loci, with EBNA2 implicated in autoimmunity. <i>Nature Genetics</i> , 2018, 50, 699-707.	21.4	286
5	GO-Elite: a flexible solution for pathway and ontology over-representation. <i>Bioinformatics</i> , 2012, 28, 2209-2210.	4.1	268
6	Alternative splicing regulates mouse embryonic stem cell pluripotency and differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10514-10519.	7.1	222
7	Single-nucleus RNA-seq identifies transcriptional heterogeneity in multinucleated skeletal myofibers. <i>Nature Communications</i> , 2020, 11, 6374.	12.8	187
8	The Human Cell Atlas bone marrow single-cell interactive web portal. <i>Experimental Hematology</i> , 2018, 68, 51-61.	0.4	168
9	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003517.	3.2	167
10	U2AF1 mutations induce oncogenic IRAK4 isoforms and activate innate immune pathways in myeloid malignancies. <i>Nature Cell Biology</i> , 2019, 21, 640-650.	10.3	165
11	The kSORT Assay to Detect Renal Transplant Patients at High Risk for Acute Rejection: Results of the Multicenter AART Study. <i>PLoS Medicine</i> , 2014, 11, e1001759.	8.4	153
12	Combinatorial Single-Cell Analyses of Granulocyte-Monocyte Progenitor Heterogeneity Reveals an Early Uni-potent Neutrophil Progenitor. <i>Immunity</i> , 2020, 53, 303-318.e5.	14.3	153
13	Defining human cardiac transcription factor hierarchies using integrated single-cell heterogeneity analysis. <i>Nature Communications</i> , 2018, 9, 4906.	12.8	147
14	DoubletDecon: Deconvoluting Doublets from Single-Cell RNA-Sequencing Data. <i>Cell Reports</i> , 2019, 29, 1718-1727.e8.	6.4	134
15	Aging Human Hematopoietic Stem Cells Manifest Profound Epigenetic Reprogramming of Enhancers That May Predispose to Leukemia. <i>Cancer Discovery</i> , 2019, 9, 1080-1101.	9.4	119
16	Asymmetrically Segregated Mitochondria Provide Cellular Memory of Hematopoietic Stem Cell Replicative History and Drive HSC Attrition. <i>Cell Stem Cell</i> , 2020, 26, 420-430.e6.	11.1	108
17	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. <i>Stem Cell Reports</i> , 2016, 7, 110-125.	4.8	101
18	Alternative Splicing of MBD2 Supports Self-Renewal in Human Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 92-101.	11.1	93

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19	Intrinsic Age-Dependent Changes and Cell-Cell Contacts Regulate Nephron Progenitor Lifespan. <i>Developmental Cell</i> , 2015, 35, 49-62.	7.0	88
20	Cross-platform single cell analysis of kidney development shows stromal cells express Gdnf. <i>Developmental Biology</i> , 2018, 434, 36-47.	2.0	88
21	Alternative Splicing in the Differentiation of Human Embryonic Stem Cells into Cardiac Precursors. <i>PLoS Computational Biology</i> , 2009, 5, e1000553.	3.2	86
22	IL-1 signaling mediates intrauterine inflammation and chorio-decidua neutrophil recruitment and activation. <i>JCI Insight</i> , 2018, 3, .	5.0	86
23	A robust method to derive functional neural crest cells from human pluripotent stem cells. <i>American Journal of Stem Cells</i> , 2013, 2, 119-31.	0.4	83
24	Mouse models of neutropenia reveal progenitor-stage-specific defects. <i>Nature</i> , 2020, 582, 109-114.	27.8	79
25	Maturation of heart valve cell populations during postnatal remodeling. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	78
26	In situ mapping identifies distinct vascular niches for myelopoiesis. <i>Nature</i> , 2021, 590, 457-462.	27.8	74
27	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 621-631.	3.8	73
28	DNMT3A Haploinsufficiency Transforms <i>FLT3</i> ITD Myeloproliferative Disease into a Rapid, Spontaneous, and Fully Penetrant Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2016, 6, 501-515.	9.4	73
29	MBNL1-mediated regulation of differentiation RNAs promotes myofibroblast transformation and the fibrotic response. <i>Nature Communications</i> , 2015, 6, 10084.	12.8	72
30	A census of the lung: CellCards from LungMAP. <i>Developmental Cell</i> , 2022, 57, 112-145.e2.	7.0	67
31	The Molecular Signature of Megakaryocyte-Erythroid Progenitors Reveals a Role for the Cell Cycle in Fate Specification. <i>Cell Reports</i> , 2018, 25, 2083-2093.e4.	6.4	64
32	TRAF6 Mediates Basal Activation of NF- κ B Necessary for Hematopoietic Stem Cell Homeostasis. <i>Cell Reports</i> , 2018, 22, 1250-1262.	6.4	62
33	Obesity alters the long-term fitness of the hematopoietic stem cell compartment through modulation of <i>Gfi1</i> expression. <i>Journal of Experimental Medicine</i> , 2018, 215, 627-644.	8.5	62
34	Coupled analysis of transcriptome and BCR mutations reveals role of OXPPOS in affinity maturation. <i>Nature Immunology</i> , 2021, 22, 904-913.	14.5	62
35	PKM2-dependent metabolic skewing of hepatic Th17 cells regulates pathogenesis of non-alcoholic fatty liver disease. <i>Cell Metabolism</i> , 2021, 33, 1187-1204.e9.	16.2	60
36	cellHarmony: cell-level matching and holistic comparison of single-cell transcriptomes. <i>Nucleic Acids Research</i> , 2019, 47, e138-e138.	14.5	57

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37	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
38	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. <i>Scientific Data</i> , 2017, 4, 170030.	5.3	48
39	DeepImmuno: deep learning-empowered prediction and generation of immunogenic peptides for T-cell immunity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	48
40	Resolving single-cell heterogeneity from hundreds of thousands of cells through sequential hybrid clustering and NMF. <i>Bioinformatics</i> , 2020, 36, 3773-3780.	4.1	42
41	MBNL1 regulates essential alternative RNA splicing patterns in MLL-rearranged leukemia. <i>Nature Communications</i> , 2020, 11, 2369.	12.8	40
42	Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods. <i>Nature Biomedical Engineering</i> , 2017, 1, 826-837.	22.5	38
43	Pathobiological Pseudohypoxia as a Putative Mechanism Underlying Myelodysplastic Syndromes. <i>Cancer Discovery</i> , 2018, 8, 1438-1457.	9.4	38
44	Whole transcriptome RNA sequencing data from blood leukocytes derived from Parkinson's disease patients prior to and following deep brain stimulation treatment. <i>Genomics Data</i> , 2015, 3, 57-60.	1.3	35
45	Monocyte and bone marrow macrophage transcriptional phenotypes in systemic juvenile idiopathic arthritis reveal TRIM8 as a mediator of IFN- β hyper-responsiveness and risk for macrophage activation syndrome. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 617-625.	0.9	31
46	Rational targeting Cdc42 restrains Th2 cell differentiation and prevents allergic airway inflammation. <i>Clinical and Experimental Allergy</i> , 2019, 49, 92-107.	2.9	28
47	PHIP drives glioblastoma motility and invasion by regulating the focal adhesion complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9064-9073.	7.1	27
48	Systems biology evaluation of cell-free amniotic fluid transcriptome of term and preterm infants to detect fetal maturity. <i>BMC Medical Genomics</i> , 2015, 8, 67.	1.5	25
49	Ontogeny and function of the circadian clock in intestinal organoids. <i>EMBO Journal</i> , 2022, 41, e106973.	7.8	24
50	Gain-of-function cardiomyopathic mutations in RBM20 rewire splicing regulation and re-distribute ribonucleoprotein granules within processing bodies. <i>Nature Communications</i> , 2021, 12, 6324.	12.8	23
51	Short-term exposure to intermittent hypoxia leads to changes in gene expression seen in chronic pulmonary disease. <i>ELife</i> , 2021, 10, .	6.0	22
52	SKI controls MDS-associated chronic TGF- β signaling, aberrant splicing, and stem cell fitness. <i>Blood</i> , 2018, 132, e24-e34.	1.4	21
53	Cxcr3-expressing leukocytes are necessary for neurofibroma formation in mice. <i>JCI Insight</i> , 2019, 4, .	5.0	21
54	miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. <i>Journal of Experimental Medicine</i> , 2018, 215, 2115-2136.	8.5	20

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55	Molecular Characterization of Pediatric Restrictive Cardiomyopathy from Integrative Genomics. <i>Scientific Reports</i> , 2017, 7, 39276.	3.3	19
56	KIF3A genetic variation is associated with pediatric asthma in the presence of eczema independent of allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 595-598.e5.	2.9	18
57	IFN- γ is essential for alveolar macrophage-driven pulmonary inflammation in macrophage activation syndrome. <i>JCI Insight</i> , 2021, 6, .	5.0	18
58	PHIP as a therapeutic target for driver-negative subtypes of melanoma, breast, and lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5766-E5775.	7.1	17
59	Prevalence of Homologous Recombination Pathway Gene Mutations in Melanoma: Rationale for a New Targeted Therapeutic Approach. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2028-2036.e2.	0.7	17
60	The balance between protective and pathogenic immune responses to pneumonia in the neonatal lung is enforced by gut microbiota. <i>Science Translational Medicine</i> , 2022, 14, .	12.4	17
61	MAAMD: a workflow to standardize meta-analyses and comparison of affymetrix microarray data. <i>BMC Bioinformatics</i> , 2014, 15, 69.	2.6	14
62	An Unbiased High-Throughput Screen to Identify Novel Effectors That Impact on Cardiomyocyte Aggregate Levels. <i>Circulation Research</i> , 2017, 121, 604-616.	4.5	13
63	Synthetic Gene Network with Positive Feedback Loop Amplifies Cellulase Gene Expression in <i>Neurospora crassa</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 1395-1405.	3.8	12
64	The Rhesus Macaque Serves As a Model for Human Lateral Branch Nephrogenesis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1097-1112.	6.1	12
65	Cannabidiol Treatment Results in a Common Gene Expression Response Across Aggressive Cancer Cells from Various Origins. <i>Cannabis and Cannabinoid Research</i> , 2021, 6, 148-155.	2.9	11
66	Systems-level perspective of sudden infant death syndrome. <i>Pediatric Research</i> , 2014, 76, 220-229.	2.3	10
67	Pbx4 limits heart size and fosters arch artery formation through partitioning second heart field progenitors and restricting proliferation. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	10
68	Progenitor transcriptome changes coordinated by Tsc1 increase perception of Wnt signals to end nephrogenesis. <i>Nature Communications</i> , 2021, 12, 6332.	12.8	10
69	Inflammatory blockade prevents injury to the developing pulmonary gas exchange surface in preterm primates. <i>Science Translational Medicine</i> , 2022, 14, eabl8574.	12.4	10
70	Analyzing alternative splicing data of splice junction arrays from Parkinson patients' leukocytes before and after deep brain stimulation as compared with control donors. <i>Genomics Data</i> , 2015, 5, 340-343.	1.3	9
71	LAMP-5 is an essential inflammatory-signaling regulator and novel immunotherapy target for mixed lineage leukemia-rearranged acute leukemia. <i>Haematologica</i> , 2022, 107, 803-815.	3.5	9
72	Unraveling bone marrow architecture. <i>Nature Cell Biology</i> , 2020, 22, 5-6.	10.3	7

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73	FOXO activity adaptation safeguards the hematopoietic stem cell compartment in hyperglycemia. <i>Blood Advances</i> , 2020, 4, 5512-5526.	5.2	7
74	Protocol for Identification and Removal of Doublets with DoubletDecon. <i>STAR Protocols</i> , 2020, 1, 100085.	1.2	6
75	Differential transcriptome response to proton versus X-ray radiation reveals novel candidate targets for combinatorial PT therapy in lymphoma. <i>Radiotherapy and Oncology</i> , 2021, 155, 293-303.	0.6	5
76	Pseudocell Tracer—A method for inferring dynamic trajectories using scRNAseq and its application to B cells undergoing immunoglobulin class switch recombination. <i>PLoS Computational Biology</i> , 2021, 17, e1008094.	3.2	5
77	GM-CSF Programs Hematopoietic Stem and Progenitor Cells During <i>Candida albicans</i> Vaccination for Protection Against Reinfection. <i>Frontiers in Immunology</i> , 2021, 12, 790309.	4.8	5
78	Investigating Cell Fate Decisions with ICGS Analysis of Single Cells. <i>Methods in Molecular Biology</i> , 2019, 1975, 251-275.	0.9	3
79	Loaded, locked, drawn: kSORT validated for patient samples. <i>Nature Reviews Nephrology</i> , 2017, 13, 60-60.	9.6	2
80	A Prognostic Human Splicing Signature That Precurses Leukemia. <i>Blood</i> , 2018, 132, 877-877.	1.4	2
81	Induced cell-autonomous neutropenia systemically perturbs hematopoiesis in <i>Cebpa</i> enhancer-null mice. <i>Blood Advances</i> , 2022, 6, 1406-1419.	5.2	2
82	A potent myeloid response is rapidly activated in the lungs of premature Rhesus macaques exposed to intra-uterine inflammation. <i>Mucosal Immunology</i> , 2022, 15, 730-744.	6.0	2
83	Integrative Analysis of Proteomics Data to Obtain Clinically Relevant Markers. <i>Methods in Molecular Biology</i> , 2017, 1788, 89-111.	0.9	1
84	Mitochondrial Morphology Controls Hematopoietic Stem Cell Self-Renewal and Confers Them Divisional Memory. <i>Blood</i> , 2017, 130, 633-633.	1.4	1
85	Long-Lasting Dysregulation of the Hematopoietic Stem Cell Compartment in Obesity. <i>Blood</i> , 2015, 126, 245-245.	1.4	0
86	Single Cell RNA seq for Analysis of Cell Fate Decisions. <i>Blood</i> , 2015, 126, SCI-20-SCI-20.	1.4	0
87	Spliceosome Mutant MDS and AML Cells Activate Innate Immune Signaling By Regulating the Expression of Therapeutically Targetable IRAK4 Isoforms. <i>Blood</i> , 2017, 130, 785-785.	1.4	0
88	Integrative Epigenetic and Single-Cell RNA-Seq Profiling of Human Hematopoietic Stem Cells Reveals Epigenetic Reprogramming of Enhancer and Regulatory Elements during Normal Aging. <i>Blood</i> , 2017, 130, 770-770.	1.4	0
89	MLL-Fusion Leukemia Dependence on MBNL1 Is Associated with Alternative Splicing of Oncogenic Proteins. <i>Blood</i> , 2018, 132, 3883-3883.	1.4	0
90	SKI Controls MDS-Associated Chronic TGF β Signaling, Aberrant Splicing, and Stem Cell Fitness. <i>Blood</i> , 2018, 132, 4350-4350.	1.4	0

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91	The Erythro-Myeloblastic Island (EMBI): A Hematopoietic Niche Balancing Erythropoiesis and Myelopoiesis. Blood, 2018, 132, 842-842.	1.4	0
92	Neutropenia-Associated Mutations Differentially Impact Developmental Cell-States. Blood, 2018, 132, 18-18.	1.4	0
93	Molecular Signature of Megakaryocyte-Erythroid Progenitors Reveals Role of Cell Cycle in Fate Specification. Blood, 2018, 132, 3828-3828.	1.4	0
94	Autism-Associated Chromatin Remodeler CHD8 Governs the Survival and Differentiation of Hematopoietic Stem/Progenitor Cells. Blood, 2019, 134, 1191-1191.	1.4	0
95	The Molecular Basis of Long First Remissions in Normal Karyotype AML Patients. Blood, 2019, 134, 3827-3827.	1.4	0
96	Divisional Memory Drives Hematopoietic Stem Cell Functional Diversity. Blood, 2021, 138, 20-20.	1.4	0
97	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