

Nir Yosef

List of Publications by Year in descending order

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Version: 2024-02-01

105
papers

21,295
citations

31976

53
h-index

29157

104
g-index

152
all docs

152
docs citations

152
times ranked

30108
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping single-cell data to reference atlases by transfer learning. <i>Nature Biotechnology</i> , 2022, 40, 121-130.	17.5	236
2	Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages. <i>Genome Research</i> , 2022, 32, 242-257.	5.5	39
3	CXCR3 regulates stem and proliferative CD8+ T cells during chronic infection by promoting interactions with DCs in splenic bridging channels. <i>Cell Reports</i> , 2022, 38, 110266.	6.4	14
4	A Python library for probabilistic analysis of single-cell omics data. <i>Nature Biotechnology</i> , 2022, 40, 163-166.	17.5	216
5	Systems-based approaches to study immunometabolism. <i>Cellular and Molecular Immunology</i> , 2022, 19, 409-420.	10.5	25
6	Batf-mediated epigenetic control of effector CD8 ⁺ T cell differentiation. <i>Science Immunology</i> , 2022, 7, eabi4919.	11.9	19
7	Massively parallel reporter perturbation assays uncover temporal regulatory architecture during neural differentiation. <i>Nature Communications</i> , 2022, 13, 1504.	12.8	16
8	PeakVI: A deep generative model for single-cell chromatin accessibility analysis. <i>Cell Reports Methods</i> , 2022, 2, 100182.	2.9	34
9	Mucosal Vaccination with Cyclic Dinucleotide Adjuvants Induces Effective T Cell Homing and IL-17 ⁺ Dependent Protection against <i>Mycobacterium tuberculosis</i> Infection. <i>Journal of Immunology</i> , 2022, 208, 407-419.	0.8	5
10	DestVI identifies continuums of cell types in spatial transcriptomics data. <i>Nature Biotechnology</i> , 2022, 40, 1360-1369.	17.5	75
11	Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision. <i>Cell Reports Methods</i> , 2022, 2, 100200.	2.9	5
12	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. <i>Science</i> , 2022, 376, eabl4896.	12.6	289
13	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. <i>Cell</i> , 2022, 185, 1905-1923.e25.	28.9	108
14	Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197.	12.6	265
15	Ets21C sustains a pro-regenerative transcriptional program in blastema cells of <i>Drosophila</i> imaginal discs. <i>Current Biology</i> , 2022, 32, 3350-3364.e6.	3.9	17
16	CD4+ and CD8+ cytotoxic T lymphocytes may induce mesenchymal cell apoptosis in IgG4-related disease. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 368-382.	2.9	53
17	Neurological Manifestations of COVID-19 Feature T Cell Exhaustion and Dedifferentiated Monocytes in Cerebrospinal Fluid. <i>Immunity</i> , 2021, 54, 164-175.e6.	14.3	119
18	Joint probabilistic modeling of single-cell multi-omic data with totalVI. <i>Nature Methods</i> , 2021, 18, 272-282.	19.0	246

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19	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021, 371, .	12.6	166
20	Single-cell transcriptomics of the <i>Drosophila</i> wing disc reveals instructive epithelium-to-myoblast interactions. <i>ELife</i> , 2021, 10, .	6.0	39
21	T cell self-reactivity during thymic development dictates the timing of positive selection. <i>ELife</i> , 2021, 10, .	6.0	17
22	Hotspot identifies informative gene modules across modalities of single-cell genomics. <i>Cell Systems</i> , 2021, 12, 446-456.e9.	6.2	78
23	The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. <i>Cell</i> , 2021, 184, 3915-3935.e21.	28.9	133
24	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. <i>Cell</i> , 2021, 184, 4168-4185.e21.	28.9	203
25	Epitome: predicting epigenetic events in novel cell types with multi-cell deep ensemble learning. <i>Nucleic Acids Research</i> , 2021, 49, e110-e110.	14.5	1
26	Benchmarked approaches for reconstruction of <i>in vitro</i> cell lineages and <i>in silico</i> models of <i>C. elegans</i> and <i>M. musculus</i> developmental trees. <i>Cell Systems</i> , 2021, 12, 810-826.e4.	6.2	36
27	Polyamine metabolism is a central determinant of helper T cell lineage fidelity. <i>Cell</i> , 2021, 184, 4186-4202.e20.	28.9	121
28	Probabilistic harmonization and annotation of single-cell transcriptomics data with deep generative models. <i>Molecular Systems Biology</i> , 2021, 17, e9620.	7.2	211
29	Oleic acid restores suppressive defects in tissue-resident FOXP3 Tregs from patients with multiple sclerosis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	56
30	Self-guarding of MORC3 enables virulence factor-triggered immunity. <i>Nature</i> , 2021, 600, 138-142.	27.8	27
31	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5' and 3' gene regions. <i>Journal of Biological Chemistry</i> , 2020, 295, 11435-11454.	3.4	25
32	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. <i>Cell Reports</i> , 2020, 33, 108433.	6.4	54
33	T Follicular Regulatory Cell-Derived Fibrinogen-like Protein 2 Regulates Production of Autoantibodies and Induction of Systemic Autoimmunity. <i>Journal of Immunology</i> , 2020, 205, 3247-3262.	0.8	13
34	Evaluation of Davis et al.: Exploring Sequence of Determinants of Transcriptional Regulation The Case of c-AMP Response Element. <i>Cell Systems</i> , 2020, 11, 2-4.	6.2	0
35	Interpretable factor models of single-cell RNA-seq via variational autoencoders. <i>Bioinformatics</i> , 2020, 36, 3418-3421.	4.1	123
36	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. <i>Nature Protocols</i> , 2020, 15, 2387-2412.	12.0	65

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37	Integrated single cell analysis of blood and cerebrospinal fluid leukocytes in multiple sclerosis. Nature Communications, 2020, 11, 247.	12.8	242
38	Inference of single-cell phylogenies from lineage tracing data using Cassiopeia. Genome Biology, 2020, 21, 92.	8.8	61
39	Enhancing scientific discoveries in molecular biology with deep generative models. Molecular Systems Biology, 2020, 16, e9198.	7.2	44
40	Coverage-dependent bias creates the appearance of binary splicing in single cells. ELife, 2020, 9, .	6.0	35
41	Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. Cell Stem Cell, 2019, 25, 713-727.e10.	11.1	76
42	MPRAnalyze: statistical framework for massively parallel reporter assays. Genome Biology, 2019, 20, 183.	8.8	58
43	Functional interpretation of single cell similarity maps. Nature Communications, 2019, 10, 4376.	12.8	169
44	Meta-analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. Human Mutation, 2019, 40, 1299-1313.	2.5	15
45	Simulating multiple faceted variability in single cell RNA sequencing. Nature Communications, 2019, 10, 2611.	12.8	89
46	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. Human Mutation, 2019, 40, 1280-1291.	2.5	46
47	Connectivity problems on heterogeneous graphs. Algorithms for Molecular Biology, 2019, 14, 5.	1.2	3
48	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. Cell Systems, 2019, 8, 315-328.e8.	6.2	117
49	Molecular recording of mammalian embryogenesis. Nature, 2019, 570, 77-82.	27.8	257
50	Mango: Exploratory Data Analysis for Large-Scale Sequencing Datasets. Cell Systems, 2019, 9, 609-613.e3.	6.2	4
51	Reconstructing B-cell receptor sequences from short-read single-cell RNA sequencing with BRAPeS. Life Science Alliance, 2019, 2, e201900371.	2.8	9
52	Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. Cell Systems, 2018, 6, 381-394.e7.	6.2	19
53	Deep generative modeling for single-cell transcriptomics. Nature Methods, 2018, 15, 1053-1058.	19.0	1,227
54	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. BMC Genomics, 2018, 19, 477.	2.8	1,562

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55	A Reproducibility-Based Computational Framework Identifies an Inducible, Enhanced Antiviral State in Dendritic Cells from HIV-1 Elite Controllers. <i>Genome Biology</i> , 2018, 19, 10.	8.8	37
56	Impulse model-based differential expression analysis of time course sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, e119.	14.5	81
57	Computation Resources for Molecular Biology: Special Issue 2018. <i>Journal of Molecular Biology</i> , 2018, 430, 2181-2183.	4.2	0
58	ImpulseDE: detection of differentially expressed genes in time series data using impulse models. <i>Bioinformatics</i> , 2017, 33, 757-759.	4.1	38
59	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	2.5	39
60	Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. <i>Nature Immunology</i> , 2017, 18, 412-421.	14.5	103
61	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , 2017, 20, 817-830.e8.	11.1	164
62	Targeted reconstruction of T cell receptor sequence from single cell RNA-seq links CDR3 length to T cell differentiation state. <i>Nucleic Acids Research</i> , 2017, 45, e148-e148.	14.5	77
63	Use antibiotics in cell culture with caution: genome-wide identification of antibiotic-induced changes in gene expression and regulation. <i>Scientific Reports</i> , 2017, 7, 7533.	3.3	67
64	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , 2017, 21, 775-790.e9.	11.1	67
65	An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. <i>Cell Reports</i> , 2017, 19, 2853-2866.	6.4	26
66	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
67	A new way to build cell lineages. <i>ELife</i> , 2017, 6, .	6.0	2
68	Protein Sialylation Regulates a Gene Expression Signature that Promotes Breast Cancer Cell Pathogenicity. <i>ACS Chemical Biology</i> , 2016, 11, 2131-2139.	3.4	43
69	FastProject: a tool for low-dimensional analysis of single-cell RNA-Seq data. <i>BMC Bioinformatics</i> , 2016, 17, 315.	2.6	59
70	Protein C receptor (PROCR) is a negative regulator of Th17 pathogenicity. <i>Journal of Experimental Medicine</i> , 2016, 213, 2489-2501.	8.5	48
71	Writ large: Genomic dissection of the effect of cellular environment on immune response. <i>Science</i> , 2016, 354, 64-68.	12.6	46
72	Antiviral CD8+ T Cells Restricted by Human Leukocyte Antigen Class II Exist during Natural HIV Infection and Exhibit Clonal Expansion. <i>Immunity</i> , 2016, 45, 917-930.	14.3	59

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73	The epigenetic landscape of T cell exhaustion. <i>Science</i> , 2016, 354, 1165-1169.	12.6	694
74	Revealing the vectors of cellular identity with single-cell genomics. <i>Nature Biotechnology</i> , 2016, 34, 1145-1160.	17.5	534
75	Pluripotency Transcription Factor Oct4 Mediates Stepwise Nucleosome Demethylation and Depletion. <i>Molecular and Cellular Biology</i> , 2015, 35, 1014-1025.	2.3	47
76	MicroRNA-21 promotes Th17 differentiation and mediates experimental autoimmune encephalomyelitis. <i>Journal of Clinical Investigation</i> , 2015, 125, 1069-1080.	8.2	201
77	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1594-603.	7.1	65
78	Oct1 and OCA-B are selectively required for CD4 memory T cell function. <i>Journal of Experimental Medicine</i> , 2015, 212, 2115-2131.	8.5	50
79	CD5L/AIM Regulates Lipid Biosynthesis and Restrains Th17 Cell Pathogenicity. <i>Cell</i> , 2015, 163, 1413-1427.	28.9	313
80	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. <i>Cell</i> , 2015, 163, 1400-1412.	28.9	504
81	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. <i>Nature Immunology</i> , 2014, 15, 373-383.	14.5	289
82	Understanding Th17 cells through systematic genomic analyses. <i>Current Opinion in Immunology</i> , 2014, 28, 42-48.	5.5	18
83	Small-Molecule ROR γ t Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. <i>Immunity</i> , 2014, 40, 477-489.	14.3	253
84	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	27.8	872
85	Sodium chloride drives autoimmune disease by the induction of pathogenic TH17 cells. <i>Nature</i> , 2013, 496, 518-522.	27.8	1,136
86	Dynamic regulatory network controlling TH17 cell differentiation. <i>Nature</i> , 2013, 496, 461-468.	27.8	608
87	Induction of pathogenic TH17 cells by inducible salt-sensing kinase SGK1. <i>Nature</i> , 2013, 496, 513-517.	27.8	851
88	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013, 498, 236-240.	27.8	1,103
89	Metallothioneins negatively regulate IL-27-induced type 1 regulatory T-cell differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7802-7807.	7.1	48
90	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	9.7	375

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91	Induction and molecular signature of pathogenic TH17 cells. <i>Nature Immunology</i> , 2012, 13, 991-999.	14.5	980
92	Nanowire-Mediated Delivery Enables Functional Interrogation of Primary Immune Cells: Application to the Analysis of Chronic Lymphocytic Leukemia. <i>Nano Letters</i> , 2012, 12, 6498-6504.	9.1	154
93	Systematic identification of gene annotation errors in the widely used yeast mutation collections. <i>Nature Methods</i> , 2012, 9, 373-378.	19.0	78
94	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	28.9	843
95	Impulse Control: Temporal Dynamics in Gene Transcription. <i>Cell</i> , 2011, 144, 886-896.	28.9	227
96	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. <i>Cell</i> , 2011, 147, 1628-1639.	28.9	303
97	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. <i>Cell</i> , 2011, 147, 853-867.	28.9	177
98	ANAT: A Tool for Constructing and Analyzing Functional Protein Networks. <i>Science Signaling</i> , 2011, 4, pl1.	3.6	78
99	Network-Free Inference of Knockout Effects in Yeast. <i>PLoS Computational Biology</i> , 2010, 6, e1000635.	3.2	11
100	Transcriptional Regulation by CHIP/LDB Complexes. <i>PLoS Genetics</i> , 2010, 6, e1001063.	3.5	28
101	Prediction of Phenotype Information from Genotype Data. <i>Communications in Information and Systems</i> , 2010, 10, 99-114.	0.5	7
102	Toward accurate reconstruction of functional protein networks. <i>Molecular Systems Biology</i> , 2009, 5, 248.	7.2	90
103	A genome-wide screen for essential yeast genes that affect telomere length maintenance. <i>Nucleic Acids Research</i> , 2009, 37, 3840-3849.	14.5	83
104	A complex-centric view of protein network evolution. <i>Nucleic Acids Research</i> , 2009, 37, e88-e88.	14.5	24
105	Medical Sequencing at the Extremes of Human Body Mass. <i>American Journal of Human Genetics</i> , 2007, 80, 779-791.	6.2	199